

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: December 10, 2003, 16:24:59 ; Search time 3400 Seconds
(without alignments)
5342.316 Million cell updates/sec

Title: US-09-719-601-5
Perfect score: 2438
Sequence: 1 MCKGNQGEAEREVSVPY.....DIIRSLKSGKWLDAVLHK 444

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -CPWT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOFL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	99.5	2425	1335	6	AX253298 Sequence
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4	99.5	2425	3083	9	AK074933 Homo sapi
5	99.5	2425	3149	9	AF084559 Homo sapi
6	99.5	2425	4089	6	AX035941 Sequence
7	2190	89.8	1335	6	BD091695 Process f
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9	2189	89.8	1508	10	AF126798 Mus muscu
10	2186	89.7	1335	6	AX253297 Sequence
11	2111	86.6	1696	9	BC009011 Homo sapi
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14	2068.5	84.8	2825	9	AK074991 Homo sapi
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17	1935	79.4	2257	6	BD082655 Methods a
18	1935	79.4	2257	6	BD092934 Methods a
19	1703	69.9	2621	9	HSM800210 Homo sapi
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21	1668	68.4	1866	5	AF301910 Oncorhync
22	1668	68.4	2558	6	BD127815 Primer fo
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24	1662	68.2	1498	5	AB074149 Oncorhync
25	1653	67.8	1365	5	AF478472 Salmo sal
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28	1646	67.5	1843	6	BD082639 Methods a
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43	1516	62.2	4205	6	AX035941 Sequence
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45	1515	62.1	1928	6	AR264714 Sequence

ALIGNMENTS

RESULT 1

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LOCUS AX253298 1335 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 4 from Patent WO0170993.
ACCESSION AX253298
VERSION AX253298.1 GI:16073842
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Winther, M.D., Smith, H.L., Allen, S.J., Ponton, A. and de Antueno, R.J.
TITLE Polynucleotides that control delta-6 desaturase genes and methods
for identifying compounds for modulating delta-6 desaturase
JOURNAL Patent: WO 0170993-A 4 27-SEP-2001;
Scotia Holdings plc (GB)
FEATURES
Location/Qualifiers
1..1335
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 307 a 405 c 336 g 287 t
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Alignment Scores:
Pred. No.: 2,71e-224 Length: 1335
Score: 2425.00 Matches: 442
Percent Similarity: 99.55% Conservative: 0
Best Local Similarity: 99.55% Mismatches: 2
Query Match: 99.47% Indels: 0
DB: 6 Gaps: 0
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Db 61 TTCAGCTGGGGAGAGATTGAGAGCATTAACCTCGCCAGCCAGAGGGTGGTGGTCAATTGAC 120
QY 41 ArgLysValTyrAsnLeuThrIleThrIleGlnHisProGlyGlyGlnArgValIle 60
Db 121 CGCAAGGTTTACAAATACCAAAATGGTCCATCCAGACCCGGGGGGGGGGGGGGGGGGT 180
QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
Db 181 GGGCACTACGCTGGAGAGATGCAACGGATGCTTCCGGCGCTTCCACCCCTGACCTGGAA 240
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Db 301 CAGGACACCGCAGAGACTCAAGATCACTAGAGACTTTCGGGGCCCTGAGGAAGCGGT 360
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Db 541 GATTATGGCCACCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 600

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QY 281 TyrGlnIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
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QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
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QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
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QY 381 PheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
Db 1141 TTCAGATTGAGCACCACTCTTCCCCACCATCCCGGACCACTTACCAAGATCGCC 1200
QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db 1201 CCGCTGTGTAAGTCTTATGTGCCAAGCATGGCATTAATACAGGAGAGCGGCTACTG 1260
QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
Db 1261 AGGCCCTGCTGGACATCATCAGTCCCTGGAAGAAGTCTGGGAAGCTGTGGCTGGACGC 1320
QY 441 TyrLeuHisLys 444
Db 1321 TACCTTCAAAA 1332
RESULT 2
AF126799 3016 bp mRNA linear PRI 21-JUN-2000
LOCUS Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.
DEFINITION AF126799
ACCESSION AF126799.1 GI:4406527
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3016)
AUTHORS Cho, H.P., Nakamura, M.T. and Clarke, S.D.
TITLE Cloning, expression, and nutritional regulation of the mammalian
Delta-6 desaturase
JOURNAL J. Biol. Chem. 274 (1), 471-477 (1999)
MEDLINE 99085046
PUBMED 9867867
REFERENCE 2 (bases 1 to 3016)
AUTHORS Cho, H.P., Nakamura, M.T. and Clarke, S.D.

TITLE Direct Submission
JOURNAL Submitted (08-FEB-1999) Nutritional Sciences, University of Texas at Austin, Painter 5.30 (A2700), Austin, TX 78712, USA
FEATURES Location/Qualifiers
source 1. 3016
organism "Homo sapiens"
mol_type "mRNA"
db_xref "taxon:9606"
cds 14..1348
notes "D6D"
codon_start 1
product "delta-6 fatty acid desaturase"
protein_id "AAD20018.1"
translation "MSGKNGSGAEREVSPTFWEIEQKHLRTDRLVIDRKVY
NITKSLQHQSGRRVIGHYAGDADTFAPFDPDLFVGVKFLKPLLIAGLAEPSOD
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Alignment Scores:
Pred. No.: 8.15e-224 Length: 3016
Score: 2425.00 Matches: 442
Percent Similarity: 99.55% Conservative: 0
Best Local Similarity: 99.55% Mismatches: 2
Query Match: 99.47% Indels: 0
DB: 9 Gaps: 0
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QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
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QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysSerGlyLysLeuTrpLeuAspAla 440
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QY 441 TyrLeuHisLys 444
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LOCUS 3083 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127375
VERSION BD127375.1 GI:23222320
KEYWORDS JP 2002017375-A/2806.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3083)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and Koga, H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002017375-A 2806 22-JAN-2002;
COMMENT HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)

Thu Dec 11 15:18:15 2003

PN JP 2002017375-A/2806
 PD 22-JAN-2002
 PF 07-JUL-2000 JP 2000253172
 PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
 PI ISHII,
 PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
 SHINICHI KOJIMA,
 PI TETSUJI OTSUKI, HISASHI KOGA
 PC
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 Primer for synthesizing full-length cDNA and use thereof FH key
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Alignment Scores:
 Pred. No.: 8,396-224 Length: 3083
 Score: 2425.00 Matches: 442
 Percent Similarity: 99.55% Conservative: 0
 Best Local Similarity: 99.55% Mismatches: 2
 Query Match: 99.47% Indels: 0
 DB: 6 Gaps: 0

US-09-719-601-5 (1-444) x BD127375 (1-3083)

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 Db 271 GGGCACTACGCTGGAGAGATGCAACGATGCTTCCGCGCTTCCACCTGACCTGGAA 330
 QY 81 PheValGlyLysPheLeuLysProLeuLeuGlyGluLeuAlaProGluGluProSer 100
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 Db 391 CAGGACCAACGCGCAAGAACTCAAGATCACTTCCGAGGACTTCCGGGCGCTGAGGAGAGCGGT 450
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 QY 281 TyrGlnIleLeuMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
 Db 931 TACCAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCTGGCGCTC 990
 QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
 Db 991 AGCTACTACATCGGTTCTTCTACCTACATCCCTTCTACGGCATCTCTGGAGCCCTC 1050
 QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
 Db 1051 CTTTCTCTCAACTTCTCATAGGTTCTCTGGAGCCACTGGTTGTGTGGGTCAACAGATG 1110
 QY 341 AsnHisIleValMetGluLeuLeuAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
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 QY 361 ThrAlaThrCysAsnValGluGlnSerPheAsnAspTrpPheSerGlyHisLeuAsn 380
 Db 1171 ACAGCCACTCGCAACTGGAGCGAGCTCTTCTCAAGCACTGGTTCAGTGGACACCTTAAC 1230
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 Db 1231 TTCAGATTGAGCACCACCTCTTCCCGCCCATGTCGGCGGCACAACTTACAGAGATCGCC 1290
 QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
 Db 1291 CCGTGTGTGAAGTCTCTATGTGCCAGCATGGCATTAATACAGGAGAGCGCTACTG 1350
 QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
 Db 1351 AGGCGCCCTGTCGACATCATCAGTCCCTGAGAGAGTCTGGGAAGCTGTGGTGGACGCC 1410
 QY 441 TyrLeuHisLys 444
 Db 1411 TACCTTCACAAA 1422

RESULT 4
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 LOCUS AK074939 cDNA FLJ30458 fis, clone NT2RP3001738, weakly similar
 DEFINITION to CYTOCHROME B5.
 ACCESSION AK074939
 VERSION AK074939.1 Gi:22760711
 KEYWORDS oligo capping; his (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 ISOGAI,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
 Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
 Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
 Kojima,S., Nagahara,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
 Akesaka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
 Ninomiya,K.
 NEDO human cDNA sequencing project
 Unpublished

```

REFERENCE 2 (bases 1 to 3083)
AUTHORS Isegai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isegai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0912, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5' - & 3' - end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).

FEATURES             Location/Qualifiers
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                     /cvs="NT2"
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                     QHAKPNI FKPDVNMVRLVGLVEQPIEYKKLKYLPYHQHEVYFFLIGPLLIP
                     MYQYQILMTIMVHKWDLAWAVSYVIRFTIYIPYGLGALLFNFTPLFLESHWF
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BASE COUNT 615 a 937 c 884 g 647 t
ORIGIN
Alignment Scores:
Pred. No.:      8.39e-224      Length:      3083
Score:          2425.00        Matches:      442
Percent Similarity: 99.55%      Conservative: 0
Best Local Similarity: 99.55%      Mismatches: 2
Query Match:      99.47%      Indels:      0
DB:              9           Gaps:      0

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QY 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
DB 151 TTCAGCTGGGAGGAGATTCAAGACATPACCTGGCCAGCCAGCGTGGCTGGTTCATTGAC 210
QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
DB 211 CGCAAGGTTTCAACATCACCAATGTGTCCATCCAGCACCGCGGGGGCCAGCGGGTGCATC 270
QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
DB 271 GGGCACTACGCTGGAGAGATGCAACGATGCTTCCGGCGCTTCCACCTGACCTGGAA 330
QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100
DB 331 TTCGTGGGCAAGTCTTGAACCCCTGCTGATGTGGTAACTGGCGGCCGCGGAGGCCGACG 390
QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120

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RESULT 5
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LOCUS

AF084559 3149 bp mRNA linear PRI 12-OCT-2000

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141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160
511 ATGCCCTGGAGAGCATTCGATGTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 570
161 ThrIleLeuThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
571 ACCCTCATCAGCGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTT 630
181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200
631 GATTATGGCCACCTGTCTGTCTACAGAAACCCAGTGGACCACTTGTCCACAAATTC 690
201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
691 GTCATTTGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATCGCCACTTCAGCAC 750
221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
751 CAGGCCAAGCTTACATCTTCCACAGGATCCCATGATGACATGCTGCACGTGTTGTT 810
241 LeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLys 260
811 CTGGCGGAATGGCAGCCCTCGAGTACGGCAAGAAAGAGCTGAATACCTCCCTACAAAT 870
261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
871 CACCAGCAGCAATCTTCTTCTGATGGCGCGCGCTGCTCATCCCATGATATTTCCAG 930
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931 TACCAGATCATCATGACCATGATCGTCCATAAGAACTGGTGGAGCTGGCTGGCGCGCT 990
301 SerTyrTyrIleAspPheIleThrTyrIleProPheTyrGlyLysLysLysLysLysLys 320
991 AGCTACTACATCCGGTCTTCTATCACCCTACATCCCTTCTTACGGCATCTCTGGAGCCCTC 1050
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1291 CGCTGTGTGAATCTTATGTGCCAAGCATGGCATTTGAATACACAGAGAGAGCGGTACTG 1350
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441 TyrLeuHisLys 444
1411 TACCTTCAAAA 1422

Qy 421 ArgAlaLeuLeuAspTllelleArgSerLeuLysSerGlyLysLeuTrpLeuAspAla 440
 Db 1411 AGGCGCCCTGTGACATCATCAGTCCCTCCTGAAGAAGCTCTGGGAAGCTGTGGCTGGACGCC 1470
 Qy 441 TyrLeuHisLys 444
 Db 1471 TACCTTCACAAA 1482

RESULT 6
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 DEFINITION Sequence 2 from Patent EP1035207.
 ACCESSION AX035941
 VERSION AX035941.1 GI:11191483
 KEYWORDS unidentified
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE
 1
 Marquardt, A. and Weber, B.H.
 Cdna molecules of the members of gene family encoding human fatty
 acid desaturases and their use in diagnosis and therapy
 Patent: EP 1035207-A 2 13-SEP-2000;
 MULTIGENE BIOTECH GMBH (DE)

FEATURES
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 ORIGIN

Alignment Scores:
 Pred. No.: 1.23e-223 Length: 4089
 Score: 2425.00 Matches: 442
 Percent Similarity: 99.55% Conservative: 0
 Best Local Similarity: 99.55% Mismatches: 2
 Query Match: 99.47% Indels: 0
 DB: 6 Gaps: 0

US-09-719-601-5 (1-444) x AX035941 (1-4089)

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 Db 81 TTCAGCTGGGAGGAGATTTCAGAAAGCATAACTCGCCACCGACAGGTGGTGGTCAATTGAC 140
 Qy 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
 Db 141 CGCAAGGTTTCAACATCACCATAATGTTCCATCCAGCACCGGGGGCCGAGCGGTGATC 200
 Qy 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
 Db 201 GGGCACTACGCTGGAGAGATTCAGCGATGCTTCGGCGCTTCACCCCTGACCTGGAA 260
 Qy 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100
 Db 261 TTCGTGGGCAAGTTCTTGAACCCCTGCTGATTGGTGAACCTGGCCCGCGAGGAGCCCGAGC 320
 Qy 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
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 Qy 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
 Db 501 ACCCTCATCAGCGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 560
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 Qy 361 ThrAlaThrCysAsnValGluGlnSerPheAsnAspTrpPheSerGlyHisLeuAsn 380
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 ACCESSION BD091695
 VERSION BD091695.1 GI:22637306
 KEYWORDS WO 0175069-A/1.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

RESULT 9
AF126798
LOCUS
DEFINITION
ACCESSION
VERSION

VERSION AX253297.1 GI:16073841
 KEYWORDS Rattus sp.
 SOURCE Rattus sp.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE Winther, M.D., Smith, H.L., Allen, S.J., Ponton, A. and de Antueno, R.J. Polynucleotides that control delta-6-desaturase genes and methods for identifying compounds for modulating delta-6-desaturase Patent: WO 0170993-A 3 27-SEP-2001; Scotia Holdings plc (GB)
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 QY 41 ArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
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 QY 61 GlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
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 QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluProSer 100
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 Db 481 ACCGTCATCAGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 181 AspTrpGlyHisLeuSerValTrpArgLysProLysTrpAsnHisLeuValHisLysPhe 200
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Db 601 GTCAATGGCCACCTTAAAGGGTGCCTCCGCCAACTGGTGAACCATCGACATTTCCAGCAC 660
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 QY 441 TyrLeuHisLys 444
 Db 1321 TACCTCCACAAA 1332
 RESULT 11
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 LOCUS 1696 bp mRNA linear PRI 12-JUL-2001
 DEFINITION Homo sapiens, fatty acid desaturase 2, clone MGC:17124
 IMAGE:4181037, mRNA, complete cds.
 ACCESSION BC009011 GI:14290485
 VERSION BC009011.1
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1696)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.

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226	IlePheHisIysAspProAspValAsnMetLeuHLeValPheValLeuGlyLeuTrpGln	245			
619	ATCTTCACAGGATCCCGATGTGAACATGCTGCGACGTGTGTGTTCTGGCGAATGGCAG	678			
246	ProIleGluTyrGlyIysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyr	265			
679	CCATCGAGTACGGCAAGAAAGCTGAATACCTCCCTACAATCACGACACGAATAC	738			
266	PhePheLeuIleGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIleIleMet	285			
739	TTCTTCTGATGGCGCGCGCTGCTCATCCCATGTATTTCAGATACAGATCATCATG	798			
286	ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg	305			
799	ACCATGATGTCCTCAAGAACTGGGTGGACCTCGCCCTGGCGCGTCACTACATCCGG	858			
306	PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe	325			
859	TTCTTCATCACTATACCTCTTCACGGCATCTGGAGGCCCTCTTTCTCTCACTTC	918			
326	IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet	345			
919	ATCAGGTTCCTGGAGAGCACTGTGTTGTGTGGTCAACAGATGAATCACATCGTCATG	978			
346	GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn	365			
979	GGATTTGACAGGAGGCTACCGTGACTGGTTCAGTAGCCAGCTGACGCCACCTGCAAC	1038			
366	ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis	385			
1039	GTGGAGCAGTCTCTTCTCAACAGCTGTGTTCAGTGGACACCTTAACCTTCAGATTGAGCA	1099			
386	HisLeuPheProThrMetProArgHisAsnLeuHisIysIleAlaProLeuValIysSer	405			
1099	CACCTCTTCCCAACCATGCCCCCGGCACAACTTACACAGATCGCCCGCTGGTGAAGTCT	1159			
406	LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp	425			
1159	CTATGTGCCAAGCATGGCATTTGAATACACAGAGAAGCCGTACTAGGGGCCCTTGCTGAC	1219			
426	IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisIys	444			
1219	ATCATCAGTCTCCTGAAGAAGTCTGGGAAGTGTGGCTGGACGCTACCTTCACAA	1275			
RESULT 13	BD127406	2825 bp	DNA	linear	PAT 18-SEP-2000
LOCUS	BD127406				
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.				
ACCESSION	BD127406				
VERSION	BD127406.1	GI:23222351			
KEYWORDS	JP 2002017375-A/2837.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 2825) Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and Koga, H.				
TITLE	Primer for synthesizing full-length cDNA and use thereof				
JOURNAL	Patent: JP 2002017375-A 2837 22-JAN-2002;				
COMMENT	HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002017375-A/2837 PD 22-JAN-2002 PF 07-JUL-2000 JP 2000253172 PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO PI ISHII, PI YUKI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINTCHI KOIWA, PI TETSUJI OTSUKI, HISASHI KOGA				

PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12Q1/68, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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Pred. No.: 1,86e-189 Length: 2825
Score: 2068.50 Matches: 378
Percent Similarity: 98.44% Conservative: 0
Best Local Similarity: 98.44% Mismatches: 3
Query Match: 84.84% Indels: 3
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DB 127 CAGGACACGCGCAAGAACTCAAGATCACTGAGGACTTCCGCGCCCTGAGGAAGCGCT 186
QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuLeuLeuLeuLeu 140
DB 187 GAGGACATGAACCTGTTCAAGACCAACCACTGCTTCTTCTCTCTCTCTCTCTCTCTCTCT 246
QY 141 IleAlaLeuCluSerIleLeuAlaThrPheThrValPheThrPheGlyAsnGlyThrIlePro 160
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QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
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QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
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QY 261 HisGlnHisGluTrpPhePheLeuIleGlyProProLeuLeuIleProMetTyPheGln 280
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QY 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
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QY 301 SerTyTrpIleArgPhePheIleThrTyTrpIleProPheTrpGlyIleLeuGlyAlaLeu 320
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QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyArgAspTrpPheSerSerGlnLeu 360
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DEFINITION AK074991
ACCESSION AK074991
VERSION AK074991.1 GI:22760798
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S.,
Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,
Kojima, S., Nagahara, K., Masuko, Y., Ono, T., Okano, K., Yoshikawa, Y.,
Notsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2825)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@helix.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5' & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
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precursor cells after 2-weeks retinoic acid (RA)
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BASE COUNT 562 a 868 c 778 g 617 t
ORIGIN

Alignment Scores:
Pred. No.: 1,86e-189 Length: 2825
Score: 2068.50 Matches: 378
Percent Similarity: 98.44% Conservative: 0
Best Local Similarity: 98.44% Mismatches: 3
Query Match: 84.84% Indels: 3
DB: 9 Gaps: 1

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Qy 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100
Db 67 TTCGTGGGCAAGTCTTGAAACCCCTGCTGATGGTGAAGTGGCCCGGAGAGCCACG 126
Qy 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
Db 127 CAGGACACCGCAAGAACTCAAAGATCACTAGGACTTCGGGCCCTGAGGAAGACGGCT 186
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Db 187 GAGACATGACACCTGTTCAAGACCAACACGCTGTTCTTCCTCTCTCTCTCTCTCTCT 246
Qy 141 IleAlaLeuGluSerIleAlaIlePheThrValPheTyrPheGlyAsnGlyTyrIlePro 160
Db 247 ATGCGCCTGGAGACATTCATGATGTTCACTGTCTTTTACTTTGGCAATGGCTGGATCT 306
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Db 367 GATTATGCCACCTGTCTGTCTCAGAAACCCCAAGTGAACACACCTGTGTCCAAATTC 426
Qy 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
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Qy 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
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LOCUS AR221960 2257 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 8 from patent US 6428990.
ACCESSION AR221960
VERSION AR221960.1 GI:23329263
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2257)
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.
TITLE Human desaturase gene and uses thereof
JOURNAL Patent: US 6428990-A 8 06-AUG-2002;
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Best Local Similarity: 81.86% Mismatches: 44
Query Match: 79.37% Indels: 4
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Db 187 CACATCAACAAGCGCTTGTGAAGAAGTATATGAACCTCTCTCTCTCTCTCTCTCTCTCT 246
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Qy	195	HisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsn	214
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Db	667	ATGCTGCACGTGTTGTCTGGCGAATGGAGCCCATCGAGTACGGCAAGAAAGACTG	726
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Db	1207	CAGGAGAAGCCGCTACTAGGGGCCCTCTGCTGGACATCATCAGTCTCCCTGAAGAAGTCTGGG	1266
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poly-unsaturated fatty acids.			
BD082640			
VERSION			
KEYWORDS			
SOURCES			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN			
PATENT: JP 2001523091-A 20 20-NOV-2001;			
CAUGENE LLC, ABBOTT LABORATORIES			
PN JP 2001523091-A/20			
PD 20-NOV-2001			
PF 10-APR-1998 JP 1998544053			
PR 11-APR-1997 US 08/834655			
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI			
THURMOND,			
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD			
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Alignment Scores:			
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Percent Similarity: 88.84% Conservative: 30			
Best Local Similarity: 81.86% Mismatches: 44			
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DB: 6 Gaps: 2			
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Db	127	GGTCCCGGTTCATCAGCCATCAGCGGCGGAGGATGCCAGGATCCCTTTGTGGCTTC	186
Qy	76	HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla	95
Db	187	CACATCAACAAGGCGCTTGTGAAGAAGTATAGAACTCTCTCTGATTGAGAACTGTCT	246
Qy	96	ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla	115
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Qy	156	AsnGlyTyrPileProThrLeuIleThrAlaPheValIleu---	AlaThrSerGlnAlaGln	174
Db	427	ACGTCCTTTTGGCCCTTCTCCTCTGCGGGTCTGCTCAGTGCAGCTT	CAGCAGGCGCCAA	486
Qy	175	AlaGlyTyrLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn	194	
Db	487	GCTGGATGGCTGCACATGATTAATGGCCACCTGCTGTCTACAGAAAACCAAGTGGAC	546	
Qy	195	HisLeuValHisLysPheValIleGlyHisLeuLysGlyValaserAlaAsnTrpTrpAsn	214	
Db	547	CACCTTGTCACAAATTCGTCAATGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAAT	606	
Qy	215	HisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsn	234	
Db	607	CATCGCCACTTCAGACACACAGCCAGCCTAACATCTTCCACAGGATCCGATGTGAAC	666	
Qy	235	MetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeu	254	
Db	667	ATGCTGCACGTGTTTGTCTGGGCGAATGCGCCATCGAGTACGGCAAGAAGAAGCTG	726	
Qy	255	LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeu	274	
Db	727	AAATACCTGCCCTACAAATCACACAGCAGCAATCTTCTCTGATGGCGCGCGCTGCTC	786	
Qy	275	IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpVal	294	
Db	787	ATCCCCATGTATTTCCAGTACCAGATCATCATGACCATGATCGTCCATAGAAGACTGGTG	846	
Qy	295	AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr	314	
Db	847	GACCTGCCCTGGGCGCTCAGCTACTACATCGGTCTTTCATCATCCTACATCCCTTTCTAC	906	
Qy	315	GlyTyrLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe	334	
Db	907	GGCATCTCTGGAGGCCCTCTTTCTCTCACTTCATCAGGTCTCTGGAGAGCCACTGGTTT	966	
Qy	335	ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAsp	354	
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Qy	375	PheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHis	394	
Db	1087	TTCACTGGACACCTTAACTTCCAGATTGAGCACCATCTTCTCCCAACATGCCCCGCAC	1146	
Qy	395	AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr	414	
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Qy	415	GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGly	434	
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Db	1267	AAGCTGTGGCTGAGCGCCTACCTTCACAAA	1296	
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DEFINITION	BD082655	Methods and compositions for synthesis of long chain polyunsaturated fatty acids.		
ACCESSION	BD082655			
VERSION	BD082655.1	GI:22628265		
KEYWORDS	JP 2001523092-A/15.			
SOURCE	unidentified			
ORGANISM	unclassified.			
REFERENCE	1 (bases 1 to 2257)			
AUTHORS	Knutzen,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and			

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 Qy 255 LysTrpLeuProTrpAsnHisGlnHisGluTrpPhePheLeuIleGlyProProLeuLeu 274
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RESULT 18

BD092934
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 DEFINITION Methods and compositions for synthesis of long chain polyunsaturated fatty acids in plants.
 ACCESSION BD092934
 VERSION BD092934.1 GI:22638545
 KEYWORDS JP 2001527395-A/21.
 SOURCE synthetic construct
 ORGANISM artificial construct
 REFERENCE 1 (bases 1 to 2257)
 AUTHORS Knutson, D., Mukerji, P., Huang, Y. S., Thurmond, J., Chaudhary, S. and Leonard, A. E. Y.
 TITLE Methods and compositions for synthesis of long chain polyunsaturated fatty acids in plants
 JOURNAL Patent: JP 2001527395-A 21 25-DEC-2001;
 COMMENT CALGENE LLC, ARBOTT LABORATORIES
 PN JP 2001527395-A/21
 PD 25-DEC-2001
 PF 10-APR-1998 JP 1998544175
 PR 11-APR-1997 US 08/833610, 11-APR-1997 US 08/834033 PR

11-APR-1997 US 08/834655, 24-OCT-1997 US 08/956985 PI
 DEBORAH KNUTSON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
 THURMOND,
 PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
 PC
 C12N15/53 C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
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 CC Topology: Linear;
 PH Key Location/Qualifiers
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 Best Local Similarity: 81.86% Mismatches: 44
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US-09-719-601-5 (1-444) x BD092934 (1-2257)
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DEFINITION     partial cds.
ACCESSION      AL050118
VERSION        AL050118.1  GI:4884143
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 2621)
JOURNAL        Wambutt, R., Heubner, D., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
COMMENT        Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152
                Martinsried, GERMANY
                Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
                consortium of the German Genome Project.
                This clone (DKFZp586C201) is available at the RZPD in Berlin.
                Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
                information about the clone and the sequencing project is available
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Score:          1703.00      Matches:      305
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 DEFINITION
 ACCESSION AY055749
 VERSION AY055749.1 GI:23428437
 KEYWORDS
 SOURCE Sparus aurata (gilthead seabream)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
 Percoidae; Sparidae; Sparus.
 1 (bases 1 to 1745)
 Salliez,I.; Panserat,S., Kaushik,S. and Bergot,P.
 Cloning, tissue distribution and nutritional regulation of a delta
 6-desaturase-like enzyme in gilthead seabream
 Unpublished
 2 (bases 1 to 1745)
 Salliez,I., Panserat,S., Kaushik,S. and Bergot,P.
 Direct Submission
 Submitted (11-SEP-2001) Fish Nutrition Laboratory, INRA,
 St-Pee-sur-Nivelle 64310, France
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 DS: 5 Gaps: 2

US-09-719-601-5 (1-444) x AY055749 (1-1745)

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 QY 218 PheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHis 237
 Db 810 TTCCAGCATCAGCTTAACCAACATCTTCAGCAGGAGCCCTGATGTGTCATGTTGTCAC 869
 QY 238 ValPheValLeuGlyGluTyrGlnPheProIleGluTyrGlyLysLysLysLeuLysTyrLeu 257
 Db 870 ATCTTTGTGCTGGAGACACTCAGCCAGTCGAGTACCGCATTAAGAGATCAAAATATCTG 929
 QY 258 ProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProLeuLeuLeuLeuProMet 277
 Db 930 CCTATATCATCACCAGCACCACTACTTCTCTCTCTGCGAGCGCGCTCTCTCATTCACGATT 989

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Qy 278 TvrPheGlnTyrGlnIlelleMetThrMetIleValHisLysAsnTrpValAspLeuAla 297
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Qy 298 TrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeu 317
Db 1050 TGGTCTATGCTTACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1109
Qy 318 GlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVal 337
Db 1110 GGCTCAGTGGCGCTCATCAGCTTGTGAGGTTTGTGAGAGTCACATGTTTGTCTGGGTG 1169
Qy 338 ThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSer 357
Db 1170 ACTCAGATGATCATCTGCGATGAGCATCCAGCAGCAGAGCAGCATCAGTGGCTGACC 1229
Qy 358 SerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGly 377
Db 1230 ATGAGTTTACAGCCACTGCAATGAGAGTCCGCTTTCACAGCATGGTTTACAGCGA 1289
Qy 378 HisLeuAsnPheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHis 397
Db 1290 CACCTCACTTCAATTCGAGCAGCACTTGTTCCTACGATGCGCGCCACCACTACCAC 1349
Qy 398 LysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLys 417
Db 1350 CTGGTGGCCCGCTTGTCCAGCACTGTGTGAGAAATGCGATCCCTTACACAGTGAA 1409
Qy 418 ProLeuLeuArgAlaLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrp 437
Db 1410 ACAATGTGGCAGGCACTGTCAGCATATCAGGTATCAGTGAAGAACTCAGGGGACCTCTGG 1469
Qy 438 LeuAspAlaTyrLeuHisLys 444
Db 1470 CTGGATGCTATCTCCATAAA 1490

RESULT 21
AF301910 1866 bp mRNA linear VRT 10-AUG-2001
LOCUS Oncorhynchus mykiss putative delta 6-desaturase (FD6D) mRNA,
DEFINITION complete cds.
ACCESSION AF301910.1 GI:13447754
VERSION AF301910.1
KEYWORDS
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 1866)
Seilliez,I., Panerati,S., Kaushik,S. and Bergot,P.
Cloning, tissue distribution and nutritional regulation of a
delta-6-desaturase-like enzyme in rainbow trout
Comp. Biochem. Physiol., B 130, 83-93 (2001)
2 (bases 1 to 1866)
Seilliez,I., Panerati,S., Kaushik,S. and Bergot,P.
Direct Submission
Submitted (30-AUG-2000) Fish Nutrition Laboratory, INRA,
St-Pee-sur-Nivelle 64310, France
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Alignment Scores:
Pred. No.: 4,66e-151 Length: 1866
Score: 1668.00 Matches: 292
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Best Local Similarity: 66.82% Mismatches: 82
Query Match: 68.42% Indels: 1
DB: 5 Gaps: 0
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Qy 28 LysHisAsnLeuLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr 47
Db 215 AGCACTCCACAGAGGACGACAGTGGTTGGTTCATGNCAGAGAGGTCTATAATATACC 274
Qy 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67
Db 275 CAGTGGCGAAGACAGACACCCAGGGGGCATCAGGTCATCAGTCTTGTCTGGAGAGAT 334
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Qy 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187
Db 635 CTGGCCACATCTCAGTCCAGGCTGGCTGGCTGGAGCATGACTAGCCACCATCTGTCTG 694
Qy 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 695 TGCAGACATCCAGCTGGGAATCAGTACTGCAAGATTTGTCTATGGACACCTCAAGGCT 754
Qy 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
Db 755 GCGTCTGTCTAAGTGGTGAACCATCGTCACTTCTCCAGCACCAGCTPAGCCCAACCTGTT 814
Qy 228 HisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlyTrpGlnProIle 247
Db 815 AGTAAAGATCTGATGTCAACTCACTGCAATGCTTCTGCTCTGGAGAGAAAAACAGCTGTA 874
Qy 248 GluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 267
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Qy 268 LeuileGlyProProLeuLeuileProMetTyrPheGlnTyrGlnIleMetThrMet 287
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Qy 288 IleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePhe 307
Db 995 TTTTCACAGGAACTGGGTGGATCTGGGCGGATGACATTCATCTCTCTCTCTCTCT 1054
Qy 308 IleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArg 327
Db 1055 TGCTGTACTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1114
Qy 328 PheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIle 347
Db 1115 TTTTGGAAAGCCACCTGGTTGTATGGTGACCCAGATGATCACTCTCTATGGAGATA 1174
Qy 348 AspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGlu 367
Db 1175 GATCAGAGAGACACAGGAGCTGGCTCACCATGCACTGGAGTGGTACTTGCACATGAA 1234
Qy 368 GlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeu 387
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Qy 388 PheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCys 407
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Qy 428 ArgSerLeuLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 1415 GGGTCACTGAAGAAGTCAGGGGATCTGTGGCTGGATCGTATCTCCATAAA 1465

RESULT 22
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LOCUS
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127815
VERSION BD127815.1 GI:23222760
KEYWORDS JP 2002017375-A/3246
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
1 (bases 1 to 2558)
Patent: JP 2002017375-A 3246 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/3246
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT CDS Location/Qualifiers
source 1..2558

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Alignment Scores:

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Pred. No.: 7,148-151 Length: 2558
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Percent Similarity: 59.67% Conservatives: 1
Best Local Similarity: 99.93% Mismatches: 1
Query Match: 68.42% Indels: 0
DB: 6 Gaps: 0

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US-09-719-601-5 (1-444) x BD127815 (1-2558)

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Qy 166 PheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeu 185
Db 61 TTTGTCTTGTACCTCTCAGGCCCAAGCTGGATGGTGCACATGATTATGGCCACTG 120
Qy 186 SerValTyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeu 205
Db 121 TCTGTCTACAGAAACCCCAAGTGGAAACCACTTGTCCACAAATTCATCATTTGGCCACTTA 180
Qy 206 LysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsn 225
Db 181 AAGGTGCTCTGCCCACTGGTGGATCATGCCACITCCAGCACCCAGCCAGCCTAAC 240
Qy 226 IlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGln 245
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Qy 246 ProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyr 265
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LOCUS Homo sapiens cDNA FLJ90444 f1s, clone NT2RP3001159.
DEFINITION AK074925
ACCESSION AK074925
VERSION AK074925.1 GI:22760689
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Tsogai, T., Ota, T., Nishikawa, T., Hayashi, K., Sugano, S., Ishii, S.,
Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S.,
Kawai-Hiro, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,
Kojima, S., Nagahara, K., Masuno, Y., Ono, T., Okano, K., Yoshikawa, Y.,
Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2558)
AUTHORS Tsogai, T. and Otsuki, T.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction;
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5' - & 3' - end one pass
sequencing and clone selection; Helix Research Institute (supported
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Pred. No.: 7.14e-151 Length: 2558
Score: 1668.00 Matches: 297
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Query Match: 68.42% Indels: 0
DB: 9 Gaps: 0
US-09-719-601-5 (1-444) x AK074925 (1-2558)
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Qy 166 PheValIleuAlatrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeu 185
Db 61 TTGTGCTGTGTACTCTCAGGCCCAAGCTGGATGGCTGGCAACATGATTTGGCCACTG 120
Qy 186 SerValTyrAlaGlySProLystrpAsnHisLeuValHisLysPheValIleGlyHisLeu 205
Db 121 TCTGCTACAGAAACCCCAAGTGGAAACCACTTGTCCCAAAATTCATCATTTGGCCACTTA 180

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241 ATCTTCACCAAGGATCCGATGTAACATGCTGCACGTGTTTGTCTTGGCGGAATGGCAG 300
246 ProIleGluTyrGlyLysLysLysLeuLysLeuProTyrAsnHisGlnHisGluTyr 265
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266 PhePheLeulleGlyProProLeuLeulleProMetTyrPheGlnTyrGlnIleMet 285
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DEFINITION cds.
ACCESSION AB074149
VERSION AB074149.1 GI:16904664
KEYWORDS Oncorhynchus masou (cherry salmon)
SOURCE Oncorhynchus masou
ORGANISM Oncorhynchus masou
REFERENCE 1 Sirisuy, S., Yoshizaki, G., Kiron, V., Takeuchi, T. and Gen, K.
AUTHORS delta6-desaturase-like cDNA in masou salmon form2
TITLE Unpublished
JOURNAL 2 (bases 1 to 1498)
REFERENCE 1 Sirisuy, S., Yoshizaki, G., Kiron, V., Takeuchi, T. and Gen, K.
AUTHORS Direct Submission
TITLE Submitted (10-NOV-2001) Soranuth Sirisuy, Tokyo University of
JOURNAL Fisheries, Aquatic Bioscience, 4-5-7 Konan, Minato-ku, Tokyo
108-8477, Japan (E-mail: soranuth@yahoo.com, Tel:81-3-5463-0555,
Fax:81-3-5463-0553)
Location/Qualifiers
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DB: 5 Gaps: 1

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QY 12 aGluArgGluValSerValP-otrPhSerTrpGluGluLeuLeuGlnLysHisAsnLeuAr 32
DB 139 GGAGGGCGAGGTGGCAGTGCA-GTCTACACCTGGGAGAGGTCCAGAGGACTGCCACAG 197
QY 32 gThrAspSerGlyLeuValLeuAlaAspArgLysValTyRsnLleThrLysTrpSerLleGl 52
DB 198 AAGCGACCAAGGTGTTGGTCATCGACAGGAGGTCTATATATACCCAGTGGGGGAGAG 257
QY 52 nhisProGlyGlyGlnArgValLleGlyHisTyRAlaGlyGluAspAlaThrAspAlaPh 72
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QY 72 eaArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuLleGl 92
DB 318 TGTGCGATTCCATCCCGATTCTAATTTTGTGAGGAAGTTTCTGAAGCGGTGCTGATTGG 377
QY 92 yGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLysLleThrGluAs 112
DB 378 AGAGCTGGCACCACAGACCCCGACGAGGACCATCGGAAACGAGTACTGGGGCAGGA 437
QY 112 pPheArgAlaLeuArgLysTyRAlaGluAspMetAsnLeuPheLysThrAsnHisValPh 132
DB 438 CTTCCAGGCCCTCGCGGACCGGTGATAGAGGAGGCTCTCTCCGTGCCGCCCTCTCT 497
QY 132 ePheLeuLeuLeuLeuAlaHisLleAlaLeuGluSerLleAlaTTPPheThrValPh 152
DB 498 CTTACGCTCTACCTGGGCGCACATCTGTCTACTAGAGGCCCTGGCTTTGGGCTGCTCTG 557
QY 152 eTyRPhGlyAsnGlyTyRileProThrLeuLleThrAlaPheValLeuAlaThrSerGl 172
DB 558 GTCTGGGGGACCGAGCTGAGCGCTCACACTGTCTGTCTCTCTCTCTCTCTCTCTCTCA 617
QY 172 nAlaGlnAlaGlyTrpLeuGlnHisAspTyRgLyHisLeuSerValTyRArgLysProLy 192
DB 618 GTCCAGGCTGGTGGCTGCAGCATCAGTACCGCCACCTGTCTGAGTCTGCAAGAAATCTGG 677
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678 CTGAACCAACAACTGCACAGTTTGTCAATTGGACACCTAAAGGTGCCTCTGCTAACTG 737
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232 pValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProLleGluTyRgLyLysLy 252
798 TATCAACTCACTGATGCTTTCGCTCGGGAGACAAACAGCCTGTAGATATGTATATAA 857
252 sLysLeuLysTyRLeuProTyRAsnHisGlnHisGluTyRPhPheLeuLleGlyProPr 272
858 GAAGTGAAGTACATGCCCTACCATCACCAACACAGTACTTCTCTCATTTGACCTCC 917
272 cLeuLeuLleProMetTyRPhGlnTyRglnLleAlaMetThrMetLleValHisLysAs 292
918 ACTCATCGTTCAGAGTTTTCATCAATCCAGATATCCGGACCATGTTTTCACACACAGA 977
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312 oPheTyRgLyLleLeuGlyAlaLeuLeuPheLeuAsnPhelleArgPheLeuGluSerHi 332
1038 CTTCTTGTGTTTCTTGTGCTCAGTAGCATTGATCAGCTTCGTCAAGTTTGTGAAAGCCA 1097
332 sTrpPheValTrpValThrGlnMetAsnHisLleValMetGluLleAspGlnGluAlaTy 352
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1218 CGACTGTTTCAGTGCCACCTCACTTTCAGATTGACACCATCTGTTTCTTCTACCATGCC 1277
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RESULT 25
AF478472 1365 bp mRNA linear VRT 27-FEB-2002
LOCUS Salmo salar putative delta-6 fatty acyl desaturase (Fads6) mRNA,
DEFINITION complete cds.
ACCESSION AF478472
VERSION AF478472.1 GI:18959527
KEYWORDS Salmo salar (Atlantic salmon);
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
REFERENCE 1 (bases 1 to 1365)
AUTHORS Hastings, N. Jr., Agaba, M.K., Tocher, D.R. and Teale, A.J.
TITLE The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and
JOURNAL Freshwater Teleosts
REFERENCE 2 (bases 1 to 1365)
AUTHORS Hastings, N. Jr., Agaba, M.K., Tocher, D.R. and Teale, A.J.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2002) Institute of Aquaculture, Pathfoot
Building, Stirling FK9 4LA, Scotland

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	1..1365	/protein_id="AA182631.1"		251	LysLysLysLeuLysTrpLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
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CDS	1..1365	1		841	CCTCCACTAAATCGTTCAGTGTCTTTTCAACATCCAGATATTCGCGACCATGTTTTCACAA 900
	1..1365	2		291	LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
	1..1365	3		901	CGGACTGGGTGGATCTGGCGTGGTGCATGATGTTTCTACCTTCGCTTCTCTGCTGTAC 960
	1..1365	4		311	IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
	1..1365	5		961	TATCCCTCTTTGGTTCTTTTGGCTCAGTAGCATTTCAGTTCAGTTCAGTTCAGTTCAGT 1020
BASE COUNT		310 a 361 c 359 g 334 t 1 others			
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Alignment Scores:					
Pred. No.:	8.56e-150	Length:	1365		
Score:	1653.00	Matches:	288		
Percent Similarity:	78.63%	Conservative:	69		
Best Local Similarity:	63.44%	Mismatches:	87		
Query Match:	67.80%	Indels:	10		
DB:	5	Gaps:	2		
US-09-719-601-5 (1-444) x AF478472 (1-1365)					
Qy	1	MetGlyLysGlyGlyAsnGlnGlyGluGlyAla-----AlaGluArgGluValSerVal 18			
Db	1	ATGGGGGCGGAGCCAGCAGCAGGAGTCAAGCGGCGCGCCAGGGTGACGGGCTTGAG 60			
Qy	19	Pro-----ThrPheSerTrpGluGluIleGlnLysHisAsn 30			
Db	61	CCCGATGAGGCGAAGGTGGCAGTGCAGTCTACACCTGGGAAGAGGTCCAGAGGCACTCC 120			
Qy	31	LeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSer 50			
Db	121	CACAGAACACACAGTGGTGGTTCATCCAGGAGGCTCTATATATATACCGAGTGGCA 180			
Qy	51	IleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAsp 70			
Db	181	AAGAGACACCCGGGTGGCATCAGGTCATCAGTCACTTTGTGTGAGAAGATGCCACGGAA 240			
Qy	71	AlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeu 90			
Db	241	GCAITTTCCGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 300			
Qy	91	IleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThr 110			
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Qy	111	GluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHis 130			
Db	361	CAGGACTTCCAGGCTTCGTCGACCATGTGAGAGGAGGGGTCTCTCCGTCGCCGCTC 420			
Qy	131	ValPhePheLeuLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThr 150			
Db	421	CTGTCTTCAGCTCTACTGGCCACATCTGCTACTAGAGGCGCTGGCTTTGGGCGTG 480			
Qy	151	ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170			
Db	481	CTCTGGGTGGGGGACGAGCTGGAGCGCTCACACTGCTCTGCTCTCTCTCTCTCTCTCT 540			
Qy	171	SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190			

AF309556	1590 bp	mRNA	linear	VRT 05-DEC-2001
Danio rerio putative delta-6 fatty acyl desaturase (Fads6) mRNA,				
complete cds.				
AF309556				
AF309556.1	GI:10954034			
Danio rerio (zebrafish)				
Danio rerio				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Actinopterygii; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes; 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RESULT 26

AF309556

LOCUS

DEFINITION

complete cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AF309556 1590 bp mRNA linear VRT 05-DEC-2001
 Danio rerio putative delta-6 fatty acyl desaturase (Fads6) mRNA,
 complete cds.

AF309556 GI:10954034
 Danio rerio (zebrafish)

Danio rerio
 Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 1590)
 Hastings, N., Agaba, M., Tocher, D.R., Leaver, M.J., Dick, J.R.,
 Sargent, J.R. and Reale, A.J.

A vertebrate fatty acid desaturase with Delta 5 and Delta 6
 activities

Thu Dec 11 15:18:15 2003

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (25), 14304-14309 (2001)
PUBMED 11724940
REFERENCE 2 (bases 1 to 1590)
AUTHORS Hastings N., Agaba M.K., Tocher D.R., Teale A.J. and Sargent J.R.
TITLE Direct Submission
JOURNAL Submitted (28-Sep-2000) Genetics, Institute of Aquaculture,
Stirling FK9 4LA, Scotland
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BASE COUNT 416 a 390 c 408 g 376 t
ORIGIN

Alignment Scores:
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Best Local Similarity: 64.64% Mismatches: 94
Query Match: 67.51% Indels: 0
DB: 5 Gaps: 0

US-09-719-601-5 (1-444) x AF309556 (1-1590)

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QY 41 ArgGlyValThrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
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QY 61 GlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
Db 181 GGACATATCTGGAGAAGCGCCACCGAGGCGCTCACTGCGTTTCATCCAAACCTTCAG 240
QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100
Db 241 CTGTGTAGGAATATACCTGAGAGCGCTCTAATCGGAGAGCTGGAGCGTCTGNACCAT 300
QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
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QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
Db 361 GAGGCTGAAGGCTCTTTTAAACACCGCCGCTGTTTTCGCTCTGCAATTTGGGCCACAT 420
QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTrpPheGlyAsnGlyTrpIlePro 160
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QY 241 LeuGluGluTrpGlnProIleGluTrpGlyLysLysLysLeuLysTrpLeuProTrpAsn 260
721 GGGGAAACCTGACGCCCGTGGAGTATGGCGTTAAGAGATCAAGCATCTGCCCTACAAC 780
QY 261 HisGlnHisGluTrpPhePheLeuIleGlyProProLeuLeuIleProMetTrpPheGln 280
781 CATCAGCAAGTACTTCTTCTTCTGCTGCTCCCTGCTCATCCAGTGTATTTCAG 840
QY 281 TyrGlnIleLeuMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
841 TTCCAAATCTTCACAATATGATCAGTCATGCGATCGGTGGTGACCTGCTGTGGTGTATC 900
QY 301 SerTrpTrpIleArgPhePheIleThrTrpIleProPheTrpGlyLysLeuGlyAlaLeu 320
901 AGCTACTAGTCGATCTCTTCTTACACGCGATCTTACGCGCTCTTTTGGGCTATT 960
QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
961 ATCTCTTTAATTTCTGTCAGGTTTATGGAGGCCACTGTTGTTGTTGGTTCACAGATG 1020
QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTrpArgAspTrpPheSerSerGlnLeu 360
1021 AGCCACATCCCATGAACATGACTATGAGAAAAATCAGGACTGCTCAGCATGCAGCTG 1080
QY 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
1081 GTCGCGACCTGTAACTCGAGCAGTCTGCCCTTCAAGACTGTTTACGCGGACACCTCAAC 1140
QY 381 PheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
1141 TTCAGATCGGACATCATCTCTTCCACAGTCCCTCGGCACAACTACTGGCGCGCGCT 1200
QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTrpGlnGlyLysProLeuLeu 420
1201 CCACGGTGGAGCGTTGTGTGAGAAATACGGAGTCAATACCAAGAGAGACCTTGTAC 1260
QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysSerGlyLysLeuTrpLeuAspAla 440
1261 GGACATTTGGGATATCATTAGTCTTTGGAGAAATCTGGCAGATCTGGCTGGATGCG 1320
441 TyrLeuHisLys 444
1321 TATCTCAACAA 1332

RESULT 27
AR221959 1943 bp DNA linear PAT 26-SEP-2002
LOCUS Sequence 7 from patent US 6428990.
DEFINITION AR221959
ACCESSION AR221959
VERSION AR221959.1 GI:23329262
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1843)
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.

TITLE Human desaturase gene and uses thereof
JOURNAL Patent: US 6428990-A 7 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..1843

BASE COUNT 356 a 598 c 466 g 423 t
ORIGIN /organism="unknown"

Alignment Scores:

Pred. No.: 6,08e-149 Length: 1843
Score: 1646.00 Matches: 294
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.51% Indels: 0
DB: 6 Gaps: 0

US-09-719-601-5 (1-444) x AR221959 (1-1843)

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Qy 171 SerGlnAlaGlnAlaGlyTrrPleGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
Db 61 TCTCAGGCCCAAGCTGGTGGCTGCACATGATTATGGCCACCTGTCTGTACAGAAA 120
Qy 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
Db 121 CCCAAGTGGAGAACCACTTGTCCAAAATGCTATTGGCCACTTAAAGGGTGGCTCTGCC 180
Qy 211 AsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePheHisLysAsp 230
Db 181 AACTGGTGGATATCCCACTTCCAGACCAAGCTTACATCTTCCACAGGAT 240
Qy 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250
Db 241 CCCGATGTGAACATGCTGCAGCTGTTTGTCTGGCGAATGGCAGCCCATCGAGTAGCGC 300
Qy 251 LysLysLysLysLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
Db 301 AAGAAGAGCTGGAATACCTGCTCCCTTACATCACCAGCAGGAATCTTCTTCGATGGG 360
Qy 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
Db 361 CCGCGCTGCTCATCCCATGATATTTCCAGTACAGATCATCATGACCATGCTCCAT 420
Qy 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
Db 421 AAGAAGCTGGTGGACCTGGCTGGCGCTCAGCTACTACATCCGGTTCCTTCATCACCCTAC 480
Qy 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
Db 481 ATCCCTTTCTACGGCATCTCGGAGCCCTCTTTTCTCACTTCATCAGGTTCTCTGGAG 540
Qy 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
Db 541 AGCCACTGGTTGTGTGGGTCCACAGATGAATCACAATCGTCATGGAGATGACAGGAG 600
Qy 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
Db 601 GCCTTACCCTGACTGTTTCAGTAGCGCTGACAGCCACCTGCAACGTGGAGCAGTCTCTTC 660
Qy 371 PheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThr 390
Db 661 TTCACGACTGGTTTCAGTGGACACCTTAACCTCCAGATTGAGCACCACCTCTTCCCCACC 720
Qy 391 MetProArgHisAsnLeuHisIleValProLeuValLysSerLeuCysAlaLysHis 410
Db 721 ATGCCCCCGCCAACTTACACAGATCGCCCGCTGGTGGAACTCTCTATGGCCCAAGCAT 780
Qy 411 GlyIleGluTyrGlnGlySerProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430
Db 781 GGCATTGAATACACAGAGAGCCGCTACTGAGGCGCTGTGGACATCATCAGGTCCCTG 840

Qy 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 841 AAGAAGCTCTGGAGAGCTGTGGCTGACCGCTTACCTTACAAA 882

RESULT 28
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LOCUS

DEFINITION 1843 bp DNA linear PAT 27-AUG-2002
Methods and compositions for synthesis of long chain
poly-unsaturated fatty acids.

ACCESSION BD082639
VERSION BD082639.1 GI:22628249
KEYWORDS JP 2001523091-A/19.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 1843)

AUTHORS Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and
Leonard,A.E.Y.

TITLE Methods and compositions for synthesis of long chain

JOURNAL poly-unsaturated fatty acids

COMMENT Patent: JP 2001523091-A 19 20-NOV-2001;
CALGENE LLC,ABBOTT LABORATORIES

PN JP 2001523091-A/19

PD 20-NOV-2001

PF 10-APR-1998 JP 1998544053

PR 11-APR-1997 US 08/834655

PI DEBORAH KNUZON,PRADIP MUKERJI,YUNG SHENG HUANG,JENNIFER PI
THURMOND,

PI SUNITA CHAUDHARY,AMANDA EUN YEONG LOENARD

PC C12N15/53,C12N15/81,C12N5/02,C12N5/10,C12N1/19,C12P7/64 PC
.C1B1/00.A61K31/20,

PC A23L1/30

CC Strandedness: Single;

CC topology: Linear;

FH Key Location/Qualifiers.

source

1..1843

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

BASE COUNT 356 a 598 c 466 g 423 t

ORIGIN

Alignment Scores:

Pred. No.: 6,08e-149 Length: 1843
Score: 1646.00 Matches: 294
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.51% Indels: 0
DB: 6 Gaps: 0

US-09-719-601-5 (1-444) x BD082639 (1-1843)

Qy 151 ValPheTyrPheGlyAsnGlyTrrPleProThrLeuIleThrAlaPheValLeuAlaThr 170

Db 1 GTCTTTTACTTTGGCAATGGCTGGATTCTACCTCATCAGCGCTTTGTCTTGCTACC 60

Qy 171 SerGlnAlaGlnAlaGlyTrrPleGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190

Db 61 TCTCAGGCCCAAGCTGGATGGCTGCACATGATTATGGCCACCTGTCTGTCTACAGAAA 120

Qy 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210

Db 121 CCCAAGTGGAGAACCACTTGTCCAAAATGCTATTGGCCACTTAAAGGGTGGCTCTGCC 180

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Db 241 CCCGATGTGAACATGCTGCACGCTGTTTGTCTGGCGGAATGGCAGCCCATCGAGTAGCGC 300

QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuLeuGly 270
 Db 301 AAGAGAGAGTGAATACCTGCCCTACATCACACAGCAATACCTCTCTCTGATTGGG 360
 QY 271 ProProLeuLeuLeuProMetTyrPheGlnTyrGlnIleLeuMetThrMetIleValHis 290
 Db 361 CCGCGCTGCTCATCCCATGATTTCCAGTACCATCATCATGACCATGATCTGCTCAT 420
 QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheLeuTyr 310
 Db 421 AAGAACCTGGGTGGACCTGGCGCTGGCGCTGAGTACTATCATCGGTCTTTCATCACTAC 480
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 QY 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430
 Db 781 GGCATTGAATACAGAGAGAGCGCTACTGAGGGCCCTCTGCAATCATCAGGTCCCTG 840
 QY 431 LysLysSerGlyLysLeuTyrLeuAspAlaTyrLeuHisLys 444
 Db 841 AAGAGTCTGGAGCTGTGGTGGAGCGCTACCTTACAAA 882

RESULT 29
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 LOCUS 1843 bp DNA linear PAT 27-AUG-2002
 DEFINITION Methods and compositions for synthesis of long chain
 polyunsaturated fatty acids.
 ACCESSION BD082654
 VERSION BD082654.1 GI:22628264
 KEYWORDS JP 2001523092-A/14.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 1843)
 Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Leonard, A.E.Y.
 Methods and compositions for synthesis of long chain polyunsaturated fatty acids
 Patent: JP 2001523092-A 14 20-NOV-2001;
 CALGENE LLC ABBOTT LABORATORIES
 JOURNAL PN JP 2001523092-A/14
 COMMENT PD 20-NOV-2001
 PF 10-APR-1998 JP 1998544176
 PR 11-APR-1997 US 08/833610
 PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND,
 PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
 PC
 C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
 30, A23K1/00
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers.
 FEATURES Location/Qualifiers

source 1..1843
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
 BASE COUNT 356 a 598 c 466 g 423 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 6,08e-149 Length: 1843
 Score: 1646.00 Matches: 294
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 67.51% Indels: 0
 DB: 6 Gaps: 0
 US-09-719-601-5 (1-444) x BD082654 (1-1843)
 QY 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170
 Db 1 GTCCTTTTACTTTGGCAATGGCTGGATTCCTACCTCATCAGGGCTTTGCTCTGCTACC 60
 QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
 Db 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 120
 QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
 Db 121 CCCAAGTGAACACCTTGTCCACAAATTCGTATGGCCACTTAAAGGGTGGCTCTGCC 180
 QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePheHisLysAsp 230
 Db 181 AACTGGTGAATCATCGCCACTTCCAGCACCCAGCCCAAGCTTAACCTTCTCTGATTGGG 240
 QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250
 Db 241 CCGATGTGAACATGCTGCACGTGTTGTTCTGGGCGAATGCGACCATCGATACGGC 300
 QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
 Db 301 AAGAGAGCTGAATACCTGCCCTACAAATCACACAGCACGCAATACTTCTCTGATTGGG 360
 QY 271 ProProLeuLeuLeuProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
 Db 361 CCGCCCTCTCTCATCCCATGATTTCCAGTACCATCATCATGATCATGATCGTCCAT 420
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 Db 481 ATCCCTTTTCTACGGCATCTCTGGAGCCCTCTTTTCTCAACTTCATCAGGTTCCTGGAG 540
 QY 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
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 Db 601 GCCTACCGTGAATGCTTTCAGTACGAGTACAGCCCTGCAACCTGCAACCTGAGTCTTC 660
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 Db 661 TTCACAGCTGGTTCAGTGGACACCTTAATCTCCAGATTGAGCACCCACCTTCTCTCCACC 720
 QY 391 MetProArgHisAsnLeuHisIleAlaProLeuValLysSerLeuCysAlaLysHis 410
 Db 721 ATGCCCGGCACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 780
 QY 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430
 Db 781 GGCATTGAATACAGAGAGAGCGCTACTGAGGGCCCTCTGCAATCATCAGGTCCCTG 840

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QY 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 841 AAGAAGTCTGGAGAGCTGTGGCTGGAGCGCTACCTTCACAAA 882

RESULT 30
BD092933
LOCUS BD092933 1843 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids in plants.
ACCESSION BD092933
VERSION BD092933.1 GI:22638544
KEYWORDS JP 2001527395-A/20
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1843)
AUTHORS Knutzen,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and
Leonard,A.E.Y.
TITLE Methods and compositions for synthesis of long chain
polyunsaturated fatty acids in plants
JOURNAL Patent: JP 2001527395-A 20 25-DEC-2001;
CALGENE LLC,ABBOTT LABORATORIES
COMMENT PN JP 2001527395-A/20
PF 10-APR-1998 JP 1998544175
PR 11-APR-1997 US 08/833610,11-APR-1997 US 08/834033 PR
11-APR-1997 US 08/834655,24-OCT-1997 US 08/956985 PI
DEBORAH KNUTZEN, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
PC
C12N15/53, C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
30, A23K1/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 356 a 598 c 466 g 423 t
ORIGIN

Alignment Scores:
Pred. No.: 6.08e-149 Length: 1843
Score: 1646.00 Matches: 294
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.51% Indels: 0
DB: 6 Gaps: 0

US-09-719-601-5 (1-444) x BD092933 (1-1843)

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Db 1 GTCTTTTACTTTGGCAATGGCTGGATTCTCTACCTCATCAGCGCTTTGTCTGTCTACC 60

QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
Db 61 TCTCAGGCCCAAGCTGGATGGCTGCACATGATATATGSCCACTGTCTGTCTACAGAAA 120

QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
Db 121 CCCAAGTGAACACCTTGTCCACAAATTCGTCATTGGCCACTTAAAGGGTGCCTCTGCC 180

QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
Db 181 AACTGGTGAATCATCGGCACATTCAGCACCAACCGCAAGCTTAACTTCCCAAGGAT 240

QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250
Db 241 CCCGATGTGAACATGCTGCACCTGTTGTCTTCTGGCGAATGCGACCCCATCGAGTACGGC 300

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QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
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QY 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
Db 361 CCGCGCTGTCTCATCCCATGTATTTCCAGTACCATCATCATGACCATGATGCTGCAT 420

QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
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QY 311 IleProPheTyrGlyIleLeuGlyAlaIleLeuPheLeuAsnPheIleArgPheLeuGlu 330
Db 481 ATCCCTTTCTACGGCATCTCTGGAGCCCTCTCTTCTCACTTCATCAGATTCTCTGGAG 540

QY 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
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QY 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
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QY 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430
Db 781 GGCATTGAATACCAAGAGAGCGGCTACTGAGGGCCCTGCTGGACATCATCAGTCTCCTG 840

QY 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 841 AAGAAGTCTGGAGAGCTGTGGCTGGAGCGCTACCTTCACAAA 882

RESULT 31
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LOCUS Oncorhynchus masou FD6D mRNA for putative delata 6-desaturase,
DEFINITION complete cds.
ACCESSION AB070444
VERSION AB070444.1 GI:15281353
KEYWORDS Oncorhynchus masou (cherry salmon)
SOURCE Oncorhynchus masou
ORGANISM Oncorhynchus masou
REFERENCE 1 Yoshizaki,G., Ishikawa,A., Takeuchi,T. and Gen,K.
AUTHORS delata-6-desaturase-like cDNA in masou salmon
TITLE Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 1692)
AUTHORS Yoshizaki,G., Ishikawa,A., Takeuchi,T. and Gen,K.
TITLE Direct Submission
JOURNAL Submitted (21-AUG-2001) Goro Yoshizaki, Tokyo University of
Fisheries, 4-5-7 Kounan, Minato-ku 108-8477, Japan
[ E-mail:goro@tokyo-u-fish.ac.jp, Tel:81-3-5463-0558,
Fax:81-3-5463-0558 ]
Location/Qualifiers
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BASE COUNT 400 a 428 c 446 g 418 t
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Query Match: 67.35% Indels: 1
DB: 5 Gaps: 0

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DB 285 AGCACTGCCACAGAGGACGAGGTGGTGGTCATCGACAGAGAGGTCTATAATATACC 344
QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67
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QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
DB 405 GCCACGAGAGCATTTGTCGATCTCCATCTCGAACCGAATTTTGTTCAGGAAGTTTCTGAAG 464
QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
DB 465 CCGTTCGTCGATGGAGAGTGGCAGCAGAGAGCCAGCCAGGACGAGGAGGAGAAATGCA 524
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
DB 525 GTACTGGTCGAGCATTTCCAGGCCCTCGTGGCCGTGTGAGAGTGGAGGTCTCTCCGT 584
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleAlaLeuLeuSerIleAla 147
DB 585 GCCCGCCCCCTCTCTCTACCTCTACCTGGGCGACATCTCTGCTACTAGAGCCCTGGCT 644
QY 148 TrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
DB 645 TTGGGCTGCTCTGGGTCTGGGAGCCAGCTGAGGCTCACACTGCTCTGTTCCCTCAG 704
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187
DB 705 CTGGCCACGCTCTCAGGCCCGAGGTGGTGGCTGCTGAGCATGACTACGCCACCTCTCAGTC 764
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
DB 765 TGCAGAAATCTGGCTGGAGCCACCAATGCAAGTTTCTATTGGACACCTTAAGGGT 824
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
DB 825 GCCTCTGCTAACTGGTGAACCACTCGTCACCTTCCAGCACCCAGCAGTAAAGCGTGT 884
QY 228 HisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIle 247

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DB 885 AGTAAGATCCTGATATCAACTCACTCATGTCTTCTGCTGGGAGACAAACAGCCTGTA 944
QY 248 GluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 267
DB 945 GAGTATGATATTAAGAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1004
QY 268 LeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMet 287
DB 1005 CTCGTGGACCTCCACCTCATGCTCCAGTGTCTTCAACATCCAGATATTCGGGACCATG 1064
QY 288 IleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePhe 307
DB 1065 TTTTCAACAGAGAGTGGTGGATGCTGGCGGGGAGATGATCTTCTACCTTCGCTCTCTTC 1124
QY 308 IleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArg 327
DB 1125 TGCTGTACTATCCCTCTTCTGGTGTCTTGGCTCAGTAGCATTCATCAGCTTCGTGAG 1184
QY 328 PheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIle 347
DB 1185 TTTTGGAAAGCCACTGTTGTATGGGTGAGCCAGATGAGTGCACCTTCGATGAGAGATG 1244
QY 348 AspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGlu 367
DB 1245 GATCAGAGAGACACAGGAGTGGCTCACCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1304
QY 368 GlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeu 387
DB 1305 CAGTCAACCTTCAACGACTGGTTCAGTGGACACCTTCACTTCAGATTGAACACCATCTG 1364
QY 388 PheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCys 407
DB 1365 TTTTCTTACCATGCCCCGTCTAATCACTACCATGCTGGTAGTCTCTCTGCTGCTTGTGT 1424
QY 408 AlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIle 427
DB 1425 GAGAAACATGGAGTTCCTTACCAGGTCAAGACTTTCGAGAAAGGAGGAGTCTGATGTGTC 1484
QY 428 ArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
DB 1485 AGTCACTGAAGAAGTACGGGATCTGTGGTGGATCGCTATCTCCATAAA 1535

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RESULT 32
 BC049438 1708 bp mRNA linear VRT 01-APR-2003
 LOCUS
 DEFINITION
 Dario rerio, clone MGC:56438 IMAGE:5612204, mRNA, complete cds.
 ACCESSION
 BC049438.1 GI:29436932
 VERSION
 MGC.
 KEYWORDS
 MGC.
 SOURCE
 Dario rerio (zebrafish)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 REFERENCE
 1 (Bases 1 to 1708)
 Strausberg, R.
 Direct Submission
 Submitted (31-MAR-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapsb-remail.nih.gov
 Tissue Procurement: Dr. Sumio Sugano
 cDNA Library Preparation: Dr. Sumio Sugano
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

REMARK
COMMENT

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smaluis, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 104 Row: e Column: 4.

FEATURES
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QHAKEPIFKDDVDNMLAFVGVNQPVEYVKYKHLPHVQHKYFFIFGPPLLIP
VYFQPIFHNI SHGMWDLIMCI SYVRYFLCYTFQYGVFAIILLENFVRMESHW
VYWTOMRI PMNIDYEQNDLWLMQVATCNIRQSAFNDFWFSGLHNFQIEHILFPMP
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CDS
466 a 417 c 426 g 399 t
2.6e-148 Length: 1708
Pred. No.: 1639, 00 Matches: 287
Score: 1639, 00
Percent Similarity: 78.60% Conservatives: 62
Best Local Similarity: 64.64% Mismatches: 95
Query Match: 67.23% Indels: 0
DB: 5 Gaps: 0

US-09-719-601-5 (1-444) x BC049438 (1-1708)

Qy 1 MetGlyLysGlyGlyAsnGlnGlyAlaAlaGluArgGluValSerValProThr 20
Db 95 ATGGTGGCGGAGGACACACAGACAGCGAATCCACGACCAACGCGAGATTCCAGCAGC 154
Qy 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValLileAsp 40
Db 155 TACACCTGGGAGGAGATGACAGAAACACACACCAACATGAGATCAGTGGGTGGTGAG 214
Qy 41 ArgLysValTrpAsnLileThrLysTrpSerLileGlnHisProGlyGlyGlnArgValile 60
Db 215 AGGAGAGGTTTATAAGCTCAGCGAGTGGGTGAAGAGACACCCCGGAGGACTGAGATCCTC 274
Qy 61 GlyHisLysTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
Db 275 GGACACTATGCTGGAGAGAGAGCCACGAGGAGGCTTCACTGGCTTTCATCCAAACCTTCAG 334
Qy 81 PheValGlyLysPheLeuLysProLeuLileGlyGluLeuAlaProGluGluProSer 100
Db 335 CTGATGAGGAATACCTGAAGCGGCTGCTATCGGAGAGCTGGAGCGGCTCTGAACCCAGT 394

Qy 101 GlnAspHisGlyLysAsnSerLysLileThrGluAspPheArgAlaLeuArgLysThrAla 120
Db 395 CAGGACCGGACAGAAAACGCTCTCTCGTGGAGGATTTCCGAGCCCTCGGTGAGCGTCTG 454

Qy 121 GluAspMetAsnLeuPheLysThrAsnHisValPheLeuLeuLeuAlaHisLile 140
Db 455 GAGGCTGAGGCTGTTTAAACACGACGCGCTGTTTTCGCTCTGCTATTTGGGCCACATT 514

Qy 141 IleAlaLeuGluSerLileAlaTrpPheThrValPheTrpPheGlyAsnGlyTrpLilePro 160
Db 515 TGTCTCTCGGAGGACATCGCTTTCGATGCTGTGATTTCGGCACCGGTTGGATCAAC 574
Qy 161 ThrLeuLileThrAlaPheValLeuLysSerGlnAlaGlnAlaGlnAlaGlnLysTrpLeuGlnHis 180
Db 575 ACGTCACTCGTGGTGTATTCTGGCTACTGCACAGTCACAGCTGATGGTGGTGCAGCAT 634
Qy 181 AspTrpGlyHisLeuSerValTrpArgLysProLysTrpAsnHisLeuValHisLysPhe 200
Db 635 GACTTCGGTCACTCTGCTCGTGTATAAACCTCTGGAATGAATCAATTTGGTGACAAATTT 694
Qy 201 ValLileGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
Db 695 GTCACTCGGACACCTTGAGGGAGCGCTTCGGGGCTGGTGGACCATCGGCATCTCCAGCAT 754
Qy 221 HisAlaLysProAsnLilePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
Db 755 CACGCTAAACCAACATCTTCAAGAGAGGACCGGACGCTCAACATGCTGAACGCGCTTGTG 814
Qy 241 LeuGlyGluTrpGlnProLileGluTrpGlyLysLysLysLeuLysTrpLeuProTrpAsn 260
Db 815 GTGGGAAACGTCGACCGCGTGGAGTACGGCGTTAAGAGATCAAGCATCTGCCCTACAAC 874
Qy 261 HisGlnHisGluTrpPhePheLeuLileGlyProProLeuLileProMetTrpPheGln 280
Db 875 CATCAGCAACAGTACTTCTTCTTATGCTCTCCCTGCTCATCCAGTGTATTTCAG 934
Qy 281 TyrGlnLileMetThrMetLileValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
Db 935 TTCCAAATCTTCAATATGATCATGTCATGTCATGTCGGTGGACCTGCTGCTGTGATC 994
Qy 301 SerTrpTrpLileArgPhePheLileThrTrpLileProPheTrpGlyLileLeuGlyAlaLeu 320
Db 995 AGCTACTACGTCGATACTTCTTTGTTTACAGCGAGTCTACGGCGCTCTTTTGGGCTATT 1054
Qy 321 LeuPheLeuAsnPheLileArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
Db 1055 ATCTCTCTTTAAATTCGTCAGGTTTATGAGAGCCACTGCTGTTTGGGTTCACAGATG 1114
Qy 341 AsnHisLileValMetGluLileAspGlnGluAlaTrpArgAspTrpPheSerSerGlnLeu 360
Db 1115 AGCGCATCCCATGAACATGACTATGAGCAAAATCAGGACTGGCTCAGCATGCGAGCTG 1174
Qy 361 ThrAlaThrCysAsnValGluLinsPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
Db 1175 GTCGGACCTGTAACATCAGCAGTCTGCTTCAACGACTGGTTCAGCGGACCTCCTCAAC 1234
Qy 381 PheGlnLileGluHisLeuPheProThrMetProArgHisAsnLeuHisLysLileAla 400
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Qy 401 ProLeuValLysSerLeuCysAlaLysHisGlyLileGluTrpGlnGluLysProLeuLeu 420
Db 1295 CCACGGTGGTATGCTGTGTGAGAAATACGAGGTCAAATACCAAGAGAGAACCTTGTATC 1354
Qy 421 ArgAlaLeuLeuAspLileArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
Db 1355 GGAGCATTTGGGATATCATTAGGCTTTGGAGAAATCTGGCAGCTCTGGCTGGATGG 1414
Qy 441 TyrLeuHisLys 444
Db 1415 TATCTCAACAA 1426

RESULT 33

AF309557 1790 bp mRNA linear VMT 05-DEC-2001
LOCUS
DEFINITION
Cyprinus carpio putative delta-6 fatty acyl desaturase (Fads6d6)
mRNA, complete cds.
AF309557
AF309557.1 GI:10954036
KEYWORDS
Cyprinus carpio (common carp)

```

ORGANISM      Cyprinus carpio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE
1 (bases 1 to 1790)
AUTHORS      Hastings,N., Acaba,M., Tocher,D.R., Leaver,M.J., Dick,J.R.,
Sargent,J.R. and Teale,A.J.
TITLE        A vertebrate fatty acid desaturase with Delta 5 and Delta 6
activities
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 98 (25), 14304-14309 (2001)
PUBMED      11724940
REFERENCE
2 (bases 1 to 1790)
AUTHORS      Hastings,N., Acaba,M.K., Tocher,D.R., Teale,A.J. and Sargent,J.R.
TITLE        Direct Submission
JOURNAL      Submitted (28-SEP-2000) Genetics, Institute of Aquaculture,
Stirling FK9 4LA, Scotland
FEATURES
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/organism="Cyprinus carpio"
/mol_type="mRNA"
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BASE COUNT  466 a 410 c 458 g 456 t
ORIGIN
Alignment Scores:
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Score:          1599.00     Matches:     278
Percent Similarity: 78.15%   Conservative: 69
Best Local Similarity: 62.61%  Mismatches: 97
Query Match:     65.59%   Indels:      0
DB:              5       Gaps:         0
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QY 1 MetGlyLysGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20
DB 1 ATGGGTGGCGGAGGACACAGACGACCGGACCATCTGGGACCAACCGGAGGTTCGGCACT 60
QY 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
DB 61 TACACCTGGGAGAGGTTCGAGAACACACCAAGTTGGAGATCAGTGGATCGAGTTGAA 120
QY 41 ArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGlyGlnArgValIle 60
DB 121 AGGAAGGTTTATATGTGACCGAGTGGGTGAAGAGACACCCCGGAGGAGTGGAGTCTC 180
QY 61 GlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
DB 181 GGACACATATCTCGAGAAGATGCCACGGAGCGTTTACTGCATTTCATCCAGACCTTCG 240
QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluLuproSer 100
DB 241 CTGTGAGAAAATACATGAGCCGCTGTTAATCGGGGAGCTTGAGCGCTGGAACCCAGT 300
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RESULT 34
AB069727
LOCUS

AB069727 1576 bp mRNA linear VRT 11-AUG-2001

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QY	59	ValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp	78
Db	251	CTTATCGGCCACCAACGCGCTGAGGACGCGCAGGATGCCCTTCGTCGCTTCATCAAGAT	310
QY	79	LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGlu	98
Db	311	CTCAATTTTGTGCCAAGTTCTTACAGCCCTCTGTGATTGGAGACTGGCTCCGGAGAA	370
QY	99	ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys	118
Db	371	CCAGCCAGGATGACCCCTGAATCGGCAGCTGGTCGAGGACTTCGCGACCCCTGCACGAC	430
QY	119	ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla	138
Db	431	GCAGCCGAGGACATGAGCTGTTGATCGCAGTCCCACTTCTTGTCTTCTTACTGGGC	490
QY	139	HisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrp	158
Db	491	CACATCTCGGCATCGGAGGTGCTGGCTGGCTCTTATCTACCTCTCGGTCCTGGCTGG	550
QY	159	IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu	178
Db	551	GTGCCAGTGGCCGCGCTTCATCTGGCCATCTCTCAGGCTCAGTCTCTGGTGTCTG	610
QY	179	GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis	198
Db	611	CAGCATGACCTGGGCCATGCTCTCATCTTCAAGAAATCCTGGTGGAAACACGTCGCCACG	670
QY	199	LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe	218
Db	671	AGTTTCGTGAGGGCAGCTAAGGGCTCTTCGGCCACTGGTGGAACTTCGGCCACTTC	730
QY	219	GlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal	238
Db	731	CAGCACCAAGCCAGCCCACTTCCAAAGAACCCAGACGTACCGTGGCGCCGCTC	790
QY	239	PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuPro	258
Db	791	TTCTCTCTGGGGAG--TCATCGTCGAGTATGGCAAGAAAGACGACGACTACCTACC	847
QY	259	TyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyr	278
Db	848	TACAAACAGCAGCACCTGTACTTCTTCGTATCGCCCGCCGCTGCTCACCTGGTGAAAC	907
QY	279	PheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp	298
Db	908	TTTGAAGTGAATAATCGCGGTACATGCTGGTGTGTCATCAGTGGCGGAATTTGCTCTGG	967
QY	299	AlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGly	318
Db	968	GGCGGCAGCTTCTATGCGCGCTTCTTATCTTACTCCCTCTCAGGGGTCCTGGG	1027
QY	319	AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThr	338
Db	1028	GTGCTGCTCTTCTTTGTTGTTGTCGTGAGGCTGCTGCTGGTTCGTGGATCACA	1087
QY	339	GlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSer	358
Db	1088	CAGATGAACCACTATCCCAAGGAGATCGGCCACGAGAACCCGGGATCGGTGAGCTCT	1147
QY	359	GlnLeuThrAlaThrCysAsnValGluInSerPhePheAsnAspTrpPheSerGlyHis	378
Db	1148	CAGCTGGCAGCACCTGCACAGCTGGAGCCCTCACTTTCCACCACTGGTTCAGCGGCAC	1207
QY	379	LeuAsnPheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLys	398
Db	1208	CTCACTTCCAGATCGAGCACCACTTTTCCCGAGATGCCAGAACCACTACAGCGCG	1267
QY	399	IleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysPro	418
Db	1268	GTGGCCCGCTGGTCAAGTGGCTGTGTGCAACAGCGGCTCTCAGTACGATGAGCGCC	1327

QY 419 LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeu 438
Db 1328 TTCCTCACCGCGCTGTGGACATGTCAGGTCCCTGAAGAAGTCTGGTGCATCTGGCTG 1387

QY 439 AspAlaTyrLeuHisLys 444
Db 1388 GACGCTACCTCCATCAG 1405

RESULT 36
AR264713
LOCUS AR264713 1717 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 2 from patent US 6492108.
ACCESSION AR264713
VERSION AR264713.1 GI:29693075
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1717)
AUTHORS Hillman,J.L., Guegler,K.J., Corley,N.C. and Shah,P.
TITLE Delta-6 desaturase homologs
JOURNAL Patent: US 6492108-A 2 10-DEC-2002;
FEATURES Location/Qualifiers
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source /organism="unknown"
BASE COUNT 330 a 563 c 482 g 342 t
ORIGIN

Alignment Scores:
Pred. No.: 9,82e-141 Length: 1717
Score: 1580.50 Matches: 278
Percent Similarity: 76.23% Conservative: 62
Best Local Similarity: 62.33% Mismatches: 103
Query Match: 64.01% Indels: 3
DB: 6 Gaps: 2

US-09-719-601-5 (1-444) x AR264713 (1-1717)

QY 1 MetGlyLysGlyLysAenGlnGly-----GluGlyAlaAlaGluArgGluValSerVal 18
Db 75 ATGGCGCGCTGCGGGAGCGCGGACCGCGGAGGAGCGCGGAGCGCGGAGCGCGGCGCTG 134

QY 19 ProThrPheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuVal 38
Db 135 CCCACCTTCGCTGGGAGCGAGATCCGCGCGCACGACCGCGCGCGCGCGCGCGCGCTG 194

QY 39 IleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArg 58
Db 195 ATCAGCGCGCGCTACGACATCAGCGCGCTGGGCGCACGCGCGCGCGCGCGCGCGCG 254

QY 59 ValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78
Db 255 CTATCGCGCCACCGCGCGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 314

QY 79 LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGlu 98
Db 315 CTCAATTTTGTGCGCAAGTCTCTACAGCGCGCTGTGATGGAGAGCTGGCTCGCGAAGA 374

QY 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118
Db 375 CCCAGCGAGGATGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 434

QY 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla 138
Db 435 GCAGCGGAGGACATGACCTTTTCATGCCAGTCCCGCGCGCGCGCGCGCGCGCGCG 494

QY 139 HisIleLeuAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrp 158
Db 495 CACATCTCTGGCGATGAGGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 554

QY 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178
Db 1599 CACATCTCTGGCGATGAGGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1788

Db 555 GTCCCGAGTCCCTGGCGCGCTTCATCTCGGCGCATCTCTCAGGCTCAGTCTGGTCTG 614

QY 179 GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis 198
Db 615 CAGCATGACCTGGCGCATGCTCTCATCTTCAAGAAGTCTGTGGTGAACACACGCTGGCCAG 674

QY 199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218
Db 675 AAGTTCGTGATGGCGCAGCTAAAGGGCTTCTCGCGCCACTGGTGGAACTTCCGCCCATTC 734

QY 219 GlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238
Db 735 CAGCACCGACCGACCGACCATCTTCCACAAAGACCCACACGCTGACGGTGGCGCGCTC 794

QY 239 PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuPro 258
Db 795 TTCCTCTCTGGCGGAG--TCATCCGTCAGTATGGCAAGAAACGACGACCTACCTACCC 851

QY 259 TyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyr 278
Db 852 TACAAACGACGACCGACCTGTACTTCTCTGATCGGCGCGCGCTGCTCACCTCGGTGAC 911

QY 279 PheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298
Db 912 TTTCAAGTGGAAATCTGGCGTACATGCTGTGTGTCATGAGTGGCGGAGTTTCTCTCG 971

QY 299 AlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGly 318
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DEFINITION Sequence 3 from Patent EP1035207.
ACCESSION AX035942
VERSION AX035942.1 GI:11191484
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Marquardt,A. and Weber,B.H.
TITLE Cdna molecules of the members of gene family encoding human fatty acid desaturases and their use in diagnosis and therapy
JOURNAL Patent: EP 1035207-A 3 13-SEP-2000;

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DEFINITION	Homo sapiens fatty acid desaturase 3 (FADS3)				mRNA, complete cds.	
ACCESSION	AF084560					
VERSION	AF084560.1			GI:10798852		
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
TITLE	1 (bases 1 to 1757)					
JOURNAL	Marquardt,A., Stohr,H., White,K. and Weber,B.H.					
MEDLINE	cDNA cloning, genomic structure, and chromosomal localization of					
PUBMED	three members of the human fatty acid desaturase family					
REFERENCE	Genomics 66 (2), 175-183 (2000)					
AUTHORS	20138619					
TITLE	10860662					
JOURNAL	2 (bases 1 to 1757)					
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USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>

REMARK
COMMENT
NIH-MGC Project URL: <http://www.genome.gov/27532811>
Contact: MGC help desk

Contact: WCC help desk
Email: c9apbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLUM)
CDNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
Contact: amadan@systemsbio.org
Greene, Mark Ketterman and Anuradha Madan
Stephanie For

Clones distribution: WGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLT at: <http://image.llnl.gov>
Series: IRAL Plate: 11 Row: B Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4858345.

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BASE COUNT

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DEFINITION Mus musculus brain cDNA, clone MNCB-0629, similar to Homo sapiens
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ACCESSION  AB041560
VERSION     1
KEYWORDS    fis (full insert sequence).
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (sites)
AUTHORS     Osada,N., Kusuda,J., Tanuma,R., Ito,A., Hirata,M., Sugano,S. and
            Hashimoto,K.
TITLE       isolation of full-length cDNA clones from mouse brain cDNA library
            made by oligo-capping method
            Unpublished
JOURNAL     2 (bases 1 to 1818)
REFERENCE   Hashimoto,K., Osada,N., Kusuda,J. and Sugano,S.
AUTHORS     Direct Submission
TITLE       Submitted (12-APR-2000) Katsuyuki Hashimoto, National Institute of
            Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
            1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            (E-mail: khashienh.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
            Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181)
            URL: http://www.nih.go.jp/yoken/genebank/
LIB NAME    Sugano mouse brain mncb
LAB HOST    TOPI0
VECTOR      pME18S-FL3
            1st strand cDNA was primed with an oligo(dT) primer
            [ATGTCGCTTTTATTTTATTTT]; double-stranded cDNA was synthesized
            using specific 5' and 3' primers and amplified by PCR. The PCR
            product was digested with SfiI and size selection was performed to
            exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
            into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
            the DraIII sites can be used to isolate the cDNA insert. Library
            was constructed by Sugano et al. (University of Tokyo, Institute of
            Medical Science). Custom primer used for sequencing (5' end primer
            [CTTCTGCTCTAAAGCTGCG]; 3' end primer
            [CGACTCGCTGAGCACA]).
FEATURES   A part of this sequence is reported in AU035600.
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BASE COUNT 390 a 535 c 498 g 395 t
ORIGIN
Alignment Scores:
Pred. No.: 7,83e-140 Length: 1818
Score: 1551.50 Matches: 277
Percent Similarity: 75.11% Conservative: 61

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Best Local Similarity: 61.56% Mismatches: 105
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Search completed: December 10, 2003, 19:33:44
Job time : 3474 secs

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; Sequence 7, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; PENDING FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
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US-09-439-261-7

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy 2430 CAGCCAACTCCCTGGCCATTTGGCCCGGAGGAGCTGGGCCCTG 2473
Db 1801 CAGCCAACTCCCTGGCCATTTGGCCCGGAGGAGCTGGGCCCTG 1843

RESULT 4
US-09-227-613-7
; Sequence 7, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.PI
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-7

Query Match 57.5%; Score 1830.4; DB 4; Length 1843;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 630 GTCTTCTACTTGGCAATGGCTGGATTCCTACCTCATACGCGCTTTGTCTTGTAC 689
Db 1 GTCTTTTACTTTGGCAATGGCTGGATTCCTACCTCATACGCGCTTTGTCTTGTAC 60
Qy 690 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAGAAA 749
Db 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAGAAA 120
Qy 750 CCCAAGTGGAAACCACTTGTCCAAATTCGTATTTGGCCCACTTAAAGGGTGTCTTGGC 809
Db 121 CCCAAGTGGAAACCACTTGTCCAAATTCGTATTTGGCCCACTTAAAGGGTGTCTTGGC 180
Qy 810 AACTGGTGGATCATCGCCATTCAGCACACCCAGGCTTAACATCTTCCCAAGGAT 869
Db 181 AACTGGTGGATCATCGCCATTCAGCACACCCAGGCTTAACATCTTCCCAAGGAT 240

Qy 870 CCCGATGTGAACATGCTGACGTTGTTTCTGGGCGAATGGAGCCCATCGATGACGC 929
Db 241 CCCGATGTGAACATGCTGACGTTGTTTCTGGGCGAATGGAGCCCATCGATGACGC 300
Qy 930 AAGAAGAGCTGAATACCTGCGCTACAAATCACAGCAGAAATACCTTCTTCTGATGGG 989
Db 301 AAGAAGAGCTGAATACCTGCGCTACAAATCACAGCAGAAATACCTTCTTCTGATGGG 360
Qy 990 CCGCGCTGTCTATCCCATGTATTTCCAGTACAGATCATCATGACCATGATCGTCCAT 1049
Db 361 CCGCGCTGTCTATCCCATGTATTTCCAGTACAGATCATCATGACCATGATCGTCCAT 420
Qy 1050 AAGAACTGGGTGACCTGGCGCTGCGCTACTACTACCTCGGTCTTCTCATCACTAC 1109
Db 421 AAGAACTGGGTGACCTGGCGCTGCGCTACTACTACCTCGGTCTTCTCATCACTAC 480
Qy 1110 ATCCCTTTTACCGCATCTCTGGAGCGCTCTTTTCTTCTTCTTCTTCTTCTTCTTCT 1169
Db 481 ATCCCTTTTACCGCATCTCTGGAGCGCTCTTTTCTTCTTCTTCTTCTTCTTCTTCT 540
Qy 1170 AGCACTGGTTTCTGTGGGTACACAGATGAATACATCTCATGAGATGACACAGGAG 1229
Db 541 AGCACTGGTTTCTGTGGGTACACAGATGAATACATCTCATGAGATGACACAGGAG 600
Qy 1230 GCCTACCGTGACTGGTTTCACTAGCCAGCTGACAGCACTCTGCAAGCTGGAGAGTCTTC 1289
Db 601 GCCTACCGTGACTGGTTTCACTAGCCAGCTGACAGCACTCTGCAAGCTGGAGAGTCTTC 660
Qy 1290 TTCAACGACTGGTTTCACTAGTGAACCTTAACTTCCAGATGAGCACCACTCTTCCCCACC 1349
Db 661 TTCAACGACTGGTTTCACTAGTGAACCTTAACTTCCAGATGAGCACCACTCTTCCCCACC 720
Qy 1350 ATGCCCCGGCACAACTTACAAAGATCGCCCCCTGTGTGAAGTCTCTATGTGCAAGCAT 1409
Db 721 ATGCCCCGGCACAACTTACAAAGATCGCCCCCTGTGTGAAGTCTCTATGTGCAAGCAT 780
Qy 1410 GGAATTGAATACAGAGAGAGCCGCTACTGAGGCGCTGCTGGACATCATCAGTCTCCCTG 1469
Db 781 GGCATTGAATACAGAGAGAGCCGCTACTGAGGCGCTGCTGGACATCATCAGTCTCCCTG 840
Qy 1470 AAGAAGTCTGGGAAGCTGTGTGTGAGCGCTTACCTTCAAAATGAAGCCACAGCCCCGG 1529
Db 841 AAGAAGTCTGGGAAGCTGTGTGTGAGCGCTTACCTTCAAAATGAAGCCACAGCCCCGG 900
Qy 1530 GACACCGTGGGAAGGGGTGAGTGGGTGATGCGCCAGAGGATGATGGCTTTTCTTC 1589
Db 901 GACACCGTGGGAAGGGGTGAGTGGGTGATGCGCCAGAGGATGATGGCTTTTCTTC 960
Qy 1590 TGAGGGGTGTCGAGAGAGCTGTGTATGCACTGCTCACGAGCCCATGTTGGATCTTCT 1649
Db 961 TGAGGGGTGTCGAGAGAGCTGTGTATGCACTGCTCACGAGCCCATGTTGGATCTTCT 1020
Qy 1650 CCGTTTCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1709
Db 1021 CCGTTTCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
Qy 1710 CTGCGCTCCCTCAGCCGTCAGCCATCAGCCATGCGCTTCCAGTGCCTTCTTCTTCTTCT 1769
Db 1081 CTGCGCTCCCTCAGCCGTCAGCCATCAGCCATGCGCTTCCAGTGCCTTCTTCTTCTTCT 1140
Qy 1770 TTCCAAGAGCAGAGAGTGGCCACCGGGGTGGTCTGTCTTCTTCTTCTTCTTCTTCT 1829
Db 1141 TTCCAAGAGCAGAGAGTGGCCACCGGGGTGGTCTGTCTTCTTCTTCTTCTTCTTCT 1200
Qy 1830 CTAAAGATGGGAGAGAGCCAGCGGTCCATGGGTCTGGGCTGTGAGTCTTCTTCTTCT 1889
Db 1201 CTAAAGATGGGAGAGAGCCAGCGGTCCATGGGTCTGGGCTGTGAGTCTTCTTCTTCT 1260
Qy 1890 TGCTCACTAGGCATCACCCCCCTTTTGGTTCTTCAAGTGTCTTCTTCTTCTTCTTCT 1949
Db 1261 TGCTCACTAGGCATCACCCCCCTTTTGGTTCTTCAAGTGTCTTCTTCTTCTTCTTCT 1320
Qy 1950 GGTCTCTAGTCGGGAGGAGCCCTTGACCTCCCGGCTTCTTCTTCTTCTTCTTCTTCT 2009

Db 1321 GGTCTTAGTGGGAGGGCCCTGACCTCCGGCTGGGTTTCACTCTCCCTGACGGCTG 1380
Qy 2010 CCATTGTCCACCCCTTTATAGAGAGCCCTGCTTTGTTTAAAGAGTGGGTCTCCCTCCT 2069
Db 1381 CCATTGTCCACCCCTTTATAGAGAGCCCTGCTTTGTTTAAAGAGTGGGTCTCCCTCCT 1440
Qy 2070 GCAGCTGGTTAAGTACCCGAGGCTCTCTTAAGATGTCAGAGGCCCCAGGCCCGGGG 2129
Db 1441 GCAGCTGGTTAAGTACCCGAGGCTCTCTTAAGATGTCAGAGGCCCCAGGCCCGGGG 1500
Qy 2130 ACAGCCAGCCCAACCTTTGGGCCCTGGAAGAGTCTCCACCCCATCACTAGAGTGTCTG 2189
Db 1501 ACAGCCAGCCCAACCTTTGGGCCCTGGAAGAGTCTCCACCCCATCACTAGAGTGTCTG 1560
Qy 2190 ACCCTGGGCTTACAGGGCCCTTCCAGCCCTCCCACTTGAAGCTGTGACCTTGG 2249
Db 1561 ACCCTGGGCTTACAGGGCCCTTCCAGCCCTCCCACTTGAAGCTGTGACCTTGG 1520
Qy 2250 ACCAAAGGGGAGTCCCTGCTCTTGTGACTCAGCAGAGGCAAGTGGCCAGTTCAAGGA 2309
Db 1621 ACCAAAGGGGAGTCCCTGCTCTTGTGACTCAGCAGAGGCAAGTGGCCAGTTCAAGGA 1680
Qy 2310 GGGGCGGCTGGCTGAGGCTCAGCCACCTCCAGCTTTTCTCAGGCTGCTCAGG 2369
Db 1681 GGGGCGGCTGGCTGAGGCTCAGCCACCTCCAGCTTTTCTCAGGCTGCTCAGG 1740
Qy 2370 TCCAAAGATTCTGAGCAATCTGACCTTCTCCAAAGGCTCTGTTATCAGCTGGGCAATGC 2429
Db 1741 TCCAAAGATTCTGAGCAATCTGACCTTCTCCAAAGGCTCTGTTATCAGCTGGGCAATGC 1800
Qy 2430 CAGCAATCCCTGGCAATTTGGCCCGCAGGGGAGCTGGGCCCTG 2473
Db 1801 CAGCAATCCCTGGCAATTTGGCCCGCAGGGGAGCTGGGCCCTG 1843

RESULT 5

US-09-439-261-6
; Sequence 6, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-6

Query Match 52.6%; Score 1675; DB 4; Length 1686;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 787 GCACCTTAAGGTTGCTTGCACCTGTTGAATCATGCCACTTCCAGCACCAAGCCCA 846
Db 1 GCACCTTAAGGTTGCTTGCACCTGTTGAATCATGCCACTTCCAGCACCAAGCCCA 60
Qy 847 AGCCTAACATCTTCCACAGGATCCCGATGTGAACATGTGCACCTGTTTGTGGGCG 906

Db 61 AGCCTAACATCTTCCACAGGATCCCGATGTGAACATGTGTGACAGTGTGTTGTTCTGGGCG 120
Qy 907 AATGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTACCTGCCCTCAATCACCAGC 966
Db 121 AATGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTACCTGCCCTCAATCACCAGC 180
Qy 967 ACGAATACTTCTTCTGATTGGGCGCGGTGCTCATCCCCATATATTCAGTACCAGA 1026
Db 181 ACGAATACTTCTTCTGATTGGGCGCGGTGCTCATCCCCATATATTCAGTACCAGA 240
Qy 1027 TCATCATCAACCATGATCGTCCATAAGACTGGGTGACCTGGCCCTGGCCGTGAGCTACT 1086
Db 241 TCATCATCAACCATGATCGTCCATAAGACTGGGTGACCTGGCCCTGGCCGTGAGCTACT 300
Qy 1087 ACATCCGGTCTTTCATCACTACATCCCTTTCTACGCGCATCTCTGGGAGCCCTCTTTTTC 1146
Db 301 ACATCCGGTCTTTCATCACTACATCCCTTTCTACGCGCATCTCTGGGAGCCCTCTTTTTC 360
Qy 1147 TCAACTTTCATCAGGTTCTCTGGAGAGCCACTGTTGTGTGGTTCACACAGATGAATCACA 1206
Db 361 TCAACTTTCATCAGGTTCTCTGGAGAGCCACTGTTGTGTGGTTCACACAGATGAATCACA 420
Qy 1207 TCGTCAATGAGATTGACCAAGAGGCGCTACCGTGACTGGTTCACTAGCAGCTGACGCCA 1266
Db 421 TCGTCAATGAGATTGACCAAGAGGCGCTACCGTGACTGGTTCACTAGCAGCTGACGCCA 480
Qy 1267 CTGCAACGTGGAGAGCTCTTCTTCAACGACTGGTTCACTAGCAGCTTAACTTCCAGA 1326
Db 481 CTGCAACGTGGAGAGCTCTTCTTCAACGACTGGTTCACTAGCAGCTTAACTTCCAGA 540
Qy 1327 TTGAGCACCACTCTTCCGCCACCATGCCCCCGGCAACATTACACAAAGATCCGCCCTGG 1386
Db 541 TTGAGCACCACTCTTCCGCCACCATGCCCCCGGCAACATTACACAAAGATCCGCCCTGG 600
Qy 1387 TGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACCGAGGAAGCGCTACTGAGGGGCC 1446
Db 601 TGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACCGAGGAAGCGCTACTGAGGGGCC 660
Qy 1447 TCGTGGACATCATCAGGTCCCTTGAAGAGTCTGGGAAGCTGTGGTGGACGCTACCTTTC 1506
Db 661 TCGTGGACATCATCAGGTCCCTTGAAGAGTCTGGGAAGCTGTGGTGGACGCTACCTTTC 720
Qy 1507 ACAATGAAAGCACAGCCCCCGGACACCTGTGGGGAAGGGTGCAGGTGGGGTGTATGCC 1566
Db 721 ACAATGAAAGCACAGCCCCCGGACACCTGTGGGGAAGGGTGCAGGTGGGGTGTATGCC 780
Qy 1567 AGAGGATGATGGGCTTTTGTCTGAGGGTGTCCGAGAGGCTGTGTATGACACTGTCTCA 1626
Db 781 AGAGGATGATGGGCTTTTGTCTGAGGGTGTCCGAGAGGCTGTGTATGACACTGTCTCA 840
Qy 1627 CGGACCCCATGTTGGATCTTCTCCCTTCTCCTCTCCTCTCTCTCTCTCTCTCTCTCTCT 1686
Db 841 CGGACCCCATGTTGGATCTTCTCCCTTCTCCTCTCCTCTCTCTCTCTCTCTCTCTCTCT 900
Qy 1687 ATAGCACCTGCCCCATGAGGACCTGCCCTCCCTCAGCGCTCAGCCATCAGCCATGGGCC 1746
Db 901 ATAGCACCTGCCCCATGAGGACCTGCCCTCCCTCAGCGCTCAGCCATCAGCCATGGGCC 960
Qy 1747 TCCAGTGTCTCTAGCCCCCTTCTTCCAAAGAGCAGAGAGTGGCCACCGGGGTGGCTC 1806
Db 961 TCCAGTGTCTCTAGCCCCCTTCTTCCAAAGAGCAGAGAGTGGCCACCGGGGTGGCTC 1020
Qy 1807 TGTCTTACCTTCCACTCTCTGCCCCCTTAAAGATGGGAGGAGACCAGCGCTCCATGGGCTGG 1866
Db 1021 TGTCTTACCTTCCACTCTCTGCCCCCTTAAAGATGGGAGGAGACCAGCGCTCCATGGGCTGG 1080
Qy 1867 CTTGTGAGTCTCCCTTTGAGGCTGTGTCTAGGATCAACCCCGCTTTTGTGTTCTTCAGA 1926
Db 1081 CTTGTGAGTCTCCCTTTGAGGCTGTGTCTAGGATCAACCCCGCTTTTGTGTTCTTCAGA 1140
Qy 1927 TGTCTTTGGGTTTCATAGGGGAGGTCCTAGTGGGAGGAGGCGCTTGCACCTCCCGGCT 1986
Db 1141 TGTCTTTGGGTTTCATAGGGGAGGTCCTAGTGGGAGGAGGCGCTTGCACCTCCCGGCT 1200

QY 1098 TTCAATACCTACATCCCTTTCTACGGCATCTCGGAGCCCTCTCTTTCTCTCAATTCATC 1157
Db 996 TTCTTATCTACCTCCCTTTCTACGGCGTCCCTCGGGTGCTGCTCTTCTTTGTGTGTC 1055
QY 1158 AGGTTCTCGAGAGCCACTCGGTTGTGTGGGTACACAGATGAATCACATCGTCATGGAG 1217
Db 1056 AGGTCCTGGAAGCCACTGGTTCTGTGGATCACAGATGAACACATCCCAAGGAG 1115
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Db 1116 ATCGCCACAGAGACACCGGACTGAGTCTCTCAGTGGCAGCCACCTGCAACGTG 1175
QY 1278 GAGCAGTCTCTTCTCAACGACTGGTTTCAGTGGACACCTTAATCTTCAGATTGACACCAAC 1337
Db 1176 GAGCCTCACTTTTCAACCACTGGTTTCAGCGGCACTCTCACTTCAGATCGAGCAAC 1235
QY 1338 CTCTTCCCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1397
Db 1236 CTCTTCCCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1295
QY 1398 TGTCCCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457
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QY 1458 ATCAGGTCTCTGAGAGTCTGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1517
Db 1356 GTCAAGTCTCTGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1415
QY 1518 CACAGCCCGGG 1530
Db 1416 CACACCCAGGCG 1428

RESULT 8

US-09-048-888-4
Sequence 4, Application US/0904888
Patent No. 6492108
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,888
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Certone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0494 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 1928 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BEPINOT01
CLONE: 2056310
US-09-048-888-4

Query Match 19.1%; Score 608.2; DB 4; Length 1928;

Best Local Similarity 66.0%; Pred. No. 4.7e-140; Indels 3; Gaps 1;

Matches 896; Conservative 0; Mismatches 458;

QY 200 GGGGAGGAGGCGCGCGAGCGCGAGGTGTGCGGTCCACCTTTCAGCTGGGAGGAGATTC 259

Db 101 GGGCGCGAGAGCGCGGTCTCAGGGACCTTACCCCGGTACTTTCACCTGGGAGGAGGTGGC 160

QY 260 GAAGCATAACTTGGCCACCGGACAGTGGGTGCTGATTCATTCACCGCAAGGTTTACACATCAC 319

Db 161 CAGCGCTCAGGGTGCAGGAGCGGTGGCTAGTATGATGACCGTAAGGTGTACACATCAG 220

QY 320 CAAATGGTCCATCCAGCACCCGCGGGGCGGAGCGGTCTCATCGGGCACTACGCTGGAGAGA 379

Db 221 CGAGTTCACCGCGCGGCTCCAGGGGCTCCCGGTCTATCAGCCACTACGCGCGGCGAGA 280

QY 380 TGCACGATGCTTCCCGGCTTCCACCTGACCTGGAATTCGTGGCAATTCGTGGCAATTCGTGAA 439

Db 281 TGCCACGATCCCTTTGCGGCTTCCACATCAACAAGGCGCTTGTGAAGAAAGTATATGAA 340

QY 440 ACCCTGCTGATTTGGTGAATCTGGGCGCGGAGGAGCCAGCGGAGCCAGCCAGCCAGCCAGCC 499

Db 341 CTCCTCTCTGATTGGAGAACTGTCTCCAGAGCAGCCAGCTTTCAGCCACCAAGATAA 400

QY 500 AAAGATCACTGAGGACTTCCCGGCGCTGAGAGAGCGGTGAGACATGAACCTGTTCAA 559

Db 401 AGAGCTGACAGATGAGTTCGCGGAGCTCGCGGCGCACAGTGGAGCGGATGGGCTCATGAA 460

QY 560 GACCAACCACTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619

Db 461 GGCACCACTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 520

QY 620 ATGGTTCATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 679

Db 521 CTGGCTCACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 580

QY 680 CTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 739

Db 581 GCTCAGTGCAGTTCAGGCGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 640

QY 740 CTACAGAAAACCCAAAGTGGAAACCACTTGTCCCAAAATTCGTCATTTGGCCACTTAAAGGG 799

Db 641 CTTGAGCACTCAAAGTGGAAACCACTTGTCTACATCATTTTGTGATTGGCCACTTAAAGGG 700

QY 800 TGCCTCTGCAACTGTTGGAATCATCGCACTTCCAGCAACCAAGCCAGCCAGCCAGCCAGCCAG 859

Db 701 GGGCGCGCGAGTTCGTTGGAACCACTGACATCTTCAGCACCACCATGCGCAAGCCCAACTGCT 760

QY 860 CCACAAGGATCCGATGTGAACATCTGCAAGT---GTTTGTCTTGGCGGAATGGCAGCC 916

Db 761 CCGCAAGACCCAGACATCAACATGATCCCTTCTCTTTCCTTGGCTTGGGGAAGATCCTCTC 820

QY 917 CATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACATCAACAGCAGGATATCTT 976

Db 821 TGTGAGCTTGGGAAACAGAGAAAATAATATGCGGTACAAACCCAGCAGCAAAATCTT 880

QY 977 CTTCTGATTGGGCGCGCTCTCATCCCAATGATTTTCCAGTACCAAGATCATCATGAC 1036

Db 881 CTTCTTAATTGGCCCCCAGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 940

QY 1037 CATGATCGTCCATAAGAACTGGGTGGAACCTGGGCTGGGCGGTGAGCTACTACTACCTGGTT 1096

Db 941 TGTATCCAGCGAAGAGTGGGTGGAATTTGGCTTGGATGATTACCTTCTACCTCGCTT 1000

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QY 1097 CTTCTACCTACATCCCTTTCTACGGCATCTCGGAGCCCTCTTTTCCTCAACTTCAT 1156
DB 1001 CTTCTCTACTTATGTGCCACTATTGGGCTGAAAGCCTTCTCGGCGCTTTTCTTCATAGT 1060
QY 1157 CAGGTTCTCGGAGAGCACTGTTTGTGTGGGTCAACAGATGAATCAATCGTCATGGA 1216
DB 1061 CAGGTTCTCGGAGAGCACTGTTTGTGTGGGTGACACAGATGAACCATATTCCCATGCA 1120
QY 1217 GATTGACAGGAGGCTACCTGCTACTGTTTCTAGTAGCCAGCTGACAGCCACTGCAAGT 1276
DB 1121 CATTTGATCATGACCGGAACATGAGTGGGTTTCCACCCAGCTCCAGGCGCATGCAATGT 1180
QY 1277 GAGCAGTCTCTTCTCAACGACTGTTTCTAGTGACACCTTAACTTCCAGATTGAGCACCA 1336
DB 1181 CCACAGTCTGCTTCAATGACTGTTTCTAGTGACACCTCACTCACTTCCAGATTGAGCACCA 1240
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DB 1241 TCTTTTCCACAGTCCCGGCGACAACTTACACAGATTCGCGCCGCTGTTGAGTCTCT 1300
QY 1397 ATGTGCAAGCATGCTTGAATACCGAGAGAGCGGCTACTGAGGCGCTGCTGGACAT 1456
DB 1301 GTGTGCAAGCATGCTTGAATACCGAGAGAGCGGCTACTGAGGCGCTGCTGGACAT 1360
QY 1457 CATCAGGTCCTTGAAGTCTGGAAGCTGTGGTGTGAGCGCTTACCTTCAAAATGAAG 1516
DB 1361 CATCACTCACTAAAGGAGTCAAGGAGCTGTGGTGTGAGCGCTTATCTTCAACCAATAACA 1420
QY 1517 CCACAGCCCGGCGACACCTGCGGAGAGGGTGCAGG 1553
DB 1421 ACAGCCACCTGCTGCCAGTCTGGAAGAGAGGAGAG 1457
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RESULT 9

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US-09-439-261-1
; Sequence 1 Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-1
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Query Match 18.9%; Score 602.8; DB 4; Length 1335;
Best Local Similarity 66.6%; Pred. No. 8.7e-139;
Matches 878; Conservative 0; Mismatches 437; Indels 3; Gaps 1;

QY 200 GGGCGAGGGGGCGCGAGCGGAGGTGTGCGTGGCCACCTTCAGTGGGAGGAGATTCA 259
DB 18 GGGCGCGAGACCGCGGCTCAGGAGCCTACCCCGCGCTACTTCACTCGGAGAGGTGGC 77
QY 260 GAAGCATAACTTCGCGACCGACAGTGGGTGTGATTCAGCGCAAGGTTTACAACTAC 319
DB 78 CCAGCGCTCAGGTTGCGAGAGCGGTGGTGTGATTCAGCGCGGTAAAGTGTACAACTAG 137
QY 320 CAAATGTTCCATCCAGCACCCCGGGGCGGCGGTCATCGGCGACTACGCTGGAGAAGA 379
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DB 138 CGAGTTCCACCGCGCGCATCCAGGGGGCTCCCGGGTTCATCAGCCACTACGCGGCGAGCA 197
QY 380 TGCACGAGATGCTTCCGGCGCTTCCACCTGACCTGGAATTCGTGGGCAAGTCTTTGAA 439
DB 198 TGCACGAGATGCTTCCGGCGCTTCCACATCAACAGGGCTTGTGAAGAGATATATGAA 257
QY 440 ACCCTTGCTGATTGGTGAATCTGGCCCGGAGAGCCAGCCAGGACCAAGCAAGCAACTC 499
DB 258 CTCTCTCTCTGATTGGAGAACTGTCTCCAGAGAGCCCGCAGCTTTGAGCCCAACCAAGATAA 317
QY 500 AAGATATCATGAGGACTTCCGGGCTCTGAGGAGAGCGGTGAGGACATGAACTGTTCAA 559
DB 318 AGAGCTGACAGATGAGTTCGGGAGTCCGGGCGCACAGTGGAGCGGATGGGCTCATGAA 377
QY 560 GACCAACCACTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
DB 378 GGCACACCATGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 437
QY 620 ATGGTTCACTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679
DB 438 CTGGCTCACCTTTGGGTCTTTGGGACGCTCTTTTGGCCCTCTCTCTCTCTCTCTCTCTCT 497
QY 680 CTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 739
DB 498 GCTCAGTGCAGTTTACGCGCGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 557
QY 740 CTACAGAAAAACCAAGTGGAAACACCTTGTTCACAAATTCGTTCATTTGGGCGACTTAAAGG 799
DB 558 CTTTCAAGCACTCAAGTGGAAACCATCTGCTTACATCATTTTGTGATTGGCCACCTGAAAG 617
QY 800 TGCTCTGCGCACTGGTGGAACTCATCGCCACTTCCAGACCCAGCCCAAGCCTTAACTCT 859
DB 618 GGGCCCCCGCAGTGTGGTGGAAACCATGATGCACTTCCAGACCCAGCCCAAGCCTTAACTCT 677
QY 860 CCACAGGATCCCGAGTGTGAACATGCTGC ---ACGTGTTTGTGTTCTCGGCGAAATGGCAGCC 916
DB 678 CCGCAAGAGACCCAGACATCAACATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 737
QY 917 CATCGAGTACGGCAAGAGAGAGTGAATACCTGCGCTCAATCAATCACCAGCACCAATACTT 976
DB 738 TGTGGAGCTTGGGAAACAGAGAAATAATATATGCGGTGACACCAACAGCACCAATACTT 797
QY 977 CTTCTCTGATTGGGCGCGCTGCTCATCCCATGTTATTTCCAGTACCAAGATCATATGAC 1036
DB 798 CTTCTCTAATTGGGCGCGCCAGCTTGTGCTCTCTACTTCCAGTGGTATATTTCTATTT 857
QY 1037 CATGATCGTCATAGAACTGGGTGAGACCTGGCGCTGGCGCTCAGTACTACATCCGGT 1096
DB 858 TGTATATCCAGCGAAAGAGTGGGTGGACTTGGGCTGGATGATTACCTTCTACGTCGCTT 917
QY 1097 CTTCTATCACTTACATCCCTTTCTACGGCATCTCTGGGAGCCCTCTCTTTTCTCAACTTCAT 1156
DB 918 CTTCTCTACTTATGTGCCACTATTGGGCTGAAAGCCTTCTCTGGGCTTTTCTTCTATGT 977
QY 1157 CAGTTTCTGAGAGGCACTGTTTGTGGGTGACACAGATGAATCAGATTCGTCATGGA 1216
DB 978 CAGTTTCTGAGAGCACTGTTTGTGGGTGACACAGATGAACCATATTTCCCATGCA 1037
QY 1217 GATTGACAGGAGGCTTACCGTGTGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1276
DB 1038 CATTGATCATGACCGGAAACATGAGTGGTTCACCCAGCTCTCTGGCCACATGCAATGT 1097
QY 1277 GGACAGTCTCTTCTTAAAGTGTGTTTCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1336
DB 1098 CCACAGTCTGCTTCAATGACTGTTTCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1157
QY 1337 CTTCTTCCACCATGCGCGGACAACTTACCAAGATCGCCCGCTGGTGGTGGTGGTGGTGGTGGT 1396
DB 1158 TCTTTTCCACGATGCTCGACAAATTACCAAGTGGTCTCCCTCTGGTGGTGGTGGTGGTGGTGGT 1217
QY 1397 ATGTGCCAAGCATGGCATTTGAATACAGAGAGAGCGGCTTACTGAGGGCCCTTCTGGGACAT 1456
```

Db 1218 GTGTGCAAGCGTGGCATAGATACAGTCCAGGCCCTGCTGTGAGCCCTTGGCGGACAT 1277
Qy 1457 CATCAGTCCCTCAAGAGTCTGGGAGCTGTGGCTGGAGCGCTACCTTCAAAATGA 1514
Db 1278 CATCCACTACTAAGAGTCAAGGAGTGGGAGCTCTGGCTAGATGCTTCTTCAACAAATA 1335

RESULT 10
US-09-227-613-1
; Sequence 1, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295, US, P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-1

Query Match 18.9%; Score 602.8; DB 4; Length 1335;
Best Local Similarity 66.6%; Pred. No. 8.7e-139;
Matches 878; Conservative 0; Mismatches 437; Indels 3; Gaps 1;

Qy 200 GGGCGAGGGGCGCCCGAGCGCGAGGTGTGGTGGCCACCTTACAGCTGGGAGAGATTCA 259
Db 18 GGGCGCGAGACCGCGCTCAGGACCTACCCGCGCTACTTACCTGGGACGAGGTGGC 77
Qy 260 GAAGCATAACTGGCGACCGACAGTGGCTGGTCAATGACCGCAAGTGTACACATCAC 319
Db 78 CAGGGCTCAGGTGCGAGGAGCGGTGTAGTATGATCGACGTAAGTGTACACATCAG 137
Qy 320 CAATGTGTCATCAGACACCGGGGGCGAGCGGTGTATGGGCACTACCTCTGGAGAGA 379
Db 138 CGAGTTACCCCGCGGATCCAGGGGGTCCCGGGTTCATCAGCCACTACCGCGGCGAG 197
Qy 380 TGCAACGATGCTTCCGCGCTTCCACCTTCCAGCTGACCTGGAATTCGTGGGCAAGTTC 439
Db 198 TGCCACGGATCCCTTTGTGGCTTCCCATCAACAGGGCTTGTGAAGATATAGAA 257
Qy 440 ACCCTGCTGATGTGGTAACCTGGCCCGAGGAGCCCGAGGACCCAGCGAGCACCGCAAGACTC 499
Db 258 CTCTCTCTGATTGGAGAACTGTCTCCAGAGCAGCCCGAGCTTTGAGCCCGCAAGATAA 317
Qy 500 AAGATCACTAGCACTCCGGGCGCTGAGAGACGGCTGAGGACATGAACCTGTTCAA 559
Db 318 AGAGCTGACATGAGTTCGGGAGCTCGGGCCACAGTGGAGCGGATGGGCTCATGAA 377
Qy 560 GACCAACACAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Db 378 GGCCAAACCATGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 437
Qy 620 ATGGTCTACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679
Db 438 CTGGCTACCCCTTGGGCTTTGGGACGTCCTTTTGGCCCTCTCTCTCTCTCTCTCTCTCT 497
Qy 680 CTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 739
Db 498 GCTCAGTGCAGTTCAAGGCCCGAGCTGGCTGGCTGCAGCATGACTTGGGCACTGTCCGT 557
Qy 740 CTACAGAAAACCAAGTGAACCCCTTGTCCACAAATTCGTCATTTGGCCACTTAAAGGG 799
Db 558 CTTGACGACCTCAAGAGTGAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 617

Qy 800 TGCTCTGCCAAGTGTGGAAATCATGCCACTTCCAGCACACCGCCAGGCTTAACTCTT 859
Db 618 GGCCCCGCCAGTGTGGTGAACACACATGCACTTCCAGCACCATGCCAAGCCCACTT 677
Qy 860 CCACAGGATCCCGATGTGAACATGCTGC--AGTGTGTGTGGGCGAATGGCAGCC 916
Db 678 CCGAAGAGCCAGACATCAACATGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 737
Qy 917 CATCGAGTCGGCAAGAGAGCTGAAATACCTGCGCTTAACTCAAAATCCAGCACGAATCTT 976
Db 738 TGTGGAGCTTGGGAAACAGAGAAAAATATATGCCGTACAAACCCAGCACAAATACTT 797
Qy 977 CTTCTGATTTGGGCGCGCTGCTCATCCCATGATTTTCCAGTACAGATCATCATGAC 1036
Db 798 CTTCTAATTTGGGCCCCAGCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 857
Qy 1037 CATGATCTCCATAAGAACTGGGTGGACCTGGCGTGGCGCTGAGCTACTACATCCGGT 1096
Db 858 TGTATCCAGCGAAAGAGTGGGTGGACTTGGCCCTGATGATTACCTTACGTCGCGT 917
Qy 1097 CTTCTACCTACATCCCTTTCTACGGCATCTTGGGAGCCCTCTCTCTCTCTCTCTCTCT 1156
Db 918 CTTCTCTACTTATGTGCCACTATTGGGGCTGAAAGCCCTTCTCTGGGCTTTTCTCTCAT 977
Qy 1157 CAGGTTCTCTGAGAGCCCACTGCTTGTGTGGGTCCACAGATGAATCACATCGTCATGGA 1216
Db 978 CAGGTTCTCTGGAAGCACTGTTTGTGTGGGTGACACAGATGAACCATATTCCCATGCA 1037
Qy 1217 GATTACAGGAGGCTTACCGTGTGCTTCACTGAGTCCAGCTGAGCGCTGAGCGCTGCA 1276
Db 1038 CATTGATCATGACCGGAACATGGGATTTCCACCCAGCTCTCTGGCCCATCATGAATGT 1097
Qy 1277 GGAGCAGTCTCTTCTTCAACAGCTGCTTCACTGAGCACCTTAACTTCCAGATTTAGC 1336
Db 1098 CCACAGTCTGCTTCAATGACTGTTCACTGAGCACCTCACTTCCAGATTTAGCAGCA 1157
Qy 1337 CTTCTTCCCGACCTGCGCGGACACTTACACAGATCGCCCGCTGGTGGTGAATCTCT 1396
Db 1158 TCTTTTCCCGAGTGCCTCGACAAATTACCAAAAGTGGCTCCCTGGTGGAGTCTCT 1217
Qy 1397 ATGTCCCAAGCATGCTTGAATACAGGAGAGCGCTACTGAGGGCCCTGCTGGACAT 1456
Db 1218 GTGTCCCAAGCGTGCATAGTACAGTACAGTCCAGCCCTGCTGTCAGCGCTTCCGCG 1277
Qy 1457 CATCAGGTCCTTGAAGAGTCTGGGAGCTGTGGCTGAGCGCTTACCTTCAAAATGA 1514
Db 1278 CATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCTCTATCTTCAACAA 1335

RESULT 11
US-09-389-681-313
; Sequence 313, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-389-681-313

Query Match 13.9%; Score 443.6; DB 4; Length 456;
Best Local Similarity 99.1%; Pred. No. 8.3e-100;

Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

788 CCACCTTAAGGGTGCCTCTGCGCAACTGGTGGAAATCATCGGCACCTTCAGACACACGCCAA 847

2 CCACCTTAAGGGTGCCTCTGCGCAACTGGTGGAAATCATCGGCACCTTCAGACACACGCCAA 61

848 GCCTAAACATCTTCACCAAGGATCCCGATGTGAACATGCTGCACTGTCTTCTTCTGGGCGA 907

62 GCCTAAACATCTTCACCAAGGATCCCGATGTGAACATGCTGCACTGTCTTCTTCTGGGCGA 121

908 ATGGCAGCCCATCGAGTACGCGCAAGAAAGAGCTGAATACTGCGCCCTACAAATCACCAGCA 967

122 ATGGCAGCCCATCGAGTACGCGCAAGAAAGAGCTGAATACTGCGCCCTACAAATCACCAGCA 181

968 CGAATACCTTCTTCTGATTTGGGCGCGCTCTCTCATCCCATGTATTTCCAGTACCAGAT 1027

182 CGAATACCTTCTTCTGATTTGGGCGCGCTCTCTCATCCCATGTATTTCCAGTACCAGAT 241

1028 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGGCGCTCAGCTACTA 1087

242 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGGCGCTCAGCTACTA 301

1088 CATCCGGTCTTCTCATCACTACATCCCTTCTACGGCATCTGGGAGCCCTCCCTTTTCT 1147

302 CATCCGGTCTTCTCATCACTACATCCCTTCTACGGCATCTGGGAGCCCTCCCTTTTCT 361

1148 CAACTTCATCAGTTCTCTGGAGAGCCACTGGTTTGTGGGTGCACACAGATGAATCAGAT 1207

362 CAACTTCATCAGTTCTCTGGAGAGCCACTGGTTTGTGGGTGCACACAGATGAATCAGAT 421

1208 CACTGAGGATTTGACGAGGACCTCG 451

RESULT 12

US-09-620-405B-313

Sequence 313, Application US/05620405B

Patent No. 6528054

GENERAL INFORMATION:

APPLICANT: Jiang, Yugu

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Xu, Jiangchun

APPLICANT: Harlocker, Susan L.

APPLICANT: Hessler, William T.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210121.470C8

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 495

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 313

LENGTH: 456

TYPE: DNA

ORGANISM: Homo sapiens

US-09-620-405B-313

Query Match 13.9%; Score 443.6; DB 4; Length 456;

Best Local Similarity 99.1%; Pred. No. 8.3e-100;

Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

788 CCACCTTAAGGGTGCCTCTGCGCAACTGGTGGAAATCATCGGCACCTTCAGACACACGCCAA 847

2 CCACCTTAAGGGTGCCTCTGCGCAACTGGTGGAAATCATCGGCACCTTCAGACACACGCCAA 61

848 GCCTAAACATCTTCACCAAGGATCCCGATGTGAACATGCTGCACTGTCTTCTTCTGGGCGA 907

62 GCCTAAACATCTTCACCAAGGATCCCGATGTGAACATGCTGCACTGTCTTCTTCTGGGCGA 121

908 ATGGCAGCCCATCGAGTACGCGCAAGAAAGAGCTGAATACTGCGCCCTACAAATCACCAGCA 967

Db 122 ATGGCAGCCCATCGAGTACGCGCAAGAAAGAGCTGAATACTGCGCCCTACAAATCACCAGCA 181

Qy 968 CGAATACCTTCTTCTGATTTGGGCGCGCTCTCTCATCCCATGTATTTCCAGTACCAGAT 1027

Db 182 CGAATACCTTCTTCTGATTTGGGCGCGCTCTCTCATCCCATGTATTTCCAGTACCAGAT 241

Qy 1028 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGGCGCTCAGCTACTA 1087

Db 242 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGGCGCTCAGCTACTA 301

Qy 1088 CATCCGGTCTTCTCATCACTACATCCCTTCTACGGCATCTGGGAGCCCTCCCTTTTCT 1147

Db 302 CATCCGGTCTTCTCATCACTACATCCCTTCTACGGCATCTGGGAGCCCTCCCTTTTCT 361

Qy 1148 CAACTTCATCAGTTCTCTGGAGAGCCACTGGTTTGTGGGTGCACACAGATGAATCAGAT 1207

Db 362 CAACTTCATCAGTTCTCTGGAGAGCCACTGGTTTGTGGGTGCACACAGATGAATCAGAT 421

Qy 1208 CACTGAGGATTTGACGAGGACCTCG 451

RESULT 13

US-09-339-338-313

Sequence 313, Application US/05339338A

Patent No. 6573368

GENERAL INFORMATION:

APPLICANT: Yugu, Jiang

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.470C2

CURRENT APPLICATION NUMBER: US/09/339,338A

CURRENT FILING DATE: 1999-06-23

NUMBER OF SEQ ID NOS: 315

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 313

LENGTH: 456

TYPE: DNA

ORGANISM: Homo sapiens

US-09-339-338-313

Query Match 13.9%; Score 443.6; DB 4; Length 456;

Best Local Similarity 99.1%; Pred. No. 8.3e-100;

Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

788 CCACCTTAAGGGTGCCTCTGCGCAACTGGTGGAAATCATCGGCACCTTCAGACACACGCCAA 847

2 CCACCTTAAGGGTGCCTCTGCGCAACTGGTGGAAATCATCGGCACCTTCAGACACACGCCAA 61

848 GCCTAAACATCTTCACCAAGGATCCCGATGTGAACATGCTGCACTGTCTTCTTCTGGGCGA 907

62 GCCTAAACATCTTCACCAAGGATCCCGATGTGAACATGCTGCACTGTCTTCTTCTGGGCGA 121

908 ATGGCAGCCCATCGAGTACGCGCAAGAAAGAGCTGAATACTGCGCCCTACAAATCACCAGCA 967

122 ATGGCAGCCCATCGAGTACGCGCAAGAAAGAGCTGAATACTGCGCCCTACAAATCACCAGCA 181

968 CGAATACCTTCTTCTGATTTGGGCGCGCTCTCTCATCCCATGTATTTCCAGTACCAGAT 1027

182 CGAATACCTTCTTCTGATTTGGGCGCGCTCTCTCATCCCATGTATTTCCAGTACCAGAT 241

1028 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGGCGCTCAGCTACTA 1087

242 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGGCGCTCAGCTACTA 301

1088 CATCCGGTCTTCTCATCACTACATCCCTTCTACGGCATCTGGGAGCCCTCCCTTTTCT 1147

302 CATCCGGTCTTCTCATCACTACATCCCTTCTACGGCATCTGGGAGCCCTCCCTTTTCT 361

Qy	1148	CAACTTCATCAGGTTCTCGAGAGCCACTGGTTTGTGTGGTTCACACAGATGAATCACAT	1207
Db	362	CAACTTCATCAGGTTCTCGAGAGCCACTGGTTTGTGTGGTTCACACAGATGAATCACAT	421
Qy	1208	CGTCATGGAGATTGACCAGGAGGCGCTACCG	1237
Db	422	CGTCATGGAGATTGACCAGGAGGACCTCGG	451

RESULT 14

US-09-433-826B-313

; Sequence 313, Application US/09433826B

; Patent No. 6579973

; GENERAL INFORMATION:

; APPLICANT: Giang, Yuqui

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.470C4

; CURRENT APPLICATION NUMBER: US/09/433.826B

; CURRENT FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 474

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 313

; LENGTH: 456

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-433-826B-313

; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jiaangchun
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Hepler, William T.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121.470C7
 ; CURRENT APPLICATION NUMBER: US/09/604,287A
 ; CURRENT FILING DATE: 2000-06-22
 ; NUMBER OF SEQ ID NOS: 489
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 313
 ; LENGTH: 456
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-604-287A-313

Query Match 13.9%; Score 443.6; DB 4; Length 456;
 Best Local Similarity 99.1%; Pred. No. 8.3e-100;
 Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	788	CCACTTTAAAGGGTGCCCTCTGCCAACTGGTGGGAATCATCGCCACTTCCAGCACACGCCCAA	847
DB	2	CCACTTTAAAGGGTGCCCTCTGCCAACTGGTGGGAATCATCGCCACTTCCAGCACACGCCCAA	61
QY	848	GCCTAACATCTTCCACAAGATCCCGATGTGAACATGCTGCACGTGTTTGTCTGGCGA	907
DB	62	GCCTAACATCTTCCACAAGATCCCGATGTGAACATGCTGCACGTGTTTGTCTGGCGA	121
QY	908	ATGGCAGCCCATCGAGTAGCGGCAAGAAGCTGAAATACCTGCCCTACAATCACAGCA	967
DB	122	ATGGCAGCCCATCGAGTAGCGGCAAGAAGCTGAAATACCTGCCCTACAATCACAGCA	181
QY	968	CGAATACTTCTTCTGATTTGGGCGCGCTGCTCATCCCCATGTTTCCAGTACCAGAT	1027
DB	182	CGAATACTTCTTCTGATTTGGGCGCGCTGCTCATCCCATGTTTCCAGTACCAGAT	241
QY	1028	CATCATGACCATGATCGTCCATAAAGAACTGGGTGGACCTGGCGCGGTCAAGTACTA	1087
DB	242	CATCATGACCATGATCGTCCATAAAGAACTGGGTGGACCTGGCGCGGTCAAGTACTA	301
QY	1088	CATCCGGTCTTTCATCACCTACATCCCTTCTACGGCATCTCGGAGCCCTCCTTTTCC	1147
DB	302	CATCCGGTCTTTCATCACCTACATCCCTTCTACGGCATCTCGGAGCCCTCCTTTTCC	361
QY	1148	CAACTTCATCAGGTTCTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCACAT	1207
DB	362	CAACTTCATCAGGTTCTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCACAT	421
QY	1208	CGTCATGGAGATTGACCAAGAGCCCTACCG	1237
DB	422	CGTCATGGAGATTGACCAAGAGAGCACTCGG	451

RESULT 16
 US-09-389-681-425
 ; Sequence 425, Application US/09389681A
 ; Patent No. 6518237
 ; GENERAL INFORMATION:
 ; APPLICANT: Yuqiu, Jiaang
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jiaangchun
 ; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.470C3
 ; CURRENT APPLICATION NUMBER: US/09/389,681A
 ; CURRENT FILING DATE: 1999-09-02
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-389-681-425

Query Match      13.9%; Score 443.4; DB 4; Length 446;
Best Local Similarity 99.8%; Pred. No. 9.2e-100; Indels 0; Gaps 0;
Matches 444; Conservative 0; Mismatches 1;

QY 788 CCACCTTAAAGGGTGCCTCTGCCAACTGGTGAATCATCGCCACTTCAGCAGCACCGCCAA 60
D 1 CCACCTTAAAGGGTGCCTCTGCCAACTGGTGAATCATCGCCACTTCAGCAGCACCGCCAA 60
QY 848 GCCTTAACATCTTCCACAGGATCCGATGTGAACATGTCACATGCTGTTGTCTGGGCGA 907
D 61 GCCTTAACATCTTCCACAGGATCCGATGTGAACATGTCACATGCTGTTGTCTGGGCGA 120
QY 908 ATGGCAGCCCATCGAGTACGGAAGAAAGCTGAATATCTGCCCTTACATCAATCAGCA 967
D 121 ATGGCAGCCCATCGAGTACGGAAGAAAGCTGAATATCTGCCCTTACATCAATCAGCA 180
QY 968 CGAATACTCTTCTCGATTTGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 1027
D 181 CGAATACTCTTCTCGATTTGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 240
QY 1028 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGTGGGCGCTCAGTACTA 1087
D 241 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGTGGGCGCTCAGTACTA 300
QY 1088 CATCCGGTCTTTCATCAGTACCTACATCCCTTCTACGGCATCTGGGAGCCCTCTTTTCT 1147
D 301 CATCCGGTCTTTCATCAGTACCTACATCCCTTCTACGGCATCTGGGAGCCCTCTTTTCT 360
QY 1148 CAACCTTCATCAGTCTCTGGAGAGCCACTGGTGTGGTTCACACAGATGAATCAGAT 1207
D 361 CAACCTTCATCAGTCTCTGGAGAGCCACTGGTGTGGTTCACACAGATGAATCAGAT 420
QY 1208 CGTCATGGAGATGACGAGAGGCC 1232
D 421 CGTCATGGAGATGACGAGAGGCC 445

RESULT 18
US-09-433-826B-425
; Sequence 425, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-425

Query Match      13.9%; Score 443.4; DB 4; Length 446;
Best Local Similarity 99.8%; Pred. No. 9.2e-100; Indels 0; Gaps 0;
Matches 444; Conservative 0; Mismatches 1;

QY 788 CCACCTTAAAGGGTGCCTCTGCCAACTGGTGAATCATCGCCACTTCAGCAGCACCGCCAA 847
D 1 CCACCTTAAAGGGTGCCTCTGCCAACTGGTGAATCATCGCCACTTCAGCAGCACCGCCAA 60
QY 848 GCCTTAACATCTTCCACAGGATCCGATGTGAACATGTCACATGCTGTTGTCTGGGCGA 907
D 61 GCCTTAACATCTTCCACAGGATCCGATGTGAACATGTCACATGCTGTTGTCTGGGCGA 120
QY 908 ATGGCAGCCCATCGAGTACGGAAGAAAGCTGAATATCTGCCCTTACATCAATCAGCA 967
D 121 ATGGCAGCCCATCGAGTACGGAAGAAAGCTGAATATCTGCCCTTACATCAATCAGCA 180
QY 968 CGAATACTCTTCTCGATTTGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 1027
D 181 CGAATACTCTTCTCGATTTGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 240
QY 1028 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGTGGGCGCTCAGTACTA 1087
D 241 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGTGGGCGCTCAGTACTA 300
QY 1088 CATCCGGTCTTTCATCAGTACCTACATCCCTTCTACGGCATCTGGGAGCCCTCTTTTCT 1147
D 301 CATCCGGTCTTTCATCAGTACCTACATCCCTTCTACGGCATCTGGGAGCCCTCTTTTCT 360
QY 1148 CAACCTTCATCAGTCTCTGGAGAGCCACTGGTGTGGTTCACACAGATGAATCAGAT 1207
D 361 CAACCTTCATCAGTCTCTGGAGAGCCACTGGTGTGGTTCACACAGATGAATCAGAT 420
QY 1208 CGTCATGGAGATGACGAGAGGCC 1232
D 421 CGTCATGGAGATGACGAGAGGCC 445

RESULT 17
US-09-620-405B-425
; Sequence 425, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-425

Query Match      13.9%; Score 443.4; DB 4; Length 446;
Best Local Similarity 99.8%; Pred. No. 9.2e-100; Indels 0; Gaps 0;
Matches 444; Conservative 0; Mismatches 1;

QY 788 CCACCTTAAAGGGTGCCTCTGCCAACTGGTGAATCATCGCCACTTCAGCAGCACCGCCAA 847

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QY 1028 CATCATGACCATGATCGTCCATTAAGAACTGGTGGAGCACTGGCCCTGGGCGCTCAGCTACTA 1087
 Db 241 CATCATGACCATGATCGTCCATTAAGAACTGGTGGAGCACTGGCCCTGGGCGCTCAGCTACTA 300
 QY 1088 CATCGGTTCTTCATACCTACATACCTCTTCTACGGCATCTGGGAGCCCTCTCTTTTCCT 1147
 Db 301 CATCGGTTCTTCATACCTACATACCTCTTCTACGGCATCTGGGAGCCCTCTCTTTTCCT 360
 QY 1148 CAATTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCACAAT 1207
 Db 361 CAATTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCACAAT 420
 QY 1208 CGTCATGAGATTGACCAAGGAGGCC 1232
 Db 421 CGTCATGAGATTGACCAAGGAGGCC 445
 RESULT 19
 US-09-604-287A-425
 ; Sequence 425, Application US/09604287A
 ; Patent No. 6586572
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Dillon, Devin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Hepler, William T.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121.470C7
 ; CURRENT APPLICATION NUMBER: US/09/604,287A
 ; PRIOR FILING DATE: 2000-06-22
 ; NUMBER OF SEQ ID NOS: 489
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 425
 ; LENGTH: 446
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-604-287A-425
 Query Match 13.9%; Score 443.4; DB 4; Length 446;
 Best Local Similarity 99.8%; Pred. No. 9.2e-100;
 Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 788 CCACTTAAGGTTGCTCTGCCAATCTGGTGGATCATGCCACTCCAGCACCAGCCAA 847
 Db 1 CCACTTAAGGTTGCTCTGCCAATCTGGTGGATCATGCCACTCCAGCACCAGCCAA 60
 QY 848 GCCTAACATCTTCCACAGGATCCCGATGTGAACATGCTGCACTGTTGTCTGGGCGA 907
 Db 61 GCCTAACATCTTCCACAGGATCCCGATGTGAACATGCTGCACTGTTGTCTGGGCGA 120
 QY 908 ATGGAGCCCATCGAGTACGCGAAGAGAGTGAATACCTGCCCTACATCACCAGCA 967
 Db 121 ATGGAGCCCATCGAGTACGCGAAGAGAGTGAATACCTGCCCTACATCACCAGCA 180
 QY 968 CCAATCTTCTTCTGATTGGGCGCGCTGCTCATCCCATGATATTTCCAGTACCAGAT 1027
 Db 181 CCAATCTTCTTCTGATTGGGCGCGCTGCTCATCCCATGATATTTCCAGTACCAGAT 240
 QY 1028 CATATGACCATGATGTCCTAAGAACTGGGTGACCTGGCTGGGCGGTGAGTACTA 1087
 Db 241 CATATGACCATGATGTCCTAAGAACTGGGTGACCTGGGCGGTGAGTACTA 300
 QY 1088 CATCGGTTCTTCATCACCCTACATCCCTTTCTACGGCATCTGGGAGCCCTCTTTTCCT 1147
 Db 301 CATCGGTTCTTCATCACCCTACATCCCTTTCTACGGCATCTGGGAGCCCTCTTTTCCT 360
 QY 1148 CAATTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCACAAT 1207
 Db 361 CAATTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCACAAT 420

QY 1208 CGTCATGAGATTGACCAAGGAGGCC 1232
 Db 421 CGTCATGAGATTGACCAAGGAGGCC 445
 RESULT 20
 US-09-439-261-12
 ; Sequence 12, Application US/09439261
 ; Patent No. 6428990
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pardiip
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295.US.P2
 ; CURRENT APPLICATION NUMBER: US/09/439,261
 ; CURRENT FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: US 08/833,610
 ; PRIOR FILING DATE: 1997-04-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422
 ; PRIOR FILING DATE: 1998-04-10
 ; PRIOR APPLICATION NUMBER: US 09/227,613
 ; PRIOR FILING DATE: 1999-01-08
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 864
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-439-261-12
 Query Match 13.2%; Score 421.6; DB 4; Length 864;
 Best Local Similarity 69.9%; Pred. No. 2.8e-94;
 Matches 584; Conservative 0; Mismatches 249; Indels 3; Gaps 1;
 QY 682 TTGCTACCTCTCAGGCCCAAGCTGGATGCTGCAACATGATTATGGCCACCTGTCTGTCT 741
 Db 29 TTCCGGCAGTTTCAAGGCCCAAGCTGGCTGGCTGCGCATGACATTGGGCACTGTCTGTCT 88
 QY 742 AGAGAAACCCAGTGGAGACCACTTGTCCCAAAATTCGTCATTCGCCCACTTAAAGGGTG 801
 Db 89 TCAGCACCTCAAAGTGGAGACCACTTGTCTACATCATTTTGTGATTGGCCACCTGAGGGG 148
 QY 802 CTTCTGCCAACTGGTGGAAATCATCGCACTTCCAGCACCAACCCCAAGCCCAATCTTCC 861
 Db 149 CCCCCGCCAGTTGGTGGAAACCATGCACTTCCAGCACCAATGCAAGCCCACTGTCTTC 208
 QY 862 ACAAGATCCCGATGTAACATGCTGC---ACGTGTTTGTCTGGCGAATGGCAGCCCA 918
 Db 209 GCAAGACCCAGACATCAACATGCACTTCTTCTTCTGGGGAAGATCTCTCTCTG 268
 QY 919 TCAGTACGGCAAGAAAGAGCTGAAATACCTGCCCTTACCAATCACCAAGCAAGATCTTCT 978
 Db 269 TGAGGCTTGGGAAACAGAGAAATATATGCGGTACACCAACCAAGCAAGATCTTCT 328
 QY 979 TCTGATTGGGCGCGCTGCTCATCCCATGATATTTCCAGTACCAAGATCATCATGACCA 1038
 Db 329 TCCTAATTGGGCGCCCGAGCCTTCTGCTGCTCTCTTCTTCCAGTGGTATATTTCTATT 388
 QY 1039 TGATCGTCCATAAGAACTGGGTGCACTGGCTGGGCGGTGAGTACTACTATCCGGTCTCT 1098
 Db 389 TTATCAGCGAAAGAGTGGTGGATTTGGCTGGATGATTAACCTTCTAGCTCCGCTTCT 448
 QY 1099 TCATCACTACATCCCTTTCTACGGCATCTGGGAGCCCTCTCTTTTCCTCAATTCATCA 1158
 Db 449 TCCTCACTTATGTGCCACTATTGGGCTGAAAGCCCTCTCTCTGGGCTTTTCTTCATAGTCA 508
 QY 1159 GGTTCCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCACAATGATCATGATGAGA 1218
 Db 509 GGTTCCTGGAAAGCAACTGGTTGTGTGGGTGACACAGATGAATGATGATGATGATGATGAGA 568

1219	TTGACGAGGAGGCTACCGTGACTGCTCAGTAGCAGCTGACAGCCACCTGCAACGTGG	1278
569	TTGATCATGACCGGAACATGGACTGGGTTTCCACCAGCTCCAGGCCACATGCAATGTCC	628
1279	AGAGTCTCTTCAAAGCACTGGTTACAGTGGACACCTTAACCTCCAGATTGAGCACCA	1338
629	ACAAGTCTCCCTTCAATGACTGGTTTACAGTGGACACCTCAACTTCAGATTGAGCA	688
1339	TCTTCCCAACCACTGCCCCGGCAACAATTACACAAGATCCCCCGCTGGTGAAGTCTCTAT	1398
689	TTTTTCCACGATGCTTCACACAATTACCAAAAGTGCCTCCCTGGTGCAGTCTTTGT	748
1399	GTGCCAAGCATGGCATTTGAATACACAGGAGAGCCGCTACTGAGGGCCCTGCTGGACA	1458
749	GTGCCAAGCATGGCATGATAGTACAGTCCAAAGCCCTGCTGTCAGCCTTCGCGGACATCA	808
1459	TCAGGTCCCTGGAAGAGTCTGGGAAGCTGTGGCTGACGCGCTACCTTCACAAATGA	1514
809	TCCACTACTAAAGGAGTCAGGCAGCTCTGGCTAGATGCCTATCTTCACCAATTA	864

RESULT 21
US-09-227-613-13
; Sequence 13, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295, US, P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 09/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-13

Query Match	13.2%;	Score 421.6;	DB 4;	Length 864;	
Best Local Similarity	69.9%;	Pred. No. 2.8e-94;			
Matches 584;	Conservative	0;	Mismatches: 249;	Indels 3;	Gaps 1;

Qy	682	TTGCTACCTCTCAGCCCAAGCTGGATGGCTGCAACATGATATGGCCACCTGCTGTCT	741
Db	29	TTCCGGCAGTTTCAGGCCCAGGCTGGCTGGCTGACGATGACTTTGGGCACCTGTCGTCT	88
Qy	742	ACAGAAACCAAGTGGAAACCACTGTGCACAAATTCGTCATTGGCCACTTAAAGGGTG	801
Db	89	TCAGACCTCAAAGTGNACCATCTGTACATCATTTTGTATTGGCCACTGAGGGGG	148
Qy	802	CCTCTGCCAATGTTGGGAATCATCGCCATTTCCAGCACCGCAAGCCTAACATCTTC	861
Db	149	CCCCGCCAGTTGTTGGAAACCAATGCACTTCCAGCACCATGCGCAAGCCCACTCTTC	208
Qy	862	ACAGGATCCGATGTGAACATGCTGC---ACGTGTTTGTCTCGGCGAATGGCAGCCCA	918
Db	209	GCAAGACCCAGACATCAACATGATATGCCGTCAACACCAAGCAGACAAATCTCT	268
Qy	919	TCGAGTACGGCAAGAAGCTGAAATACCTGCCCTACAATCACACAGCAAGATCTCT	978
Db	269	TGGAGCTTGGGAAACAGAAAGAAAAATATATGCCGTCAACACCAAGCAGACAAATCTCT	328
Qy	979	TCCTGATTGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAAGTACATCATGACCA	1038
Db	329	TCCTAATTGGGCCCCCAGCCCTTGCTGCTCTACTTCCAGTGGTATATTTCTATTG	388
Qy	1039	TGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGGCCCTCAGCTACTACATCCGGTCT	1098

QY	380	TGCAACGGATGCCTTCGCGCCTTCCACCTGACCTGGAATTGCTGGCAAGTCTTGAA	439
Db	228	TGCCAAGGATCCCTTTGTGGCCCTTCCATCAACAAGGGCCTTGTGAAGAAGTATATGAA	287
QY	440	ACCCCTGCTATTGGTGAACTGGGCCCGGAGGAGCCAGCAGGACCACCGCAAGAACTC	499
Db	288	CTCTCTCCTGATTGGAGAACTGTCTCAGAGCAGCCAGCTTTGAGCCACCAAGAATAA	347
QY	500	AAAGATCACTGAGGACTTCCGGGCCCTTGAGAGACGGCTGAGACATGAACCTGTTCAA	559
Db	348	AGAGCTGACAGATGAGTTCCGGGAGCTGCGGGCCACAGTGAGCGGATGGGGCTCATGAA	407
QY	560	GACCAACCAAGTGTTCTTCTCTCCCTCTCTGGGCCACATCATGCCCTGGAGAGCATGTC	619
Db	408	GGCCAACCATGTCTTCTTCTCTGTACTGCTGCACATCTTGCTGCTGGATGCTGCAGC	467
QY	620	ATGGTTCACTGTCTTCTACTTTGGCAATGGCTGGATTCTACCTCATCAGGGCCTTGT	679
Db	468	CTGGCTCACCCCTTTGGGTCTTTGGGACGTCCTTTTGGCCCTTCCTCTCTGTGGGGTCT	527
QY	680	CCTTGTCTACCTCTCAGGCCCAAGCTGGATGGCTCAACATGATTATGGCCACCTGCTGT	739
Db	528	GCTCAGTGCAGTTCAAGCCCCAGGCTGCTGGCTGCAGCATGACTTTGGCACCTGTCCGT	587
QY	740	CTACAGAAAACCAAGTGGAAACCACTTGTGCCAAATGGTCATTGGCCACTTAAGGG	799
Db	588	CTTCAGACCTCAAAGTGGAAACCATCTGTACATCATTTTGTGATGGCCACCTGAAGGG	647
QY	800	TGCTCTTCGCAACTGGTGGAAATCATCGCACTTCAGCACCCAGCCAAAGCCTAACATCTT	859
Db	648	GGCCCCGCCAGTTGGTGGAAACCATGCACTTCAGACCATGCCAAGCCCACTGCTT	707
QY	860	CCACAAGATCCCGATGTGACATGCTGCAAGTCT--TTGTTCTGGCGGAATGGCAGCC	916
Db	708	CCGCAAGAAGCCACATCAACATGCATCCCTCTTCTTTGCCCTTGGGAAGATCCCTCTC	767
QY	917	CATCGAGTAGCGCAAGAAGAGCTGAAATACCTCCCTTACAATCACGAGCAGAACTACTT	976
Db	768	TGTGGAGCTTGGGAAAACAGAGAAAAAATATATCCGTTACAACACCAGCACAAATACTT	827
QY	977	CTTCCCTGATTGGCGCGCGCTGCTCATCCCCATGTTTTCAGTACAGATCATCATGAC	1036
Db	828	CTTCTCTAATTGGGGCCCCAGCCTTGTGCTCTCTACTTCCAGTGGTATATTCTTCTATT	887
QY	1037	CATGATCGTCCATAGAACCTGGGTGGACCTGGCCTGGGCCGTCA	1080
Db	888	TGTTATCCAGCGAAAGAAGTGGGTGGACTTGGCCTGGATCAGCA	931

```

RESULT 23
US-09-227-613-35
; Sequence 35, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda B.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US-P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-35
Query Match 11.6%; Score 370.4; DB 4; Length 960;

```

Best Local Similarity 64.5%; Pred. No. 1.2e-81;
Matches 570; Conservative 0; Mismatches 311; Indels 3; Gaps 1;

QY 200 GGGCGAGGGGGCGCGCGAGCGAGGTGTCGGTGGCCACTTCAAGTCGGAGAGATTCA 259
Db 48 GGGCGCGGAGACGGCGGCTCAGGGACCTACCCGCGCTACTTCACCTGGGACGAGTGGC 107
QY 260 GAAGCATACCTCGCGCAGCGACAGTGGGTGCTCATTTGACCGCAAGGTTTACAACATCAC 319
Db 108 CCAAGCCTCAGGTGGGAGAGCGGTGGCTAGTATCGACCGTAAAGGTATCAACATCAG 167
QY 320 CAAATGGTCCATCCAGACACCGGGGGGGCCAGCGGGTCATCGGGCACTACGCTGGAGAAGA 379
Db 168 CGAGTTACCGCGCGGACATCCAGGGGGCTCCGGGGTCATCAGGCCATCAGCCCGGGCAGGA 227
QY 380 TGAACGGATGCTTCGGGGCCTTCCACCCTGNACCTGGAATCGTGGGCAAGTTCCTTGA 439
Db 228 TGGCACCGATCCCTTTGTGGCCTTCCACATCAACAAGGGCCTTGTGAAGAAGTATATGAA 287
QY 440 ACCCTTGCTGATTGGTGAACTGGCCCCGGAGGAGCCAGCAGGATCACCGCAAGAACTC 499
Db 288 CTCTCTCCTGATTGGAGAACTGTCTCCAGAGCAGCCGAGCTTTGAGCCCCACCAAGATAA 347
QY 500 AAGATCACTGAGGATTCGGGGCCCTGAGGAAGAGCGCTGAGGACATGAACCTGTTCAA 559
Db 348 AGAGCTGACAGATGAGTTCCGGGAGCTGGCGGCCACAGTGGAGCGGATGGGGCTCATGAA 407
QY 560 GACCAACCAAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Db 408 GGGCAACCAATGTCTTCTCTCTGTGATCTGCTGCACTCTGCTGCTGATGCTGCAGC 467
QY 620 ATGGTTCACTGTCTTCTACTTTGGCAATGGCTGGATTCCTACCTCATCAGGCCCTTTGT 679
Db 468 CTGGCTCACCTTTGGTCTTTGGGAGCTCTTTGGCCCTCTCTCTCTCTCTCTCTCTCTCT 527
QY 680 CTTGTCTACTCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGT 739
Db 528 GCTCAGTGCAGTTTCAGGCCCAAGCTGGCTGGCTGCAACATGATTTGGGCACTGTCTGT 587
QY 740 CTACAGAAACCCAAAGTGGAAACCACTTGTCCACAAATTGCTATTTGGCCACTTAAAGGG 799
Db 588 CTTCAGCACCTCAAAGTGGAAACCATCTGCTACATCATTTTGTATTTGGCCACCTGAAGGG 647
QY 800 TGCCCTTGCCAACTGGTGGAAATCATGCCACTTCCAGCACCAAGCCAGCCTTAACATCTT 859
Db 648 GGGCCCCGCGAGTTGGTGGAAACCAATGCACTTCCAGCACCATGCCAAGCCCAACTGCTT 707
QY 860 CCACAGGATCCCGATGTGAAACATGTGCAACGTGT--TTGTTCTGGGCGAATGGCAGCC 916
Db 708 CCGCAAGACCCAGACATCAACATGATCCCTTCTTTCCTTGGGGAATCCTCTC 767
QY 917 CATCGAGTACGGCAAGAAGGTGAATAACTTGGCCCTACAATCAACAGCAGCAAGTACTT 976
Db 768 TGTGGAGCTTGGGAAAACAGAAGAAAAATATATGCGGTACAGCCACAGCAGCAAAATCTT 827
QY 977 CTTTCTGATTTGGCCCGCTGTCTATCCCCAGTATTTCCAGTACCAGATCATGAC 1036
Db 828 CTTCTTAATTTGGGCCCCAGCCTTGCTGCTCTCTACTTCCAGTGGTATATTTCTATTT 887
QY 1037 CATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGCCGCTCA 1080
Db 888 TGTTATCCAGGAAAGTGGGTGGACTTTGGCTGGATCAGCA 931

RESULT 24
US-09-439-261-5
; Sequence 5, Application US/09439261
; Patent No. 642890
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng

RESULT 24
US-09-439-261-5
; Sequence 5, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng

Db 495 GCAGCATGACTTTGGGACCTCTGGCTTTCAGACCTCAAGTGGAAACCATCTGCTACA 554
QY 773 CAAATTCGTCAFTGGCCCACTTAAAGGGTCTCTGCCAACTGGTGGAAATCATCGCACTT 832
Db 555 TCATTTTGTGATTGGCCACCTGAAGGGGCCCCGCCAGTTGGTGGAAACCATGCACTT 614
QY 833 CCAGCACCACGACCAAGCTTAACATCTCCACAAGGATCCGATGGAACATGCTGC--A 889
Db 615 CCAGCACCACGACCAAGCCCACTGCTTCGCAAGACCCAGACATCAACATGCACTCCCTT 674
QY 890 CGTGTGTTGTTCTGGGCGAATGGCAGCCCATCGATACGACGACCAAGAGAGCTGAATACCT 949
Db 675 CTTCTTTGCTTGGGAGATCCTCTCTGTGAGCTTGGGAAACAGAAAGAAAATATAT 734
QY 950 GGCCTACATCCAGCAGCAATATCTTCTGATTTGGGCGCGCTGCTCATCCCAT 1009
Db 735 GCGGTACACACCCAGCAGCAATATCTTCTTAATTTGGGCCCCCAGCGCTTCTGCTCT 794
QY 1010 GTATTTCCAGTACCAATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGCG 1069
Db 795 CTACTTCCAGTGTATATTTCTATTTTATCCAGCGAAAGAGTGGGTGGACTTGGC 854
QY 1070 CTGGGCGCTCA 1080
Db 855 CTGGATCAGCA 865

RESULT 26
US-09-439-261-35
; Sequence 35, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-04-11
; PRIOR FILING DATE: 1997-04-11
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-35

Query Match 11.0%; Score 351.8; DB 4; Length 990;
Best Local Similarity 64.7%; Pred. No. 4.4e-77;
Matches 540; Conservative 0; Mismatches 292; Indels 3; Gaps 1;

QY 200 GGGGAGGGGGCGCGGAGCGGAGGTGTGGTGGCCCACTTCACTGGGAGGATCA 259
Db 18 GGGCGCCGAGACCGCGGCTCAGGACCTTACCCCGCTTCTACCTGGGACGAGGTGGC 77

QY 260 GAAGCATAACTTGGCAGCCGACAGTGGGCTGGTCAATGACCGCAAGTTTACACATCAC 319
Db 78 CCAGCGCTCAGGTGCGAGGAGCGGTGGCTAGTGTGACCGTAAAGTGTACACATCAG 137

QY 320 CAAATGGTCCATCCAGACACCGGGGGCGGAGCGGCTCATCGGCACTACGCTGAGAGA 379
Db 138 CGAGTTACCCCGCGCATCCAGGGGGTCCCGGGTCAATCAGCCACTACGCGGGCAGGA 197

QY 380 TCCACGGATGCTTCCCGGCTTCCACCTGACCTGGAATCTGTGGGAGAGTTCTTGAA 439

Db 198 TGCCACGATCCCTTTGTGGCCTTCCACATCAACAAGGGCCTTGTGAAGAATATATGAA 257
QY 440 ACCCTCTGCTGATTGGTGAACCTGGCCCCGAGAGCCAGCCAGGACCAAGCAAGATC 499
Db 258 CTCTCTCTGATTGGAGAACTGTCTCAGAGCAGCCAGCTTTGAGCCCAACCAAGATAA 317
QY 500 AAAGATCACTGAGGACTTCCGGGCTTGAAGAGAGCGGTGAGGACATGAACCTGTTCAA 559
Db 318 AGAGCTGACAGATGAGTTCCGGGAGCTGGGGCCACAGTGGAGCGGATGGGGCTCATGAA 377
QY 560 GACCAACCAAGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Db 378 GGCACACCATGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 437
QY 620 ATGTTTCACTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679
Db 438 CTGGCTCACCTTTGGGTCTTTGGGACGTCCTTTTGGCCCTTCTCTCTCTCTCTCTCTCT 497
QY 580 CTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 739
Db 498 GCTCAGTGCAGTTTCCAGCCCGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 557
QY 740 CTACAGAAAAACCAAGTGGAAACCACTTGTCCCAAAATTCGTCAATTTGGTGGCCACTTAAAGG 799
Db 558 CTTTCCAGCATCTCAAGTGGAAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 617
QY 800 TGCTCTGCGCACTGGTGGATCATCGCCACTTCCAGCACCAGCCAGCCAGCCAGCCAGCC 859
Db 618 GGGCCCCCGGAGTTGGTGGAAACCACTGACATGCTCTCTCTCTCTCTCTCTCTCTCTCT 677
QY 860 CCACAAGGATCCCGATGTGAACATGTCTG---AGTGTGTTGTTCTGGGCGAATGGGAGCC 916
Db 678 CCGCAAGACCCAGACATCAACATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 737
QY 917 CATGAGTACGGGAGAGAGAGTGAATACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 976
Db 738 TGTGAGCTTGGGAAACAGAGAAATATATATGCTGCTCTCTCTCTCTCTCTCTCTCTCT 797
QY 977 CTTCTGATTTGGGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1031
Db 798 CTTCTTAATTTGGGCGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 852

RESULT 27
US-09-227-613-34
; Sequence 34, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-34

Query Match 11.0%; Score 351.8; DB 4; Length 990;
Best Local Similarity 64.7%; Pred. No. 4.4e-77;
Matches 540; Conservative 0; Mismatches 292; Indels 3; Gaps 1;

QY 200 GGGGAGGGGGCGCGGAGCGGAGGTGTGGTGGCCCACTTCACTGGGAGGATCA 259
Db 18 GGGCGCCGAGACCGCGGCTCAGGACCTTACCCCGCTTCTACCTGGGACGAGGTGGC 77

260	GAAGCATAACTGGCCCAACGACAGTGGGCTGGTCATTGACCGCAAGGTTTACAAACATCAC	319	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
78	CCAGCGCTCAGGGTGCAGGACGCGGTGGCTAGTGATCGACCGCTAAGGTGTACAAACATCAG	137	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
320	CAAAATGGTCCATCCAGACACCCGGGGGGCCAGCGGGTTCATCGGCGACTACGCTGGAGAAGA	379	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
138	CGAGTTCAACCGCGCGGCTCCAGGGGGCTCCCGGGTTCATCAGCCACTAGCCGGCGCAGA	197	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
380	TGCAACGGATGCTTCGCGGCTTCACACCTGACCTCGAAATTCGTGGGCGAAGTTCTTGAA	439	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
198	TGCCACGGATCCCTTTGTGGGCTTCACATCAACAAGGGCTTTGTGAAGAAGTATATGAA	257	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
440	ACCCCTGCTGATTTGGTGAACCTGGCCCGGAGAGGCCAGCAGCACCGCAAGAACTC	499	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
258	CTCTCTCTGATTTGGAGAACTGTCTCCAGAGCAGCCACGCTTTGAGCCCAACCAAGATAA	317	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
500	AAAGATCACTGAGGACTTCGCGGCCCTGAGGAAGAGCGCTGAGGACATGAACCTGTTCAA	559	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
318	AGAGCTGACAGATGAGTTCCGCGAGCTGCGGGCCACAGTGGAGCGGATGGGCTCATGAA	377	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
560	GACCAACACAGTGTTCCTTCCTCCTCGTGGCCACATCATCGCCTGGAGAGCATTCG	619	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
378	GGCCAAACCATGTCTCTTCCTGCTGACCTGCTGCACATCTTGCTGCTGGATGCTGCAC	437	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
620	ATGGTTCACTGTTCTCTACTTTTGGGAATGGCTGGAATTCCTACCCCTCATCAGCGCCTTGT	679	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
438	CTGGCTCACCCCTTTGGGTCCTTTGGGAGCGCTCTTTTGCCCTCTCTCTGCTGCGGTGT	497	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
680	CCTTGCTACTCTCAGGCCCAAGCTGGATGGCTGCAACATGATATGGCCACCTGTCGT	739	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
498	GCTCAGTGCAGTTCAAGGCCCAGGCTGGCTGGCTGCACATGACTTTGGGCACTGTCGT	557	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
740	CTACAGAAAACCAAGTGGAAACCACTTTGCCAACAATTCGTCAATTTGGGCACTTAAAGG	799	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
558	CTTCAGCACTCAAAAGTGGAAACCACTGCTACATCATTTTTGATTTGGCCACCTGAAGG	617	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
800	TGCTCTGCAACTGGTGGATCATCGGCACCTCCAGCACCGCCAAAGCCTAACATCTT	859	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
618	GGCCCCCGCCAGTTGGTGGAAACCATGCACTTCCAGCACATGCCAAGCCCAACTGCTT	677	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
860	CCACAAGGATCCCGATGTAACATGCTGCG --- AGTGTTTGTCTGGGGGAATGGCAGCG	916	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
678	CGCGAAAGACCCAGACATCAACATGCAATCCCTCTTCTTTGCTTTGGGAAGATCCCTCTC	737	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
917	CATCGAGTACGGCAAGAGAAGCTGAATACCTGCCCTACAATCAACAGCAGCAATCACTT	976	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
738	TGTGGAGCTTGGAAACAGAGAAAATAATATGCCGTACAAACCAACGACCAATACTT	797	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
977	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC	1031	CTTCTGATATGGGCCCGCGCTGCTCATCCCACTGATATTTCCAGTACCATCATC
798	CTTCTGATATGGGCCCGCGCTGCTGCTCTCTACTTGCAGTGGTATATTTTC	852	CTTCTGATATGGGCCCGCGCTGCTGCTCTCTACTTGCAGTGGTATATTTTC

RESULT 28
US-09-439-261-4
; Sequence 4, Application US/09439261

```

; Patent No. 6428990
;
; GENERAL INFORMATION:
;
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Faridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
;
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
;
; FILE REFERENCE: 6295, US, P.2
;
; CURRENT APPLICATION NUMBER: US/09/439,261
;
; CURRENT FILING DATE: 1999-11-12
;
; PRIOR APPLICATION NUMBER: US 08/833,610
;
; PRIOR FILING DATE: 1997-04-11
;
; PRIOR APPLICATION NUMBER: PCT/US98/07422
;
; PRIOR FILING DATE: 1998-04-10
;
; PRIOR APPLICATION NUMBER: US 09/227,613
;
; PRIOR FILING DATE: 1999-01-08
;
; NUMBER OF SEQ ID NOS: 60

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? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 4
? LENGTH: 304
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-439-261-4

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Query Match	9.58;	Score	302.4;	DB	4;	Length	304;
Best Local Similarity	99.7%;	Pred. No.	3.9e-65;				
Matches	303;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
QY	630	GTCTTCTACTTTGGCAATGGCTGGATTCTACCTCATCAGCGCCTTTGTCTCTGCTACCC	689				
Db	1	GTCTTTTACTTTGGCAATGGCTGGATTCTACCTCATCAGCGCCTTTGTCTCTGCTACCC	60				
QY	690	TCTCAGGCCCCAAGCTGCATGGCTGCAACATGATTATGGCCACCTCTGTCTACAGAAA	749				
Db	61	TCTCAGGCCCCAAGCTGCATGGCTGCAACATGATTATGGCCACCTCTGTCTACAGAAA	120				
QY	750	CCCAAGTGGAAACCACTTTGTTCACAAATTGGCATATGGCCACTTAAAGGGTGCTCTGCCC	809				
Db	121	CCCAAGTGGAAACCACTTTGTTCACAAATTGGCATATGGCCACTTAAAGGGTGCTCTGCCC	180				
QY	810	AACTCGTGGGAATCATCGCCACTTCCAGCACCGCCAGCCCTTAACATCTTCCACAAGAT	869				
Db	181	AACTCGTGGGAATCATCGCCACTTCCAGCACCGCCAGCCCTTAACATCTTCCACAAGAT	240				
QY	870	CCCGATGTGAACATGTGCAAGTGTGTTGTCTTGGGCGAATGGCAGCCCATCGATACGCC	929				
Db	241	CCCGATGTGAACATGTGCAAGTGTGTTGTCTTGGGCGAATGGCAGCCCATCGATACGCC	300				
QY	930	AAGA	933				
Db	301	AAGA	304				

RESULT 29
US-09-227-613-4
; Sequence 4, Application US/09227613A

Patent No. 6432684
GENERAL INFORMATION:
APPLICANT: MUKERJI, Pradip
APPLICANT: LEONARD, Amanda E.
APPLICANT: HUANG, Yung-Sheng
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.PI
CURRENT APPLICATION NUMBER: US/09/227,613A
CURRENT FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: 08/833,610
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 42
SOFTWARE: SEQ ID for Windows Version 3.0

	Query Match	9.5%	Score 302.4;	DB 4;	Length 304;
	Best Local Similarity	99.7%;	Pred. No. 3.9e-65;		
	Matches 303;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	630	GTCTTCTACTTTGGCAATGCTGGATTCTACCCCTCATCAGGCGTTTGTCTTGTCTTAC	689		
Db	1	GTCTTTTACTTTGGCAATGGCTGGATTCTACCCCTCATCAGGCGTTTGTCTTGTCTTAC	60		
Qy	690	TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTCTCTGTCTACAGAAA	749		
Db	61	TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTCTCTGTCTACAGAAA	120		
Qy	750	CCCAAGTGGAAACCACTTGTGCCAAATTCGTATTGGCCACTTAAAGGGTGCCCTCTGCC	809		
Db	121	CCCAAGTGGAAACCACTTGTGCCAAATTCGTATTGGCCACTTAAAGGGTGCCCTCTGCC	180		

QY 810 AACTGGTGAATATCCCACTTCCAGACACAGCCAGGCTTAACATCTTCCACAGGAT 869
DB 181 AACTGGTGAATATCCCACTTCCAGACACAGCCAGGCTTAACATCTTCCACAGGAT 240
QY 870 CCCGATGTAACATGCTGCAGCTGTTTGTCTGGCGAATGGCAGCCCATCGAGTACGGC 929
DB 241 CCCGATGTAACATGCTGCAGCTGTTTGTCTGGCGAATGGCAGCCCATCGAGTACGGC 300
QY 930 AAGA 933
DB 301 AAGA 304

RESULT 30
US-09-439-261-37
; Sequence 37, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-37

Query Match 8.0%; Score 253.8; DB 4; Length 473;
Best Local Similarity 71.6%; Pred. No. 4.2e-53;
Matches 333; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1050 AAGAACTGGGTGAGCTGGCCCTGAGCTACTACATCCGGTCTTCTCATCACCTAC 1109
DB 9 AAGAACTGGGTGAGCTGGCCCTGAGCTACTACATCCGGTCTTCTCATCACCTAT 68
QY 1110 ATCCCTTTCTACGGCATCTGGAGCCCTCTTTCTCTCAACTTTCATCAGGTTCTCTGGAG 1169
DB 69 GTGCCACTATTGGGCTGAAGCCTTCTGGGCCCTTTCTTTCATAGTCAGGTTCTCTGGAA 128
QY 1170 AGCCACTGGTTGTGGTGCACAGATGAATACATCGTCATGGAGATTGACCAAGAG 1229
DB 129 AGCAACTGGTTGTGGTGCACAGATGAATACATCGTCATGGAGATTGACCAAGAG 188
QY 1230 GCTACCGTGAATGCTTCACTAGTACAGCCAGCTGACAGCCACTTCCCAAGTGTGAGCAGTCTTC 1289
DB 189 CGGAACATGAGTGGTTTCCACCCAGCTTCCAGTGTGAGCAGTCTTCCTCCAGC 248
QY 1290 TTCAACGACTGGTTGAGTGGACACCTTAACCTTCCAGATTGACAGCAGCTCTTCCCCACC 1349
DB 249 TTCAATGACTGGTTGAGTGGACACCTTAACCTTCCAGATTGAGCAGCAGCTCTTCCCCACC 308
QY 1350 ATGCCCCGGCACAACTTACCAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 1409
DB 309 ATGCTCTGCACAAATACCAAGTGGTCCCTGGTGCAGTCTTGTGTGCCAAGGCT 368
QY 1410 GGCAATTGAATACAGAGAGCCGCTTACAGAGGCGCTGCTGGAGCATATCAGGTCCCTG 1469
DB 369 GGCAATAGATACAGTCCAGAGCCCTGCTGTGAGCCTTGGCCGACATCATCCACTCACTA 428

RESULT 32
US-09-439-261-3
; Sequence 3, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng

QY 1470 AAGAACTGGGAAGCTGTGCTGGAGCCCTACCTTACAAATGA 1514
DB 429 AAGAACTGGGAAGCTGTGCTGGAGCCCTTATCTTCCCAATAA 473

RESULT 31
US-09-227-613-36
; Sequence 36, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-227-613-36

Query Match 8.0%; Score 253.8; DB 4; Length 473;
Best Local Similarity 71.6%; Pred. No. 4.2e-53;
Matches 333; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1050 AAGAACTGGGTGAGCTGGCCCTGAGCTACTACATCCGGTCTTCTCATCACCTAC 1109
DB 9 AAGAACTGGGTGAGCTGGCCCTGAGTATACCTTCTAGTCCGCTTCTTCTCATCTAT 68
QY 1110 ATCCCTTTCTACGGCATCTGGAGCCCTCTTTCTCTCAACTTTCATCAGGTTCTCTGGAG 1169
DB 69 GTGCCACTATTGGGCTGAAGCCTTCTGGGCCCTTTCTTTCATAGTCAGGTTCTCTGGAA 128
QY 1170 AGCCACTGGTTGTGGTGCACAGATGAATACATCGTCATGGAGATTGACCAAGAG 1229
DB 129 AGCAACTGGTTGTGGTGCACAGATGAATACATCGTCATGGAGATTGACCAAGAG 188
QY 1230 GCTACCGTGAATGCTTCACTAGTACAGCCAGCTGACAGCCACTTCCCAAGTGTGAGCAGTCTTC 1289
DB 189 CGGAACATGAGTGGTTTCCACCCAGCTTCCAGTGTGAGCAGTCTTCCTCCAGC 248
QY 1290 TTCAACGACTGGTTGAGTGGACACCTTAACCTTCCAGATTGACAGCAGCTCTTCCCCACC 1349
DB 249 TTCAATGACTGGTTGAGTGGACACCTTAACCTTCCAGATTGAGCAGCAGCTCTTCCCCACC 308
QY 1350 ATGCCCCGGCACAACTTACCAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 1409
DB 309 ATGCTCTGCACAAATACCAAGTGGTCCCTGGTGCAGTCTTGTGTGCCAAGGCT 368
QY 1410 GGCAATTGAATACAGAGAGCCGCTTACAGAGGCGCTGCTGGAGCATATCAGGTCCCTG 1469
DB 369 GGCAATAGATACAGTCCAGAGCCCTGCTGTGAGCCTTGGCCGACATCATCCACTCACTA 428

; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-09-227-6113-3
 Query Match 7.2%; Score 230.4; DB 4; Length 655;
 Best Local Similarity 69.1%; Pred. No. 2.8e-47;
 Matches 329; Conservative 0; Mismatches 146; Indels 1; Gaps 1;
 QY 1078 TCAGCTACTACATCCGGTTCCTTCATCACCTACATCCCTTTTACGGCATCTCTGGAGCCC 1137
 Db 1 TTACCTTCTACGTCGGCTCTTCTCCTCACCTATGTGCCACTATTGGGGCTT-GAAAGCTTCC 59
 QY 1138 TCCTTTTCTCCTCAACTTCATCAGGTTCTCTGAGAGCCACTGGTTTGTGTGGGTACACAGA 1197
 Db 60 TGGGCGCTTTTCTCATAGTCAGGTTCTTGGAAAGCACTGGTTTGTGTGGGTACACAGA 1119
 QY 1198 TGAATCACATCGTTCATGGAAGATTGACAGAGGCCCTACCGTGACTGTTTCACTAGCCAGC 1257
 Db 120 TGAACCATATTCCATGSCATTTGATCATGACCGGAACATGGACTGGGTTTCACCCAGC 179
 QY 1258 TGACAGCCACCTTCAACGCTGGAGCAGTCCCTTCTTCAACGACTGGTTTCACTGGGACCTTTA 1317
 Db 180 TCCAGGCCACATGCATGTCACAACTCTCGCAAGTCTGCTTCAATGACTGTTTCACTGGGACCTCA 239
 QY 1318 ACTTCAGATTGAGCAGCACCTCTTCCACACCATGCCCGGACCACTTACACAAAGATCG 1377
 Db 240 ACTTCCAGATTGAGCAGCACCTCTTTCCTCCACGATGCTCGACACAACTTACCAAAAGTGG 239
 QY 1378 CCCCCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACCAAGAGAACCCGCTAC 1437
 Db 300 CTCCTCTGTGTCAGTCTCTGTGTGCCAAGCATGGCATAGAGTACCAAGTCCCAAGCCCTGC 359
 QY 1438 TGAGGGCCCTGCTGGACATCATCAGTCCCTGAAAGAGTCTGGGAGCTGTGCTGGAGC 1497
 Db 360 TGTGAGCCTTTCGCGGACATCATCACTCACTAAAGAGTCAAGGAGTCAAGGAGCTCTGCTAGATG 419
 QY 1498 CCTACCTTCAAAATGAAGCCACAGCCCGGACACCGTGGGAAAGGGGTGCAGG 1553
 Db 420 CCTATCTTCAACATAACACAGCCACCTGCTCCAGTCTGGAAGAGAGAGGAGGAAG 475
 RESULT 34
 US-09-439-261-38
 ; Sequence 38, Application US/09439261
 ; Patent No. 6428990
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Paridip
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295.US.P2
 ; CURRENT APPLICATION NUMBER: US/09/439,261
 ; CURRENT FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: US 08/833,610
 ; PRIOR FILING DATE: 1997-04-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422
 ; PRIOR FILING DATE: 1998-04-10
 ; PRIOR APPLICATION NUMBER: US 09/227,613
 ; PRIOR FILING DATE: 1999-01-08
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 449
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (5)...(5)
 ; OTHER INFORMATION: k = g or t/u at position 5
 ; NAME/KEY: misc.feature
 ; LOCATION: (5)...(6)
 ; OTHER INFORMATION: m = a or c at position 6

US-09-439-261-38		7.1%; Score 226.8; DB 4; Length 449;	
Query Match		71.0%; Pred. No. 1.8e-46;	
Best Local Similarity		0; Mismatches 127; Indels 1; Gaps 1;	
Matches 314; Conservative			
QY	1078	TGAGTACTACATCCGGTCTTTCATACCTTACATCCCTTTCACGGCATCTCGGAGCCC	1137
DB	7	TTACCTTCTAGCTCCGCTTCTTCTCATATGTCACCTATTGGGGCT-GAAAGCTTCC	65
QY	1138	TCCTTTTCTCAACTTCATCAGGTCTCTGGAGAGCCACTGGTTTGTGGGTACACAGA	1197
DB	66	TGGGCTCTTCTTTCATAGTCAGGTCTCTGGAAGCAACTGGTTTGTGGGTACACAGA	125
QY	1198	TGAATCATCTGTCATCGATGACAGGAGGCTACCGTACTGCTCAGTAGCCAGC	1257
DB	126	TGAACCATATTCCTATGATCATACCGGACATGACTGGTTTCCACCCAGC	185
QY	1258	TGACAGCCACTGCAACGTGGAGAGTCCTTCTTCAACGACTGGTTTCAAGTGACACTTA	1317
DB	186	TCCAGGCCACATGCAATGTCCCAAGTCTGCTTCAATGACTGGTTTCAAGTGACACTTA	245
QY	1318	ACTTCCAGATTGAGCACCACCTCTTCCACCACATGCTCCCGGCACTTACACAAGATCG	1377
DB	246	ACTTCCAGATTGAGCACCACCTCTTCCACCAGATGCTCCGACAAATACCAAAAGTGG	305
QY	1378	CCCGCTGGTGAAGTCTCTATGTGCGAAGCATGTCATGATACGAGAGAGCCGCTAC	1437
DB	306	CTCCCTGGTGCAGTCTCTGTGTGCCAAGCATGTCATGATACGAGAGAGCCGCTAC	365
QY	1438	TGAGGGCCCTGCTGCATCATCATCAGGTCCTCTGAAGAAAGTCTGGGAAGCTGTGGTGAAG	1497
DB	366	TGTCAGCCTTCCGCGACATCATCCACTCCTAAAGGAGTCAGGCGAGCTCTGGCTAGATG	425
QY	1498	CCTACCTTCAAAATGAAGCCA	1519
DB	426	CCTATCTTCAACAATAACAACA	447
RESULT 36			
US-09-172-108-35			
; Sequence 35, Application US/09172108			
; Patent No. 6160104			
; GENERAL INFORMATION:			
; APPLICANT: Cunningham, Mary Jane			
; APPLICANT: Zweiger, Gary B.			
; APPLICANT: Panzer, Scott R.			
; APPLICANT: Seilhammer, Jeffrey J.			
; TITLE OF INVENTION: MARKERS FOR PEROXISOMAL PROLIFERATORS			
; FILE REFERENCE: PA-0012 US			
; CURRENT APPLICATION NUMBER: US/09/172,108			
; CURRENT FILING DATE: 1998-10-13			
; NUMBER OF SEQ ID NOS: 56			
; SOFTWARE: PERL Program			
; SEQ ID NO 35			
; LENGTH: 259			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: unsure			
; LOCATION: 219			
; OTHER INFORMATION: a o r g o r c o r t, unknown, or other			
; FEATURE:			
; OTHER INFORMATION: 700483475H1			
; US-09-172-108-35			
Query Match		6.2%; Score 198; DB 3; Length 259;	
Best Local Similarity		87.6%; Pred. No. 1.8e-39;	
Matches 227; Conservative		0; Mismatches 31; Indels 1; Gaps 1;	
QY	631	TCTTCTACTTTGGCAATGGCTGATCTTACCTCATACGCGCTTGTCTTGTACTCT	690
DB	2	TCTCGTACTTGGCAATGGCTGATCTTACCTCATACGCGCTTGTCTTGTACTCT	61
QY	691	CTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAGAAAC	750
DB	62	CCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTTCTGTCTATAGAAAT	121
QY	751	CCAAGTGGAAACCACTTGTCCCAAAATTCGTATGGCCACTTAAGGGTGTCTGTGCA	810
DB	122	CCATATGGAACCACTTGTCCCAAAATTCGTATGGCCACTTAAGGGTGTCTGTGCA	181
QY	811	ACTGGTGGATCATGCGCACTTCCAGCACACAGCCCAAGCTTAACATCTTCCCAAGGATC	870
DB	182	ACTGGTGGAAACCACTTGTCCCAAAATTCGTATGGCCACTTAAGGGTGTCTGTGCA	240
QY	871	CCGATGTGAACATGCTGTCA	889
US-09-227-613-37			
; Sequence 37, Application US/09227613A			
; Patent No. 6432684			
; GENERAL INFORMATION:			
; APPLICANT: MUKERJI, Pradip			
; APPLICANT: LEONARD, Amanda E.			
; APPLICANT: HUANG, Yung-Sheng			
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF			
; FILE REFERENCE: 6295.US.P1			
; CURRENT APPLICATION NUMBER: US/09/227,613A			
; CURRENT FILING DATE: 1999-01-08			
; PRIOR APPLICATION NUMBER: 08/833,610			
; PRIOR FILING DATE: 1997-04-11			
; NUMBER OF SEQ ID NOS: 42			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 37			
; LENGTH: 449			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-09-227-613-37			
Query Match		7.1%; Score 226.8; DB 4; Length 449;	
Best Local Similarity		71.0%; Pred. No. 1.8e-46;	
Matches 314; Conservative		0; Mismatches 127; Indels 1; Gaps 1;	
QY	1078	TGAGTACTACATCCGGTCTTTCATACCTTACATCCCTTTCACGGCATCTCGGAGCCC	1137
DB	7	TTACCTTCTAGCTCCGCTTCTTCTCATATGTCACCTATTGGGGCT-GAAAGCTTCC	65
QY	1138	TCCTTTTCTCAACTTCATCAGGTCTCTGGAGAGCCACTGGTTTGTGGGTACACAGA	1197
DB	66	TGGGCTCTTCTTTCATAGTCAGGTCTCTGGAAGCAACTGGTTTGTGGGTACACAGA	125

Db 287 AACTTCAGATCGAGCACACCTCTTCCCGAGGATCCGAGACACAACTACAGCGGGTG 228
Qy 1377 GCGCCGCTGGTGAAGTCTCTATGTGCAAGCATGGCAATTGAATACAGGAGAGCGCTA 1436
Db 227 GCGCCGCTGGTGAAGTCTCTATGTGCAAGCATGGCAATTGAATACAGGAGAGCGCTT 168
Qy 1437 CTGAGGCGCTCTGAGCATCATCAGGTCCCTGAAGAAGTCTGGGAAGCTGTGGCTGGAC 1496
Db 167 CTCACCGCGCTGGTGGACATCGTCAGTCCCGAAGAAGTCTGGTGACATCTGGCTGGAC 108
Qy 1497 GCCTACCTTCACAAATGAAGCCACAGCCCCCGG 1530
Db 107 GCCTACCTTCATCAGTGAAGGCAACACCCAGGCG 74

RESULT 40
US-09-440-315A-3/C
; Sequence 3, Application US/09440315A
; Patent No. 6551812
; GENERAL INFORMATION:
; APPLICANT: Gould-Rothberg, Bonnie
; TITLE OF INVENTION: Compositions and Methods Relating to the
; TITLE OF INVENTION: Peroxisomal Proliferator Activated Receptor-Alpha
; TITLE OF INVENTION: Mediated Pathway
; FILE REFERENCES: 15966-533
; CURRENT APPLICATION NUMBER: US/09/440,315A
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/108,293
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/126,465
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 253
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: g0m0_173.1
; NAME/KEY: misc_feature
; LOCATION: (11)...(204)
; OTHER INFORMATION: wherein n may be a or t or g or c
US-09-440-315A-3

Query Match 3.2%; Score 102; DB 4; Length 253;
Best Local Similarity 65.3%; Pred. No. 7.4e-16;
Matches 147; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
Qy 334 AGCACCGGGGGGCGAGCGGCTCATCGGGCACTACGCTGGAGAGATGCAACGATGCCT 393
Db 225 ACCACCGGGAGGCTCCCGGTGATCAGCCACTACGCTGGTGGATGCCAGGATCCT 166
Qy 394 TCCGCGCTTCCACCTGACCTGAATTCGTGGGCAAGTCTTGAACCCCTGCTGATTG 453
Db 165 TTGTGGCATTCACATTAAAGGGCTTGTGAGAAAGTATATGAACCTCTCTTCTGATTG 106
Qy 454 GTGACTGCGCCCGGAGAGCGCCAGCGGACCGCAAGCAACTCAAGATCACTGAGG 513
Db 105 GAGAGCTAGCTCCGGAGAGCGCCAGCTTTGAACCCACCAAGATAAGCGCTNACTGATG 46
Qy 514 ACTTCGGGGCCCTGAGGAAGACGGCTGAGGACATGAACCTGTTCA 558
Db 45 AATTCGGGGGCTGGGGCCACAGTGGAGCGAATNGSCCTCATGA 1

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Job time : 157 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2003, 18:18:30 ; Search time 73 Seconds
(without alignments)

2684.577 Million cell updates/sec

Title: US-09-719-601-5

Perfect score: 2438

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Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued Patents NA -QWMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=BITS -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFWT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09719601@cgn_1_44 @runat 09122003 094909 21199 -NCPUS=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1935	79.4	2257	4	US-09-439-261-8
2	1935	79.4	2257	4	US-09-227-613-8
3	1646	67.5	1843	4	US-09-439-261-7
4	1646	67.5	1843	4	US-09-227-613-7
5	1560.5	64.0	1717	4	US-09-048-888-2
6	1515	62.1	1928	4	US-09-048-888-4
7	1508	61.9	1335	4	US-09-439-261-1
8	1508	61.9	1335	4	US-09-227-613-1
9	1348	55.3	1686	4	US-09-439-261-6
10	1348	55.3	1686	4	US-09-227-613-6
11	1103	45.2	864	4	US-09-439-261-12
12	1103	45.2	864	4	US-09-227-613-13

13	960	39.4	990	4	US-09-439-261-35	Sequence 35, Appl
14	960	39.4	990	4	US-09-227-613-34	Sequence 34, Appl
15	933	38.3	960	4	US-09-439-261-36	Sequence 36, Appl
16	933	38.3	960	4	US-09-227-613-35	Sequence 35, Appl
17	923	37.9	918	4	US-09-439-261-5	Sequence 5, Appl
18	923	37.9	918	4	US-09-227-613-5	Sequence 5, Appl
19	834	34.2	446	4	US-09-389-681-425	Sequence 425, App
20	834	34.2	446	4	US-09-620-405B-425	Sequence 425, App
21	834	34.2	446	4	US-09-433-826B-425	Sequence 425, App
22	834	34.2	446	4	US-09-604-287A-425	Sequence 425, App
23	834	34.2	456	4	US-09-389-681-313	Sequence 313, App
24	834	34.2	456	4	US-09-620-405B-313	Sequence 313, App
25	834	34.2	456	4	US-09-339-338-313	Sequence 313, App
26	834	34.2	456	4	US-09-433-826B-313	Sequence 313, App
27	834	34.2	456	4	US-09-604-287A-313	Sequence 313, App
28	620	25.4	473	4	US-09-439-261-37	Sequence 37, Appl
29	620	25.4	473	4	US-09-227-613-36	Sequence 36, Appl
30	585	24.0	304	4	US-09-439-261-4	Sequence 4, Appl
31	585	24.0	304	4	US-09-227-613-4	Sequence 4, Appl
32	566	23.2	449	4	US-09-439-261-38	Sequence 38, Appl
33	566	23.2	449	4	US-09-227-613-37	Sequence 37, Appl
34	566	23.2	655	4	US-09-439-261-3	Sequence 3, Appl
35	566	23.2	655	4	US-09-227-613-3	Sequence 3, Appl
36	459	18.8	1617	2	US-08-834-655-1	Sequence 1, Appl
37	459	18.8	1617	3	US-08-834-033A-1	Sequence 1, Appl
38	459	18.8	1617	3	US-09-363-574-1	Sequence 1, Appl
39	459	18.8	1617	4	US-09-363-526-1	Sequence 1, Appl
40	459	18.8	1617	4	US-09-330-235-17	Sequence 17, Appl
41	435.5	17.9	1684	2	US-08-831-570-1	Sequence 1, Appl
42	435.5	17.9	1684	2	US-08-831-575-1	Sequence 1, Appl
43	435.5	17.9	1685	1	US-08-366-779-4	Sequence 4, Appl
44	435.5	17.9	1685	1	US-08-789-936-4	Sequence 4, Appl
45	435.5	17.9	1685	4	US-08-934-254-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-439-261-8
; Sequence 8, Application US/09439261
; Patent No. 6438990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2257
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-8

Alignment Scores:
Pred. No.: 1.96e-215 Length: 2257
Score: 1935.00 Matches: 352
Percent Similarity: 88.84% Conservative: 30
Best Local Similarity: 81.86% Mismatches: 44
Query Match: 79.37% Indels: 4
DB: 4 Gaps: 2

US-09-719-601-5 (1-444) x US-09-439-261-8 (1-2257)

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Qy 375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHis 394
Db 1087 TTCAGTGAGACACCTTAACCTTCAGATTGAGCACACACCTCTCCACCACCATCCCGCGCAC 1146
Qy 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
Db 1147 NACTTACACAAGATCGCCCGCTGGTGGAAGTCTCTATGTGCCAAGCATGGCATTGAATAC 1206
Qy 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGly 434
Db 1207 CAGGAGAAGCGCTACTGTAGGCGCCCTGTGGACATCATCAGATCCCTGAGAAAGTCTGGG 1266
Qy 435 LysLeuTyrLeuAspAlaTyrLeuHisLys 444
Db 1267 AAGCTGTGGTGGAGCGCTACCTTCACAAA 1296

RESULT 2
US-09-227-613-8
; Sequence 8, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: NUKERJTI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-8

Alignment Scores:
Pred. No.: 1,96e-215 Length: 2257
Score: 1935.00 Matches: 352
Percent Similarity: 88.84% Conservative: 30
Best Local Similarity: 91.86% Mismatches: 44
Query Match: 79.37% Indels: 4
DB: Gaps: 2

US-09-719-601-5 (1-444) x US-09-227-613-8 (1-2257)
Qy 19 ProThr-----PheSerTyrGluGluIleGlnLysHisAsnLeuArgThrAspSer 35
Db 7 CTATCCCGCGCTACTTCACTGGACGAGGTGGCCAGCGCTCAGGTGGCGAGAGCGG 66
Qy 36 GlyLeuValIleAspArgLysValTyrAsnIleThrLysTyrSerIleGlnHisProGly 55
Db 67 TGGCTAGTGTATCGACCGTAGGTGTACAACATCAGCGAGTTCAACCGCGCATCCAGGG 126
Qy 56 GlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
Db 127 GGCTCCGGGTCAACCCACTACGCGCGGCGAGGATGCCACGGATCCCTTTGTGCGCTTC 186
Qy 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95
Db 187 CACATCAACAAGCGCCCTTGTGAAGAAGTATATGAACCTCTCTCTGATTGGAGAACTGTCT 246
Qy 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115
Db 247 CCAGACGAGCCGCTTTGAGCCCAACCAAGATAAAGAGCTGCACAGATGAGTTCGGGAG 306
Qy 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135
Db 307 CTCGCGGGCCAGTGGAGCGGATGGGGCTCATGAAGGCCCAACCATGTCTCTTCTCTGCTG 366
Qy 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTyrPheThrValPheTyrPheGly 155

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Db 661 TTCAACGACTGGTTCTAGTGGACACCTTAATCTCCAGATTGAGCACCACCTCTTCCCCACC 720
 Qy 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuValAlaLysHis 410
 Db 721 ATGCCCGGACAACTTACACAGATGCGCCGCTGGTGAATCTCTATGTGCCAAGCAT 780
 Qy 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleLeuArgSerLeu 430
 Db 781 GGCATTGAATACAGGAGAGCCGCTACTGAGGCGCCCTGCTGGACATCATCAGGTCCCTG 840
 Qy 431 LysLysSerGlyLysLeuTyrLeuAspAlaTyrLeuHisLys 444
 Db 841 AAGAGCTGGGAGCTGTGGCTGGAGCGCTACTTCCACAAA 882

RESULT 4

US-09-227-613-7
 ; Sequence 7, Application US/09227613A
 ; Patent No. 6432684
 ; GENERAL INFORMATION:
 ; APPLICANT: MUKERJI, Pradip
 ; APPLICANT: LEONARD, Amanda E.
 ; APPLICANT: HUANG, Yung-Sheng
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295-US.P1
 ; CURRENT APPLICATION NUMBER: US/09/227,613A
 ; CURRENT FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: 08/833,610
 ; PRIOR FILING DATE: 1997-04-11
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 1843
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-09-227-613-7

Alignment Scores:
 Pred. No.: 7,16e-182 Length: 1843
 Score: 1645.00 Matches: 294
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 67.51% Indels: 0
 DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-227-613-7 (1-1843)

Qy 151 ValPheTyrPheGlyAsnGlyTyrIleProThrLeuIleThrAlaPheValLeuAlaThr 170
 Db 1 GTCITTTACTTGGCAATGGCTGGATTCCTACCTTCAACGGCCCTTTGTCTTGTCTACC 60
 Qy 171 SerGlnAlaGlnAlaGlyTyrLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
 Db 61 TCTCAGGCCCAAGCTGGATGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 120
 Qy 191 ProLysTyrAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
 Db 121 CCCAAGTGAACACCTTGTCCACAAATTTGTCTATGGCCACCTTAAGGTGGCTCTGCC 180
 Qy 211 AsnTyrPheAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
 Db 181 AACTGGTGAATCATCGCACTTCCAGCAGCAGCCCAAGCCTAACATCTTCCACAGGAT 240
 Qy 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTyrGlnProIleGluTyrGly 250
 Db 241 CCCGATGTGAACATGCTGCAGCTTTTGTCTGGCGAATGGCAGCCCATCGATGAGGC 300
 Qy 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
 Db 301 AAGAAGAGAGCTGAATACTCCCTTACAATCACCAGCAGCAATACTTCTCTCTGATTGGG 360
 Qy 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
 Db 361 CCGCGCTGCTCATCCCATGTATTTTCAGTACCATCATCATGACCATGATGCTTCAT 420

Qy 291 LysAsnTyrValAspLeuAlaTyrAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
 Db 421 AAGAACTGGGTGGACCTGGCCCTGGCCCTGAGCTACTACATCCGGTTCTTTCATCACCTAC 480
 Qy 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
 Db 481 ATCCCTTTTCTACGGGATCTCTGGAGCCCTCTCTTCTTCTCAACTTCATCAGGTTCTCGAG 540
 Qy 331 SerHisTyrPheValTyrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
 Db 541 AGCCACTGGTTGTGGGTCAACACAGATGAATCACATCGTCGTGAGATTGACAGGAG 600
 Qy 351 AlaTyrArgAspTyrPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
 Db 601 GCTTACCGTGAAGTGTTCAGTAGCCAGCTGACAGCCACCTGCAACGTGAGCAGTCTTTC 660
 Qy 371 PheAsnAspTyrPheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThr 390
 Db 661 TTCAACGACTGGTTCTAGTGGACACCTTAATCTCCAGATTGAGCACCACCTCTTCCCCACC 720
 Qy 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuValAlaLysHis 410
 Db 721 ATGCCCGGACAACTTACACAGATGCGCCGCTGGTGAATCTCTATGTGCCAAGCAT 780
 Qy 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleLeuArgSerLeu 430
 Db 781 GGCATTGAATACAGGAGAGCCGCTACTGAGGCGCCCTGCTGGACATCATCAGGTCCCTG 840
 Qy 431 LysLysSerGlyLysLeuTyrLeuAspAlaTyrLeuHisLys 444
 Db 841 AAGAGCTGGGAGCTGTGGCTGGAGCGCTACTTCCACAAA 882

RESULT 5

US-09-048-888-2
 ; Sequence 2, Application US/09048888
 ; Patent No. 6492108
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Dr.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/048,888
 ; FILING DATE: Filed Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cerrone, Michael C.
 ; REGISTRATION NUMBER: 39,132
 ; REFERENCE/DOCKET NUMBER: PF-0494 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1717 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: ENDANOT01
CLONE: 2451043
US-09-048-888-2

Alignment Scores:

Pred. No.: 5,986-172 Length: 1717
Score: 1560.50 Matches: 278
Percent Similarity: 76.23% Conservatives: 62
Best Local Similarity: 62.33% Mismatches: 103
Query Match: 64.01% Indels: 3
DB: 4 Gaps: 2

US-09-719-601-5 (1-444) x US-09-048-888-2 (1-1717)

QY 1 MetGlyLysGlyGlyAsnGlnGly-----GluGlyAlaAlaGluAArgGluValSerVal 18
DB 75 ATGGCGCGGCTGGGGAGCGCGGAGCGCGGAGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 134
QY 19 ProThrPheSerTrpGluGluGlnGlyHisAsnLeuA-gThrAspSerGlyLeuVal 38
DB 135 CCCACCTTCTGCTGGAGCGATCCGCGCGACGACCGCGCGGCGGAGCGCGGAGCGCGGAGCGCG 194
QY 39 IleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArg 58
DB 195 ATCGAGCGCGGCTACGACATCAGCGCTGGGCGACGACCGCGCGGAGCGCGGAGCGCGGAGCGCG 254
QY 59 ValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78
DB 255 CTCATCGCGCACCGCGCGCTGAGGACCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCG 314
QY 79 LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGlu 98
DB 315 CTCATTTTGTGGCAAGTTCCTACAGCCCTGTGATGGAGAGCTGGCTCCGGAAGA 374
QY 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118
DB 375 CCAGCGAGGATGAGCCCGCTGAATGCGAGCTGGTGGAGGAGCTCCGAGCGCTCCGAGCGCG 434
QY 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla 138
DB 435 GCAGCGGAGGATGAGGAGCTGTTGATGCGAGCTCCGAGCTCCGAGCGCTCCGAGCGCG 494
QY 139 HisIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrp 158
DB 495 CACATCCTGGCCATGAGGAGTGGCTGGCTGGCTCCCTATCTACCTCTCTGGCTGGCTGGCTGG 554
QY 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178
DB 555 GTCCCCAGTGGCTGGCGCGCTTCATCTCGGCGATCTCTCAGGCTCAGCTGGCTGGCTGGCTGG 614
QY 179 GlnHisAspTrpGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis 198
DB 615 CAGCATGACCTGGGCGCATGCTCCATCTTCAAGAGTCTGGTGGAGAACCAACGCTGGCGCGCAG 674
QY 199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218
DB 675 AAGTTGTGATGGGCGAGCTAAAGGGCTTCTCGCGCCACTGGTGGAGAACTCCGCGCACCTTC 734
QY 219 GlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238
DB 735 CAGCACCGCCAGCCACACATCTTCCACAGAGCCAGAGCTGAGCGGTGGCGCGCGCTG 794
QY 239 PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeuLysTrpLeuPro 258
DB 795 TTCCTCTGGGGGAG---TCATCCGTGAGTATGGCAAGAGAAACGAGATCCTACCC 851
QY 259 TyrAsnHisGlnHisGlyTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyr 278
DB 852 TACACCGCAGGACCTGTACTTCTTCTGATCGGCGCGCGCTGTCTCACCCTGGTGAGC 911

QY 279 PheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298
DB 912 TTGGAAGTGAATAATCTGGCGTACATGCTGGTGTGCATGTCAGTGGCGGATTTGCTCGG 971
QY 299 AlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyLeuGly 318
DB 972 GCGCGCAGCTTCTATGCGCGCTTCTTTATCTACCTCCCTTCTACGCGCTCCCTGGG 1031
QY 319 AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThr 338
DB 1032 GTGCTCTCTTTTCTTCTCTCTGAGGCTCTGGAAAGCCATGCTGCTGGTGGATCACA 1091
QY 339 GlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSer 358
DB 1092 CAGATGAACACATCCCAAGGAGATCGGCCACGAGACACCGGAGCTGGGTCTAGCTCT 1151
QY 359 GlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHis 378
DB 1152 CAGCTGGCGGACCTGCAACGCTGGAGCCCTCCTTTTCCACCACTGGTTCAGCGGCGAC 1211
QY 379 LeuAsnPheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLys 398
DB 1212 CTCACCTTCCAGATCGAGCACCACTCTTCCCGAGGATCCGAGACACAACTACAGCGCG 1271
QY 399 IleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysPro 418
DB 1272 GTGCGCGCGCTGGTCAAGTGGCTGTGTGCCAAGCACGCGCTCAGCTCAGAGTGAGCGCC 1331
QY 419 LeuLeuAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeu 438
DB 1332 TTCTTACCGCGCTGGTGACATCGTCAGTCCCTGCAAGAGTCTGTGTGACATCTGGCTG 1391
QY 439 AspAlaTyrLeuHisLys 444
DB 1392 GAGCGCTACCTCCATCAG 1409
RESULT 6
US-09-048-888-4
Sequence 4, Application US/09048888
Patent No. 6492108
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,888
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0494 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555


```

/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1928 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: BFPINOT01
/ CLONE: 2056310
/
US-09-048-888-4

Alignment Scores:
Pred. No.: 1,45e-166 Length: 1928
Score: 1515.00 Matches: 272
Percent Similarity: 76.08% Conservatives: 62
Best Local Similarity: 61.96% Mismatches: 99
Query Match: 62.14% Indels: 6
DB: Gaps: 3

US-09-719-601-5 (1-444) x US-09-048-888-4 (1-1928)

QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluLileGln 27
Db 102 GCGCCGACACCGCGCTCAGGACCTACCCCGCTACTTCCCTGGGACGAGTGCC 161
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTrzAsnIleThr 47
Db 162 CAGCGCTCAGGTCGCGAGCGGTGGCTAGTATCGACCGTAAGGTGTACAAATCAGC 221
QY 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTrzAlaGlyLysAsp 67
Db 222 GAGTTCACCGCGCGATCCAGGGGCTCCCGGGTCTATCAGGCATACCGCGGCGAGAT 281
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 282 GCCACGGATCCCTTTGTGGCTTCCACATCAACAGGGCTTGTGAAGAAGTATATGAAC 341
QY 88 ProLeuLeuIleGlyLysLeuAlaProGluProSerGlnAspHisGlyLysAsnSer 107
Db 342 TCTCTCTGATTTGGAGAACTGTCTCCAGAGACAGCCCGAGCTTTGAGCCACCAAGATAAA 401
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 402 GAGCTGACATGAGTTCCGGAGCTCGCGCCACAGTGGAGCGGTGGGCTCATGAG 461
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
Db 462 GCCAACCATGCTCTTCTCTGCTGTACTCTGTCACATCTTGTCTGTGATGCTGCAGCC 521
QY 148 TrpPheThrValPheTrpPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
Db 522 TGGCTCACCTTTGGGCTTTGGAGCGCTCTTTTGGCCCTCTCTCTCTGCGGTGCTG 581
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerVal 187
Db 582 CTCAGTCAGTTACGGCCCGAGCTGGCTGCTGTCAGCATGACTTGGCCACCTGTGCGTC 641
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 642 TTCAGCACCTCAAAAGTGAACCACTCTGTACATCATTTGTGATGTCACCTTGAAGGG 701
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
Db 702 GCCCCCGCCAGTTGGTGAACCAACATGCTCTCCAGCACCATGTCAGCCCAACTGCTTC 761
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 762 CGCAAAGACCCAGACATCAACATG---CATCCCTTCTCTTGTGCTTGGGAGATCCTC 818
QY 246 ProIleGluTrpGlyLysLysLeuLysTrpLeuProTrpAsnHisGlnHisGluTrp 265
Db 819 TCTGTGGAGCTTGGAAACAGAGAAAAATATATGCGGTACACCAACCAGCACAAATAC 878

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QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTrpGlnIleIleMet 285
Db 879 TTTCTTCTTAATTGGGCCCCCAGCCCTGCTGCTCTCTACTTCCAGTGGTATATTTCTAT 938
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTrpTrzIleArg 305
Db 939 TTTGTTATCCAGCGAAAGAGTGGTGGACTTGGCTGGATGATTACCTTCTACGTCGCG 998
QY 306 PhePheIleThrTrpIleProPheTrpGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db 999 TTTCTTCTTACITATGTGCACATATTGGGGCTGAAAGCCCTTCTGGGCCCTTTCTTCA 1058
QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
Db 1059 GTCAGGTTCTCGAAAGCAACTGGTTGTGTGGGTGACACAGATGAACCATATTTCCATG 1118
QY 346 GluIleAspGlnGluAlaTrpArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
Db 1119 CACATTGATCATGACCGGAACATGGACTGGTTCACCCAGCTCCAGGCCACATGCAAT 1178
QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
Db 1179 GTCCACAAGTCTGCTTCAATGACTGGTTCAGTGGACACCTCAACTTCCAGATTGACAC 1238
QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
Db 1239 CATCTTTTCCCGAGATGCTCTGACACATATACCAAAAGTGGCTCCCTGGTGCAGTCC 1298
QY 406 LeuCysAlaLysHisGlyIleGluTrpGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
Db 1299 TTGTGTCCCAAGCATGGCATAGAGTACCAGTCCCAAGCCCTGCTGTCAGCCITTCGCGC 1358
QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTrpLeuHisLys 444
Db 1359 ATCATCCACTCACTAAAGGAGTCAGGCGAGCTCTGCTAGATGCTTCTTCAACCA 1415

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RESULT 7

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US-09-439-261-1
; Sequence 1, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P2
; CURRENT FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-04-11
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-439-261-1

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Alignment Scores:
Pred. No.: 5,34e-166 Length: 1335
Score: 1508.00 Matches: 271
Percent Similarity: 75.85% Conservatives: 62
Best Local Similarity: 61.73% Mismatches: 100
Query Match: 61.85% Indels: 6
DB: Gaps: 3

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US-09-719-601-5 (1-444) x US-09-439-261-1 (1-1335)

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QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluIleGln 27
Db 19 GCGCGGAGACCGCGGCTCAGGACCTACCCCGCGCTACTTCCCTGGGACGAGGTGGCC 78
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr 47
Db 79 CAGCGCTCAGGTCGCGAGCGGTGGCTAGTGTACCGTAAAGGTGTACCAACATCAGC 138
QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67
Db 139 GAGTTTCACCCCGCGCATCCAGGGGCTCCCGGGTCATCAGCCACTACCGCGGCGAGAT 198
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 199 GCCACGGATCCCTTTGTGGCTTCCACATCAACAGGGCTTTGTGAGAGTATATGAAC 258
QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
Db 259 TCTCTCTGATTTGGAGAACTGTCTCCAGAGCAGCCAGCTTTGAGCCGCCAAGAATAAA 318
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 319 GAGCTGACAGATGCTTCGGGAGCTGGGCCACAGTGGAGCGGATGGGCTCATGAAG 378
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
Db 379 GCCAACCATGCTTCTCTGCTGTACCTGTCTGCACATCTTGTCTGGTGGATGGTGCAGCC 438
QY 148 TrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
Db 439 TGCTCAACCTTTGGTCTTTGGAGCTCTTTTGGCTTTCCTCTCTGCTGGCTGCTG 498
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187
Db 499 CTAGTGCAGTTCAGGCCAGCTGGCTGGCTGCAGCATGACTTTGGGCACCTGTCTGCTC 558
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 559 TTCAGCACTCAAGTGGAAACCATCTGTACATCATTTTGTGATTTGGCCACTGAAGGG 618
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePhe 227
Db 619 GCGCCGCGAGTGTGTGGAAACACATGCATCTCCAGCACCATGCGCAAGCCCAACTGCTTC 678
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 679 CGCAAGACCCAGACATCAACATG---CATCCCTTCTTCTTTCCTTTGGGGAAGATCTC 735
QY 246 ProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 265
Db 735 TCTGTGGAGCTTTGGGAAACAGAGAAATAATATATGCGGTACCAACACCAGCACAAATAC 795
QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMet 285
Db 796 TTCTTCTAATTGGGCGCCAGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 855
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg 305
Db 856 TTGTGTTATCAGGAAAGAGTGGGTGGACTTGGCTGGATGATTAACCTTCTACGTCGCG 915
QY 306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db 916 TTCTTCTCTACTTATGTGGCACTATTGGGGCTGAAAGCCTTCTCTGGGCTTTTCTCTATA 975
QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
Db 976 GTCAGTTCTCTGAAAGCAACTGTTTGTGTGGTGACACATGATGACCATATTCCTCATG 1035
QY 346 GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
Db 1036 CACATTGATCATGACCCGGAACATGGACTGGGTTTCCACCCAGCTCTCTGCGCACATGCAAT 1095
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QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
Db 1096 GTCCACAAGTCTGCTTCAATGACTGGTTCAGTGACACCTCACTTCCAGATTGAGCAC 1155
QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
Db 1156 CATCTTTTCCACCATGCTCGACACAATTACCAAGTGGTCCCTTGTGTGAGTCC 1215
QY 406 LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
Db 1216 TTGTGTGCCAAGCGTGGCATAGTACCAAGCCCTCTGTGTGAGCTTCCCGGAC 1275
QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 1276 ATCATCCACTCTAAAGAGTCAGGCGCTCTGTGTAGATGCTATCTTCCACCA 1332
RESULT 8
US-09-227-613-1
; Sequence 1, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.PI
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-1
Alignment Scores:
Pred. No.: 5 34e-166 Length: 1335
Score: 1508.00 Matches: 271
Percent Similarity: 75.85% Conservative: 62
Best Local Similarity: 61.73% Mismatches: 100
Query Match: 61.85% Indels: 6
Gaps: 3
DB: 4
US-09-719-601-5 (1-444) x US-09-227-613-1 (1-1335)
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```
QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluIleGln 27
Db 19 GCGCGGAGACCGCGGCTCAGGACCTACCCCGCGCTACTTCCCTGGGACGAGGTGGCC 78
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr 47
Db 79 CAGCGCTCAGGTCGCGAGCGGTGGCTAGTGTACCGTAAAGGTGTACCAACATCAGC 138
QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67
Db 139 GAGTTTCACCCCGCGCATCCAGGGGCTCCCGGGTCATCAGCCACTACCGCGGCGAGAT 198
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 199 GCCACGGATCCCTTTGTGGCTTCCACATCAACAGGGCTTTGTGAGAGTATATGAAC 258
QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
Db 259 TCTCTCTGATTTGGAGAACTGTCTCCAGAGCAGCCAGCTTTGAGCCGCCAAGAATAAA 318
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 319 GAGCTGACATGATTTCCGGGAGCTTCGGGCGCCACAGTGGAGCGGATGGGCTCATGAAG 378
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
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Db 663 CTGGACATCATCAGTCCCTCGAAGAGTCTGGGAAGCTGTGGCTGGAGCGCTACCTTCAC 722
QY 444 Lys 444
Db 723 AAA 725
RESULT 10
US-09-227-613-6
; Sequence 6, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-6
Alignment Scores:
Pred. No.: 3.5e-147 Length: 1686
Score: 1348.00 Matches: 241
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.23% Indels: 0
DB: 4 Gaps: 0
US-09-719-601-5 (1-444) x US-09-227-613-6 (1-1686)
QY 204 HisLeuLysGlyAlaSerAlaAsnTrpAsnHisArgHisPheGlnHisAlaLys 223
Db 3 CACTTAAGGGTGCTCTGCCACCTGGTGGATCATGCCACTCCACGACCAAG 62
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CCTAACATCTCCACAAGATCCGATGTGAACATGCTGCACGTGTGTGTCTGGGCGAA 122
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLys 263
Db 123 TGGCAGCCCATCGATGACGCGAAGAGCTGAATACCTGCCCTCAATCACCAGCAC 182
QY 264 GluTyrPhePheLeuIleGlyProPheLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATACCTCTCTGATTGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGATC 242
QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 243 ATCATGACCATGATGTCATAGAACTGGGTGGACCTGGCTGGCGCTGAGTACTAC 302
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
Db 303 ATCCGGTTCTTCATCACCTACATCCCTTTCTACGGCATCTCTGGAGCCCTCTTTCTC 362
QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACCTTCATCAGGTTCTCGAGAGCCACTCGTGGTTCAGTAGCCAGCTGACGACCATC 422
QY 344 ValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThr 363
Db 423 GTCATGGAGATTGACACAGAGGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 482
QY 364 CysAsnValGluGlnSerPheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIle 383
Db 483 TGCACGTGGAGCAGTCTCTTCTCAACGACTGGTTCAGTGGACACCTTAACCTTCCAGATT 542

QY 384 GluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuVal 403
Db 543 GAGCACCACTCTTCCCAACCATGCCCGGCACAACTACACAAGATGCCCGCGGTGGTG 602
QY 404 LysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysPheLeuArgAlaLeu 423
Db 603 AAGTCTCTATGTGCCAAGCATGGCATTGAATACCAAGGAGAACCGCTACTGAGGCGCCGTG 662
QY 424 LeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHis 443
Db 663 CTGGACATCATCAGTCCCTCGAAGAGTCTGGGAAGCTGTGGCTGGAGCGCTACCTTCAC 722
QY 444 Lys 444
Db 723 AAA 725
RESULT 11
US-09-439-261-12
; Sequence 12, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-12
Alignment Scores:
Pred. No.: 4.55e-119 Length: 864
Score: 1103.00 Matches: 194
Percent Similarity: 77.93% Conservative: 32
Best Local Similarity: 66.90% Mismatches: 52
Query Match: 45.24% Indels: 12
DB: 4 Gaps: 3
US-09-719-601-5 (1-444) x US-09-439-261-12 (1-864)
QY 157 GlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGly 176
Db 22 GGGGAATTCGGCAGTT-----CAGGCCACGGCTGGC 54
QY 177 TrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeu 196
Db 55 TGGCTGCAGCATGACATTTGGGCACCTGTGGTCTTCAGCACCTCAAAAGTGAACCATCTG 114
QY 197 ValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArg 216
Db 115 CTACATCATTTTGTGATTGGCCACCTGGAAGGGGGGCCCCCGCCAGTTGGTGAACCATCATG 174
QY 217 HisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProLysTrpAsnMetLeu 236
Db 175 CACTTCCAGCACCATGCCAAGCCAACTGCTTCCGCAAGAGCCAGACATCAACATG--- 231
QY 237 His-----ValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeu 254
Db 232 CATCCCTCTCTTTTGCCTTGGGGAGATCCTCTCTGTGGAGCTTGGGAACAGAAAGAA 291

255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuLeuGlyProProLeuLeu 274
292 AATATATGCGGTACCAACACAGACACAAATATCTTCTTAATTTGGGCCCCAGCCTTG 351
275 IleProMetTyrPheGlnTyrGlnIleleMetThrMetIleValHisLysAsnTrpVal 294
352 CTGCTCTCTACTTCCAGTGGTATATTTCTATTTTGTATCCACGGAAGAGTGGGTG 411
295 AspLeuAlaTrpAlaValSerTyrIleArgPhePheIleThrTyrIleProPheTyr 314
412 GACTTGGCTTGGATGATTAACCTTCTACGTCCTCTCTCTCTCTCTCTCTCTCTCTCT 471
315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlnSerHisTrpPhe 334
472 GGGCTGAAAGCGCTTCTGCGGCTTTCTTCTATAGTCAGGTCCTCGAAGCAACTGGT 531
335 ValTrpValThrGlnMetAsnHisIleValMetGluLeuAspGlnGluAlaTyrArgAsp 354
532 GTGTGGGTGACACAGATGAACCAATATCCATGACATTTGATGATGACCGGACATGGAC 591
355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374
592 TGGGTTTCCACCGAGCTCCAGGACACATGCAATGTCCACAAAGTCTGCTTCAATGACTGG 651
375 PheSerGlyHisLeuAsnGlnIleGluHisLeuPheProThrMetProArgHis 394
652 TTCAGTGGACACCTCACTTCCAGATGAGCACCATCTTTTCCACAGATGCTCGACAC 711
395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
712 AATTACCAAAAGTGGCTCCCTGCTGAGTCTCTGTCGCAAGCATGGCATAGATG 771
415 GlnGluLysProLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGly 434
772 CAGTCCAAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 831
435 LysLeuTrpLeuAspAlaTyrLeuHisLys 444
832 CAGCTCTGGTAGATGCTATCTTCCACCA 861

RESULT 12
US-09-719-613-13
; Sequence 13, Application US/092276:3A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-13
Alignment Scores:
Pred. No.: 4,55e-119 Length: 864
Score: 1103.00 Matches: 194
Percent Similarity: 77.93% Conservative: 32
Best Local Similarity: 66.90% Mismatches: 52
Query Match: 45.24% Indels: 12
Gaps: 3
US-09-719-601-5 (1-444) x US-09-227-613-13 (1-864)

157 GlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGly 176
22 GCGGGAATTCGCGCAGTT-----CAGCCCGAGGCTGCG 54
177 TrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeu 196
55 TGCTGACGATGACCTTGGGACCTGTCGGTCTTCAGCACCTCAAGTGAACCATCTG 114
197 ValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArg 216
115 CTACATCATTTTGTATGTCACCTGAAAGGGGGCCCCCGCCAGTGGTGGAAACCAATG 174
217 HisPheGlnHisLysAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeu 236
175 CATTTCAGACACCATGCGAAGCCCACTGCTTCGGAAGAGCCACACATCAACATG--- 231
237 His-----ValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLeu 254
232 CATCCCTTCTTCTTGGCTTGGGGAAGATCTCTCTGTGAGGCTTGGGAAACAGAA 291
255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeu 274
292 AATATATGCGGTACACACACAGCACAAATATCTTCTCTAATTGGGCCCCAGCCTTG 351
275 IleProMetTyrPheGlnTyrGlnIleleMetThrMetIleValHisLysAsnTrpVal 294
352 CTGCTCTCTACTTCCAGTGGTATATTTCTATTTTGTATCCAGCGAAGAGTGGGTG 411
295 AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314
412 GACTTGGCTTGGATGATTAACCTTCTACGTCCTCTCTCTCTCTCTCTCTCTCTCTCT 471
315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlnSerHisTrpPhe 334
472 GGGCTGAAAGCGCTTCTGCGGCTTTCTTCTATAGTACAGTCTCTGGAAGCAACTGGTT 531
335 ValTrpValThrGlnMetAsnHisIleValMetGluLeuAspGlnGluAlaTyrArgAsp 354
532 GTGTGGGTGACACAGATGAACCATATTTCCATGACATTTGATGATGACCGGACATGGAC 591
355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374
592 TGGGTTTCCACCGAGCTCCAGGACACATGCAATGTCCACAAAGTCTGCTTCAATGACTGG 651
375 PheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThrMetProArgHis 394
652 TTCAGTGGACACCTCAACTTCCAGATGAGCACCATCTTTTCCACAGATGCTCGACAC 711
395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
712 AATTACCAAAAGTGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 771
415 GlnGluLysProLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGly 434
772 CAGTCCAAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 831
435 LysLeuTrpLeuAspAlaTyrLeuHisLys 444
832 CAGCTCTGGTAGATGCTATCTTCCACCA 861

RESULT 13
US-09-439-261-35
; Sequence 35, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12

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; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-35

Alignment Scores:
Pred. No.: 2,67e-102 Length: 990
Score: 960.00 Matches: 176
Percent Similarity: 69.54% Conservative: 50
Best Local Similarity: 54.15% Mismatches: 73
Query Match: 39.38% Indels: 26
DB: 4 Gaps: 4

US-09-719-601-5 (1-444) x US-09-439-261-35 (1-990)

QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27
DB 19 GCGCGGAGACCGCGGCTCAGGACCTACCCGCGCTACTTCACTCGGAGAGGTGGCC 78
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValleAspArgLysValTyrAsnLeuThr 47
DB 79 CAGCGCTCAGGTCGAGGCGGTGGCTAGTATGATCGACCGCTAAGGTGTCAACATCAGC 138
QY 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67
DB 139 GAGTTCACCGCGGATCCAGGGGCTCCCGGGTCATCAGCCATCAGCCGCGGAGGAT 198
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
DB 199 GCCACCGATCCCTTGTGGCTTCCATCAACAGAGGCGCTTGTGAAGATATATGAAC 258
QY 88 ProLeuLeuIleGlyGluLeuAlaProGluProSerGlnAspHisGlyLysAsnSer 107
DB 259 TCTCTCCTGATGGAGACTGCTCCAGAGAGCGGCTTGGAGCCACCAAGATATAA 318
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
DB 319 GAGCTGACAGAGTTCGCGGAGCTCGGSCCAGTGGAGCGGCTCATGAG 378
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
DB 379 GCCAACCATGCTTCTTCTGCTGTACCTGTGACATCTTGTCTGGTGGTGCAGCC 438
QY 148 TrpPheThrValPheTyrPheGlyAsnGlyTTPileProThrLeuIleThrAlaPheVal 167
DB 439 TGCTCACCTTGGGTCTTGGAGCTCTTTGGAGCTCTTTGGCCCTCTCTCTGCGGTGCTG 498
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187
DB 499 CTCAGTGCAATTCAGGCCCGGCTGGCTGCGCATGACTTTGGGCGCATCTGTCGGTC 558
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
DB 559 TTCAGCACTCAAGTGGGAACCATCTGCTACATCATTTTGTGATTTGGCCACTGAGGGG 618
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
DB 619 GCGCCCGCAGTGTGGTGGAAACACATGCTTCCAGCACCACGCAAGCCCAACTGCTTC 678
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
DB 679 CGCAAGAGCCGACATCAACATG---CATCCCTTCTTCTTCTTGGGGAAGATCCTC 735
QY 246 ProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyr 265
```

```
DB 736 TCTGTGGAGCTTGGGAAACAGAGAGAAATATATGCGGTACCAACACGACCAATAC 795
QY 266 PhePheLeuIleGly-----
DB 796 TTCTTCTTAATTTGGGCCCCCAGCCCTTGTCTCTACTTCCAGTGTATATTTCTAT 855
QY 271 -----ProProLeuLeuLeuProMetTyrPheGlnTyrGlnIleleMet 285
DB 856 TTTGTATATCCAGCAGCAGCCCGCCAGCTTGTCTCTACTTCCAGTGTATATTTCTAT 915
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg 305
DB 916 TTTGTATATCCAGCAGGAAGAGTGGTGGACTTGGCTGGATGATTACCTTCTACCTCGC 975
QY 306 PhePheIleThrTyr 310
DB 976 TTCTTCTCCTCATAT 990

RESULT 14
US-09-227-613-34
; Sequence 34, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.PI
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-227-613-34

Alignment Scores:
Pred. No.: 2,67e-102 Length: 990
Score: 960.00 Matches: 176
Percent Similarity: 69.54% Conservative: 50
Best Local Similarity: 54.15% Mismatches: 73
Query Match: 39.38% Indels: 26
DB: 4 Gaps: 4

US-09-719-601-5 (1-444) x US-09-227-613-34 (1-990)

QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27
DB 19 GCGCGGAGACCGCGGCTCAGGAGCTACCCGCGCTACTTCACTCGGAGAGGTGGCC 78
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValleAspArgLysValTyrAsnLeuThr 47
DB 79 CAGCGCTCAGGTCGAGGAGCGGCTGGCTAGTATGATCGACCGCTAAGGTGTCAACATCAGC 138
QY 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67
DB 139 GAGTTCACCGCGGATCCAGGGGCTCCCGGGTCATCAGCCATCAGCCGCGGAGGAT 198
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
DB 199 GCCACCGATCCCTTGTGGCTTCCATCAACAGAGGCGCTTGTGAAGATATATGAAC 258
QY 88 ProLeuLeuIleGlyGluLeuAlaProGluProSerGlnAspHisGlyLysAsnSer 107
DB 259 TCTCTCCTGATGGAGACTGCTCCAGAGAGCGGCTTGGAGCCACCAAGATATAA 318
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
DB 319 GAGCTGACAGAGTTCGCGGAGCTCGGSCCAGTGGAGCGGCTCATGAG 378
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
DB 379 GCCAACCATGCTTCTTCTGCTGTACCTGTGACATCTTGTCTGGTGGTGCAGCC 438
QY 148 TrpPheThrValPheTyrPheGlyAsnGlyTTPileProThrLeuIleThrAlaPheVal 167
DB 439 TGCTCACCTTGGGTCTTGGAGCTCTTTGGAGCTCTTTGGCCCTCTCTCTGCGGTGCTG 498
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187
DB 499 CTCAGTGCAATTCAGGCCCGGCTGGCTGCGCATGACTTTGGGCGCATCTGTCGGTC 558
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
DB 559 TTCAGCACTCAAGTGGGAACCATCTGCTACATCATTTTGTGATTTGGCCACTGAGGGG 618
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
DB 619 GCGCCCGCAGTGTGGTGGAAACACATGCTTCCAGCACCACGCAAGCCCAACTGCTTC 678
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
DB 679 CGCAAGAGCCGACATCAACATG---CATCCCTTCTTCTTCTTGGGGAAGATCCTC 735
QY 246 ProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyr 265
```


Patent No. 6432684
GENERAL INFORMATION:
APPLICANT: MUKERJI, Pradiip
APPLICANT: LEONARD, Amanda E.
APPLICANT: HUANG, Yung-Sheng
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.P1
CURRENT APPLICATION NUMBER: US/09/227,613A
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 960
TYPE: DNA
ORGANISM: Homo Sapien
US-09-227-613-35

Alignment Scores:
Pred. No.: 3.58e-99 Length: 960
Score: 933.00 Matches: 170
Percent Similarity: 73.38% Conservative: 45
Best Local Similarity: 58.02% Mismatches: 72
Query Match: 38.27% Indels: 6
DB: 4 Gaps: 3

US-09-719-601-5 (1-444) x US-09-227-613-35 (1-960)

```
QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27
DB 49 GCGCGCGAGACCGCGCTCAGGGACCTACCGCGCTTACCTCGGAGAGGTGGCC 108
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValleAspArgLysValTrpAsnLeuThr 47
DB 109 CAGCGCTCAGGCTGCGAGGCGGTGGCTAGTATCGACCGTAAAGGTGTACAAATCAGC 168
QY 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTrpAlaGlyGluAsp 67
DB 169 GAGTTCACCGCGGATCCAGGGGGTCCCGGTTCATCAGCCATCAGCGCGGCGAGAT 228
QY 66 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
DB 229 GCCACGGATCCCTTGTGGCTCCACATCAACAAGGGCTTGTGAAGAGTATATCAAC 288
QY 86 ProLeuLeuIleGlyGluLeuAlaProGluProSerGlnAspHisGlyLysAsnSer 107
DB 289 TCTCTCTGTGATGAGAACTGTCTCAGCAGCGCCAGCTTTGAGCCCAACAGAAATAA 348
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
DB 349 GAGCTGACAGATGAGTTCGGGAGCTGGGGCCACAGTGGAGCGGATGGGGCTCATGAG 408
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
DB 409 GCCAACCACTGCTTCTCTGCTGACCTGTGACATCTTGTGCTGGATGGTGGAGCC 468
QY 148 TrpPheThrValPheTrpPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
DB 469 TGGCTCACCTTGGGTCTTTGGGAGCTCTTTTGGCTTCTCTCTCTCTCTCTCTCTCT 528
QY 168 LeuAlaThrSerGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerVal 187
DB 529 CTCAGTGAGTTCAGGCGCCAGCTGGCTGGCTGAGCATGATGATTTGGGCACTCTCGGTC 588
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
DB 589 TTCACCACTCAAGTGAAACCACTGTCTATCATATTTGTGATTTGGCCACTCGAAGGG 648
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
DB 649 GCCCGCGCAGTGTGGTGAACCAATGATGATGATGATGATGATGATGATGATGATGAT 708
```

```
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
DB 709 CGCAAGACCCAGACATCAATG---CATCCCTTCTTTTGGGGAAGATCCTC 765
QY 246 ProIleGluTrpGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys 265
DB 766 TCTGTGGAGCTTGGGAACAGAGAATAATATATGCGGTACACCCAGCACAATAC 825
QY 266 PhePheLeuIleGlyProLeuLeuIleProMetLysPheGlnTrpGlnIleIleMet 285
DB 826 TCTTCTTAATTGGGCCCCAGCTTGTGCTCTCTACTTCCAGTGTATATTTTCTAT 885
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298
DB 886 TTTGTTATCCAGCGAAAGAAAGTGGTGGACTTGGCGTGG 924
```

RESULT 17

US-09-439-261-5
Sequence 5, Application US/09439261
Patent No. 6428990
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradiip
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.P2
CURRENT APPLICATION NUMBER: US/09/439,261
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 918
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (755)...(755)
OTHER INFORMATION: r = g or a at position 755
US-09-439-261-5

Alignment Scores:
Pred. No.: 4.89e-98 Length: 918
Score: 923.00 Matches: 167
Percent Similarity: 74.04% Conservative: 44
Best Local Similarity: 58.60% Mismatches: 68
Query Match: 37.88% Indels: 6
DB: 4 Gaps: 3

US-09-719-601-5 (1-444) x US-09-439-261-5 (1-918)

```
QY 19 ProThr-----PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSer 35
DB 7 CTTACCCCGCGTACTTTCACCTGGGAGGAGTGGCGGCTCAGGCTGCGAGGCGG 66
QY 36 GlyLeuValIleAspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGly 55
DB 67 TGGCTAGTATGATCGACCTAAGGTGTACAACTACATCAGCGAGTTCACCGCGCGCATCCAGG 126
QY 56 GlyGlnArgValIleGlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
DB 127 GGCTCCCGGTCTATCAGCCACTACCGCGGAGGAGTGCACCGATCCCTTTGTGGCTTC 186
QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyLeuAla 95
DB 187 CACATCAACAAGGCGCTGTGTGAAGAAGTATATGAATCTCTCTCTGATGGAGAACTGTCT 246
```


QY 96 ProGluLeuProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115
DB 247 CAGACACCCAGCTTTCAGCCACCAAGATTAAGAGCTACAGATGAGTTCCGGAG 306
QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeu 135
DB 307 CTGCGGCCACAGTGAGCGGATGGGCTCATGAAGGCCAACCATGCTTCTTCTGCTG 366
QY 136 LeuLeuAlaHisIleLeuAlaLeuGluSerIleAlaTrpPheThrValPheThrPheGly 155
DB 367 TACCTCTGACATCTTGTCTGGATGGTGAGTGAGCTGCTCACCCTTTGGTCTTTGGG 426
QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAla 175
DB 427 ACCTGCTTTTGGCTTCTCTCTCTGCTGCGGTGCTCAGTGCGAGTTCCAGGCCAGGCT 486
QY 176 GlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHis 195
DB 487 GGTGCTGCGACATGACATTTGGGCACCTGTGCGTCTTCAGCACCTCAAGTGGGAACCAT 546
QY 196 LeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHis 215
DB 547 CTGCTACATCATTTCTGATGSCCACTGAAGGGGGCCCCCGCCAGTTGTGGGAACCA 606
QY 216 ArgHisPheGlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMet 235
DB 607 ATGCACCTTCAGACCATGCCAGCCCAACTGCTCCGCAAGAGCCACACATCAACATG 666
QY 236 LeuHis-----ValPheValLeuGlyGluTrpGlnProIleGluTrpGlyLysLys 253
DB 667 ---CATCCCTCTCTCTTGGGGAAGATCCTCTCTGCTGGAGCTTGGGAACAGAG 723
QY 254 LeuLysTrpLeuProThrAsnHisGlnHisGluTrpPhePheLeuIleGlyProLeu 273
DB 724 AAAAAATATATGCGGTACACCAACAGACACATATCTTCTTAATTTGGGCCCCCAGCC 783
QY 274 LeuIleProMetTyrPheGlnTrpGlnIleMetThrMetIleValHisLysAsnTrp 293
DB 784 TTGCTGCTCTCTACTTCCAGTGGTATATTTCTATTGTTATCCAGCGAAGAGTGG 843
QY 294 ValAspLeuAlaTrp 298
DB 844 GTGGACTTGGCTGG 858

RESULT 18

US-09-227-613-5
; Sequence 5, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-5

Alignment Scores:

Pred. No.:	4,89e-98	Length:	918
Score:	923.00	Matches:	167
Percent Similarity:	74.04%	Conservative:	44
Best Local Similarity:	58.60%	Mismatches:	68
Query Match:	37.86%	Indels:	6
DB:		Gaps:	3

US-09-719-601-5 (1-444) x US-09-227-613-5 (1-918)

QY 19 ProThr-----PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSer 35
DB 7 CTTACCCCGCGCTTCTACCTCGGAGAGTCCCGCAGCTCAGGGTCCGAGGAGCGG 66
QY 36 GlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGly 55
DB 67 TGGCTAGTATCAGCCGTAAAGTGTACACATCAGCGAGTTCCACCGCGGATCCAGGG 126
QY 56 GlyClnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
DB 127 GGTCCCGGTCTATCAGCCACTACGCGGCGAGGATGCCAGGATCCCTTTGGGCTTC 186
QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95
DB 187 CACATCAACAAGGCTTGTGAAGAAGTATATGAACCTCTCTCTGATTTGAGAACTGTCT 246
QY 96 ProGluLeuProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115
DB 247 CCAGAGCAGCCCGCTTTCAGCCCAAGAAATAAAGAGCTGACAGATGAGTTCCGGAG 306
QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeu 135
DB 307 CTGCGGCCACAGTGGAGCGGATGGGCTCATGAAGCCCAACCATGCTTCTTCTGCTG 366
QY 136 LeuLeuAlaHisIleLeuAlaLeuGluSerIleAlaTrpPheThrValPheThrPheGly 155
DB 367 TACCTGCTGACATCTTGTCTGCGATGGTGAGCTGCTCACCCTTTGGGCTTTGGG 426
QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAla 175
DB 427 ACCTCTTTTGGCTTCTCTCTCTGCTGCGGTGCTGCTCAGTCCAGTTCAGGCCAGGCT 486
QY 176 GlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHis 195
DB 487 GGTGCTGCGACATGACTTTGGGCACTCTGCGTCTTTCAGCACCTCAAAAGTGGAAACCAT 546
QY 196 LeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHis 215
DB 547 CTGCTACATCATTTGTGATTTGGCCACTGAAGGGGGCCCCCGCCAGTTGTGGGAACCA 606
QY 216 ArgHisPheGlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMet 235
DB 607 ATGCACCTTCAGACCATGCCAGCCCAACTGCTCCGCAAGAGCCACACATCAACATG 666
QY 236 LeuHis-----ValPheValLeuGlyGluTrpGlnProIleGluTrpGlyLysLys 253
DB 667 ---CATCCCTCTCTCTTGGGGAAGATCCTCTCTGCTGGAGCTTGGGAACAGAG 723
QY 254 LeuLysTrpLeuProThrAsnHisGlnHisGluTrpPhePheLeuIleGlyProLeu 273
DB 724 AAAAAATATATGCGGTACACCAACAGACACATATCTTCTTAATTTGGGCCCCCAGCC 783
QY 274 LeuIleProMetTyrPheGlnTrpGlnIleMetThrMetIleValHisLysAsnTrp 293
DB 784 TTGCTGCTCTCTACTTCCAGTGGTATATTTCTATTGTTATCCAGCGAAGAGTGG 843
QY 294 ValAspLeuAlaTrp 298
DB 844 GTGGACTTGGCTGG 858

RESULT 19
US-09-389-681-425
; Sequence 425, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: YUQUI, Jiang
; APPLICANT: DILLON, Davin C.
; APPLICANT: MITCHEM, Jennifer L.
; APPLICANT: XU, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-389-681-425

Alignment Scores:
Pred. No.: 3,776-88 Length: 446
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-389-681-425 (1-446)

QY 204 HisLeuLysGlyValAspAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
DB 2 CACTTAAAGGGTGCCTCTGCCAATCTGTGGATCATCCCACTTCCACACACGCGCAAG 61
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
DB 62 CCTAAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCACGTTGTGTTCTGGCGAA 121
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLys 263
DB 122 TGGCAGCCCATCGATGCGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
QY 264 GluTyrPhePheLeuIleGlyProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
DB 182 GAATACCTTCTTCATCCTACCTACCTACCTACCTACCTACCTACCTACCTACCTAC 241
QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyr 303
DB 242 ATCATGACCATGATCGTCATGAAGAACTGGGGAGACCTGGGCGCTGGGCGCTGACT 301
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
DB 302 ATCCGGTCTTCTCATCCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 361
QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
DB 362 AACCTTCATCAGTTCTCTGAGAGCCACTGTTGTGTGGTGCACACAGATGAATCATC 421
QY 344 ValMetGluIleAspGlnGlu 350
DB 422 GTCATGGAGATTGACCCAGGAG 442

RESULT 20
US-09-620-405B-425
; Sequence 425, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425

; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-425

Alignment Scores:
Pred. No.: 3,776-88 Length: 446
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-620-405B-425 (1-446)

QY 204 HisLeuLysGlyValAspAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
DB 2 CACTTAAAGGGTGCCTCTGCCAATCTGTGGATCATCCCACTTCCACACACGCGCAAG 61
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
DB 62 CCTAAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCACGTTGTGTTCTGGCGAA 121
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLys 263
DB 122 TGGCAGCCCATCGATGCGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
QY 264 GluTyrPhePheLeuIleGlyProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
DB 182 GAATACCTTCTTCATCCTACCTACCTACCTACCTACCTACCTACCTACCTACCTAC 241
QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyr 303
DB 242 ATCATGACCATGATCGTCATGAAGAACTGGGGAGACCTGGGCGCTGGGCGCTGACT 301
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
DB 302 ATCCGGTCTTCTCATCCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 361
QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
DB 362 AACCTTCATCAGTTCTCTGAGAGCCACTGTTGTGTGGTGCACACAGATGAATCATC 421
QY 344 ValMetGluIleAspGlnGlu 350
DB 422 GTCATGGAGATTGACCCAGGAG 442

RESULT 21
US-09-433-826B-425
; Sequence 425, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-425

Alignment Scores:
Pred. No.: 3,776-88 Length: 446
Score: 834.00 Matches: 147

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.21%	Indels:	0
DB:	4	Gaps:	0

US-09-719-601-5 (1-444) X US-09-433-826B-425 (1-446)

Qy	204	HisLeuLygGlyAlaSerAlaAsnTrpTrpAsnHisSargHisPheGlnHisHisAlaLys	223
Db	2	CACCTAAAGGGGTGCTCTGCCAACCTGGTGGAAATCATCGGCACCTCCAGCACCCACGCCAAG	61
Qy	224	ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu	243
Db	62	CCTAACATCTTCCACAGGATCCCGATGTGAACATGCTGCACGTGTTGTTCTGGSCGAA	121
Qy	244	TrpGlnProIleGluTyrGlyLysLysLysLysLysTyrLeuProTyrAsnHisGlnHis	263
Db	122	TGSCAGCCCATCGAGTACGGCAAGAAGAAGCTGAATACCTGCCCTACAATCACCAACAC	181
Qy	264	GluTyrPhePheLeuIleGlyProLeuLeuIleProMetTyrPheGlnTyrGlnIle	283
Db	182	GAATATCTTCTCGANTGGGGCGCGCTGCTCATCCCATGTAATTTCCAGTACCAAGATC	241
Qy	284	IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr	303
Db	242	ATCATGACCATGATGTCCTCCATAAGAACTGGGTGGACCTGGGCTGGGCGCTCAGCTACTAC	301
Qy	304	IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu	323
Db	302	ATCCGGTCTTCATCATCACTACATCCCTTTCACGGCATCCTGGAGAGCCCTCTTTCCCTC	361
Qy	324	AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle	343
Db	362	AACTTCATCAGGTCTCTGGAGAGCCCATCGTTGTGTGGGTCCACACAGATGAATCATCATC	421
Qy	344	ValMetGluIleAspGlnGlu	350
Db	422	GTCATGGAGATTGACCAGAG	442

RESULT 22

```

US-09-604-287A-425
; Sequence 425, Application US/09604287A
; Patent No. 6586372
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens

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Alignment Scores:	
Pred. No.:	3,778-88
Score:	834.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	34.21%
DB:	4
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 0
Length:	446
Matches:	147

US-09-719-601-5 (1-444) X US-09-604-287A-425 (1-446)

Qy	204	HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys	222
Db	2	CACCTTAAAGGGTGCTCTGCCACTGGTGAATCATTCGCCACTTCACGACCACGCCAAG	61
Qy	224	ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu	243
Db	62	CCTAACACTCTCCACAAGGATCCGATGTGAACATGTCGACGTGTTTGTTCCTGGGCGAA	121
Qy	244	TrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis	263
Db	122	TGGCAGCCCATCGAGTAGCGCAAGAAGACTGAATACCTGCGCTACAAATCACCAGCAC	181
Qy	264	GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle	283
Db	182	GAATACTTCTTCCTGATTGGGCGCGCGTGCTCATCCCCATGTATTTCAGACACCAGATC	241
Qy	284	IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr	303
Db	242	ATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGGGCGGTACGTACTAC	301
Qy	304	IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu	323
Db	302	ATCCGGTCTTCATCACCATCATCCCTTTCACGGCATCTCGGAGCGCTCCCTTTTCCTC	361
Qy	324	AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle	343
Db	362	AACTTCATCAGTTCTCTGGAGGCCACTGGTTTCTGTGGGTCCACACAGATGATCATCATC	421
Qy	344	ValMetGluIleAspGlnGlu	350
Db	422	GTCAATGAGATTGACAGGAG	445

RESULT 23

```

US-03-389-681-313
; Sequence 313, Application US/59389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqi, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.47003
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-03-389-681-313

```

Alignment Scores:					
Pred. No.:	3.91e-89	Length:	456		
Score:	834.00	Matches:	147		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	34.21%	Indels:	0		
Ds:	4	Gaps:	0		

US-09-719-601-5 (1-444) X US-09-389-681-313 (1-456)

Qy	204	Hi	st	eu	ys	gc	l	yl	a	sr	al	a	sn	t	r	p	a	sn	h	i	s	a	r	g	h	i	s	p	h	e	g	n	h	i	s	h	i	s	a	l	a	l	a	l	y	s		223								
Db	3	C	A	T	T	A	A	G	G	T	C	T	C	C	A	A	C	T	G	G	T	G	A	T	C	A	T	G	C	C	A	C	C	A	C	C	G	C	C	A	G		62													
Qy	224	P	r	a	s	n	i	l	e	p	h	e	i	s	l	y	s	a	s	p	r	o	b	a	s	v	a	l	a	n	t	w	e	t	l	e	u	i	s	v	a	l	p	h	e	v	a	l	l	e	u	G	l	u		243
Db	63	C	C	T	A	A	C	A	T	C	T	C	A	A	G	G	A	T	C	C	C	A	T	C	C	C	A	T	G	T	G	C	A	C	A	T	G	T	G	T	G	T	T	G	T	T	G	T	G	G	C	A		122		
Qy	244	T	r	p	i	n	p	r	o	i	l	e	g	u	t	r	y	l	y	s	l	y	s	l	y	s	l	e	u	s	t	y	r	e	u	p	r	o	t	y	a	s	n	h	i	s	g	l	n	h	i	s		263		

Db 123 TGGGAGCCCATCGATGACGCGCAGAGAGCTGAATATCTGCCCTACATCACCAGCAC 182
Qy 264 GluTyrPhePheLeuLeuGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATACTTCTTCTGATTGGCGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGATC 242
Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 243 ATCATGACCATGATGCTCCATAGAACTGGGTGGACCTGGCCCTGGGCGCTGAGTACTAC 302
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323
Db 303 ATCCGGTTCCTCATCACCTACATCCCTTCTACGGCATCCTGGGAGCCCTCTTTTCTC 362
Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACTTCATCAGGTTCTTGAGAGCCACTGGTTTGTGGTGCACACATGAATCACATC 422
Qy 344 ValMetGluIleAspGlnGlu 350
Db 423 GTCATGGAGATTGACCAGGAG 443

RESULT 24

US-09-620-405B-313
; Sequence 313, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-313

Alignment Scores:
Pred. No.: 3,918-88 Length: 456
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-620-405B-313 (1-456)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
Db 3 CACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATCGCCACTTCACACACACCGCCAG 62
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CCTAACATCTCCACAAGATCCCGATGTGAACATGCTGCAGTGTGTGTTCTGGGCGAA 122
Qy 244 TrpGlnProIleGluTyrGlyLysLysLysLeuLysLysLeuLysLysLeuProTyrAsnHisGlnHis 263
Db 123 TGGCAGCCCATCGATGACGCGCAGAGAAAGCTGAATATCTGCCCTACATCACCAGCAC 182
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATACTTCTTCTGATTGGCGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGATC 242

Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 243 ATCATGACCATGATGCTCCATAGAACTGGGTGGACCTGGCCCTGGGCGCTGAGTACTAC 302
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323
Db 303 ATCCGGTTCCTCATCACCTACATCCCTTCTACGGCATCCTGGGAGCCCTCTTTTCTC 362
Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACTTCATCAGGTTCTTGAGAGCCACTGGTTTGTGGTGCACACATGAATCACATC 422
Qy 344 ValMetGluIleAspGlnGlu 350
Db 423 GTCATGGAGATTGACCAGGAG 443

RESULT 25

US-09-339-338-313
; Sequence 313, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-339-338-313

Alignment Scores:
Pred. No.: 3,918-88 Length: 456
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-339-338-313 (1-456)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
Db 3 CACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATCGCCACTTCACACACACCGCCAG 62
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CCTAACATCTTCACAAGATCCCGATGTGAACATGCTGCAGTGTGTGTTCTGGGCGAA 122
Qy 244 TrpGlnProIleGluTyrGlyLysLysLysLeuLysLysLeuLysLysLeuProTyrAsnHisGlnHis 263
Db 123 TGGCAGCCCATCGATGACGCGCAGAGAAAGCTGAATATCTGCCCTACATCACCAGCAC 182
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATACTTCTTCTGATTGGCGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGATC 242
Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 243 ATCATGACCATGATGCTCCATAGAACTGGGTGGACCTGGCCCTGGGCGCTGAGTACTAC 302
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323
Db 303 ATCCGGTTCCTCATCACCTACATCCCTTCTACGGCATCCTGGGAGCCCTCTTTTCTC 362
Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343

Db 363 AACTCATCAGGTTCTGGAGCCACTGTTTGTGTGGTGCACAGATGATCATC 422
Qy 344 ValMetGluLeuAspGlnGlu 350
Db 423 GTCATGGAGATTGACCCAGGAG 443
RESULT 26
US-09-433-826B-313
; Sequence 313, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-313

Alignment Scores:
Pred. No.: 3,91e-88 Length: 456
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 4 Gaps: 0
US-09-719-601-5 (1-444) x US-09-433-826B-313 (1-456)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
Db 3 CACTTAAAGGGTGGCTCTGCCAATCGGTGGAAATCATCGCCACTTCCAGCACCCAGCAAG 62
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CCTAACATCTTCCACAGGATCCCGATGTGACATGCTGCACGTGTTTGTCTGGCGAA 122
Qy 244 TrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
Db 123 TGGCAGCCCATCGAGTACGGCAAGAGCTGAATACCTGCCCTCAACAATCACCAGCAC 182
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATACTTCTTCCTGATGGGCCCGCTGCTATCCCATGTATTTCCAGTACCCAGATC 242
Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 243 ATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGGGCGCTCAGCTACTAC 302
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323
Db 303 ATCCGGTTCCTCATCACCCTATCCCTTCTACGGCATCTCTGGAGCCCTCTTTTCTC 362
Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACTTCATCAGTTCTCTGGAGCCACTGGTTTGTGTGGTGCACACAGATGATCATC 422
Qy 344 ValMetGluLeuAspGlnGlu 350
Db 423 GTCATGGAGATTGACCCAGGAG 443

RESULT 27

US-09-604-287A-313
; Sequence 313, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-313

Alignment Scores:
Pred. No.: 3,91e-88 Length: 456
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-604-287A-313 (1-456)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
Db 3 CACTTAAAGGGTGGCTCTGCCAATCGGTGGAAATCATCGCCACTTCCAGCACCCAGCAAG 62
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CCTAACATCTTCCACAGGATCCCGATGTGACATGCTGCACGTGTTTGTCTGGCGAA 122
Qy 244 TrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
Db 123 TGGCAGCCCATCGAGTACGGCAAGAGCTGAATACCTGCCCTCAACAATCACCAGCAC 182
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATACTTCTTCCTGATGGGCCCGCTGCTATCCCATGTATTTCCAGTACCCAGATC 242
Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 243 ATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGGGCGCTCAGCTACTAC 302
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323
Db 303 ATCCGGTTCCTCATCACCCTATCCCTTCTACGGCATCTCTGGAGCCCTCTTTTCTC 362
Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACTTCATCAGTTCTCTGGAGCCACTGGTTTGTGTGGTGCACACAGATGATCATC 422
Qy 344 ValMetGluLeuAspGlnGlu 350
Db 423 GTCATGGAGATTGACCCAGGAG 443

RESULT 28

US-09-439-261-37
; Sequence 37, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.

```

RESULT 30
US-09-439-261-4
; Sequence 4, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIORITY APPLICATION NUMBER: US 08/833,610
; PRIORITY FILING DATE: 1997-04-11
; PRIORITY APPLICATION NUMBER: PCT/US98/07422
; PRIORITY FILING DATE: 1998-04-10
; PRIORITY APPLICATION NUMBER: US 09/227,613
; PRIORITY FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: SEQ ID for Windows Version 4.0

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; SEQ ID NO 4
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-4
Alignment Scores:
Pred. No.: 2,25e-59 Length: 304
Score: 585.00 Matches: 101
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.00% Indels: 0
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-439-261-4 (1-304)
QY 151 ValPheTyrPheGlyAsnGlyTrrPheProThrLeuIleThrAlaPheValLeuAlaThr 170
Db 1 GTCTTTTACTTTGGCAATGCTGGATTCTTACCTCATCAGCCCTTTGTCTTGTCTACC 60
QY 171 SerGlnAlaGlnAlaGlyTrrPheGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
Db 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGCTGCTACAGAAA 120
QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
Db 121 CCCAAGTGGAAACACCTTTGCCAATAATTCGTCATTGGCCACCTTAAAGGGTGCCTCTGCC 180
QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
Db 181 AACTGGTGGAAATCATGCCACTTCCAGCACCAAGCCTAACATCTTCCACAGGAT 240
QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyLutrrPgnProIleGlyTyrGly 250
Db 241 CCCGATGTGAACATGCTGCACGTTGTTTCTGGCGAATGGCAGCCCATCGAGTACGGC 300
QY 251 Lys 251
Db 301 AAG 303

RESULT 31
US-09-439-261-38
; Sequence 38, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: k = g or t/u at position 5
; NAME/KEY: misc_feature
; LOCATION: (6)...(6)
; OTHER INFORMATION: m = a or c at position 6
US-09-439-261-38
Alignment Scores:
Pred. No.: 6.79e-57 Length: 449
Score: 566.00 Matches: 102
Percent Similarity: 83.33% Conservative: 18
Best Local Similarity: 70.83% Mismatches: 24
Query Match: 23.22% Indels: 1
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-439-261-38 (1-449)
QY 301 SerTyrTyrIleArgPhePheIleThrTrrPheProPheTyrGlyIleLeuGlyAlaLeu 320
Db 9 ACCTTCTAGCTCGGCTTCTTCTCTACTATGTCACACTATTGGGCTGAAAGCTTCTCTGG 68
QY 321 LeuPheLeuAsnPheIleArgPheLeuGlySerHisTrpPheValTrrPheValThrIleMet 340
Db 321 LeuPheLeuAsnPheIleArgPheLeuGlySerHisTrpPheValTrrPheValThrIleMet 340
```

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Db 69 GCCTTTCTTCATA-GTCAGGTTCTCGAAGCAACTGGTTTGTGTGGTGACACAGATG 127
Qy 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTTPPheSerSerGlnLeu 360
Db 128 AACCATATCCCATGCATGATGATCATGACCGGAACATGGAGCTGGTTTCCACCAAGCTC 187
Qy 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTTPPheSerGlyHisLeuAsn 380
Db 188 CAGGCCACATGCAATGTGCCAAGTCTGCCTTCAATGATGCTGTTTCAGTGGACACCTCAAC 247
Qy 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisIleAla 400
Db 248 TTCCAGATTGACCAATCTTTTCCACAGATGCTCGACAAATATCCACAAAGTGCT 307
Qy 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db 308 CCCCTGGTGACGCTCTGTGTGCCAAGCATGCGATAGAGTACCAAGTCCAGGCCCTGCTG 367
Qy 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTTPLeuAspAla 440
Db 368 TCAGCCTTGGCGACATCATCTCACTAAGAGGATCAGGGCAGCTCTGGCTAGATGCC 427
Qy 441 TyrLeuHisLys 444
Db 428 TATCTTCAACAA 439

RESULT 33
US-09-227-613-37
; Sequence 37, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-37

Alignment Scores:
Pred. No.: 6,79e-57 Length: 449
Score: 566.00 Matches: 102
Percent Similarity: 83.33% Conservative: 18
Best Local Similarity: 70.83% Mismatches: 24
Query Match: 23.22% Indels: 1
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-227-613-37 (1-449)
Qy 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db 9 ACCTTCTAGTCGCTCTTCTCTCACTATGTGCCACTATTGGGCTGAAAGCTTCTCTGG 68
Qy 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTTPPheValTTPValThrGlnMet 340
Db 69 GCCTTTCTTCATA-GTCAGGTTCTCGAAGCAACTGGTTTGTGTGGTGACACAGATG 127
Qy 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTTPPheSerSerGlnLeu 360
Db 128 AACCATATCCCATGCATGATGATCATGACCGGAACATGGAGCTGGTTTCCACCAAGCTC 187
Qy 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTTPPheSerGlyHisLeuAsn 380
Db 188 CAGGCCACATGCAATGTGCCAAGTCTGCCTTCAATGATGCTGTTTCAGTGGACACCTCAAC 247
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Qy 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisIleAla 400
Db 248 TTCCAGATTGAGCAACCATTTTCCACAGATGCTCGACAAATATCCACAAAGTGCT 307
Qy 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db 308 CCCCTGGTGACGCTCTGTGTGCCAAGCATGCGATAGAGTACCAAGTCCAGGCCCTGCTG 367
Qy 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTTPLeuAspAla 440
Db 368 TCAGCCTTGGCGACATCATCTCACTAAGAGGATCAGGGCAGCTCTGGCTAGATGCC 427
Qy 441 TyrLeuHisLys 444
Db 428 TATCTTCAACAA 439

RESULT 34
US-09-439-261-3
; Sequence 3, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-3

Alignment Scores:
Pred. No.: 1.23e-56 Length: 655
Score: 566.00 Matches: 102
Percent Similarity: 83.33% Conservative: 18
Best Local Similarity: 70.83% Mismatches: 24
Query Match: 23.22% Indels: 1
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-439-261-3 (1-655)
Qy 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db 3 ACCTTCTAGTCGCTCTTCTCTCACTATGTGCCACTATTGGGCTGAAAGCTTCTCTGG 62
Qy 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTTPPheValTTPValThrGlnMet 340
Db 63 GCCTTTCTTCATA-GTCAGGTTCTCGAAGCAACTGGTTTGTGTGGTGACACAGATG 121
Qy 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTTPPheSerSerGlnLeu 360
Db 122 AACCATATCCCATGCATGATGATCATGACCGGAACATGGAGCTGGTTTCCACCAAGCTC 181
Qy 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTTPPheSerGlyHisLeuAsn 380
Db 182 CAGGCCACATGCAATGTGCCAAGTCTGCCTTCAATGATGCTGTTTCAGTGGACACCTCAAC 241
Qy 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisIleAla 400
Db 242 TTCCAGATTGAGCAACCATCTTTTCCACAGATGCTCGACAAATATCCACAAAGTGCT 301
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QY 401 ProLeuValysSerLeuCyAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db 302 CCCTGGTGGAGTCCTTGTGTGCAAGCATGGCATAGTACAGTCCAGGCCCTGCTG 361
QY 421 ArgAlaLeuLeuAspIleLeuArgSerLeuLysSerGlyLysLeuTrpLeuAspAla 440
Db 362 TCAGCTTCCGCGACATCATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCC 421
QY 441 TyrLeuHisLys 444
Db 422 TATCTTCACCAA 433
RESULT 35
US-09-719-601-5
; Sequence 3, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-3

Alignment Scores:
Pred. No.: 1,23e-56 Length: 655
Score: 566.00 Matches: 102
Percent Similarity: 83.33% Conservative: 18
Best Local Similarity: 70.83% Mismatches: 24
Query Match: 23.22% Indels: 1
DB: 4 Gaps: 0
US-09-719-601-5 (1-444) x US-09-227-613-3 (1-655)
QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db 3 ACCTTCTACGTCGCGCTTCTTCTCCTCCTCCTATATGTGCCACTATTTGGGGCTGAAAGCTTCTG 62
QY 321 LeuPheLeuAenPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
Db 63 GCCTTTTCTTCATA-GTCAGGTTCCTCGAAGCAACTGGTTGTGTGGGTGACACAGATG 121
QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
Db 122 AACCATATTCGATGCACTTATGATGACGCGGAACATGAGCTGGGTTCACCCAGCTC 181
QY 361 ThrAlaTrpCysAenValGluGlnSerPhePheAenAspTrpPheSerGlyHisLeuAen 380
Db 182 CAGCCACATGCAATGTCACAGTTCCTTCATGACTGGTTCAGTGACACCTCAAC 241
QY 381 PheGlnIleGluHisLeuPheProThrMetProArgHisAenLeuHisLysIleAla 400
Db 242 TTCAGATTGAGCACCATTCTTTTCCACGATGCTCGACACATATACCAAGTGGCT 301
QY 401 ProLeuValLysSerLeuCyAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db 302 CCCTGGTGGAGTCCTTGTGTGCAAGCATGGCATAGTACAGTCCAGGCCCTGCTG 361
QY 421 ArgAlaLeuLeuAspIleLeuArgSerLeuLysSerGlyLysLeuTrpLeuAspAla 440
Db 362 TCAGCTTCCGCGACATCATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCC 421

QY 441 TyrLeuHisLys 444
Db 422 TATCTTCACCAA 433
RESULT 36
US-08-834-655-1
; Sequence 1, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUZON, DEBORAH
; APPLICANT: MUKERJI, Pradip
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-834-655-1
Alignment Scores:
Pred. No.: 1,51e-43 Length: 1617
Score: 459.00 Matches: 118
Percent Similarity: 43.55% Conservative: 88
Best Local Similarity: 24.95% Mismatches: 183
Query Match: 18.83% Indels: 84
DB: 2 Gaps: 14
US-09-719-601-5 (1-444) x US-08-834-655-1 (1-1617)
QY 17 SerValProThrPheSerTrpGluGluIle-----GlnLys 28
Db 86 AGTGTGAGGACGCTTCTTCTCGGCCGCGAGTTTGAATGCGGAGGCTCTCAATGAGGCGAAG 145
QY 29 HisAenLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThrLys 48
Db 146 AAGGATGCGGAGCCACCTTCTTGATGATCATCGACACAAAGGTTGACGATGTCGCGGAG 205
QY 49 TrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyrAlaGlyGluAspAla 68
Db 206 TTTCGCTTCGATCATCCCGGTGGAAGTGTGTTCAGGCAC---GTTGGCAAGGACGCGC 262
QY 69 ThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysPro 88

Db 263 ACTGAGCTCTTACACTTTTACCCCTCTCTGAGAGACTCTTGCAC 316
Qy 89 LeuLeuLeuGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLys 108
Db 317 TTTTACGTTGGTGATATT-----GACGAGAGGACCGCGATATC---AAGAAATGATGAC 367
Qy 109 IleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThr 128
Db 368 TTTGCGGCGGAGTCCGACAGCTCGTACCTTGTTCACGCTCTCTGTTACTACGATTCT 427
Qy 129 AsnHisValPhePheLeuLeuLeuAlaHisIleLeuLeuGluSerIleAlaTrp 148
Db 428 TCCAAGGACATACGAGCTTCAAGGCTCTCGTTCAACCTCTGCATCTGGGCTTTGTGACG 487
Qy 149 PheThrValPheTyPheGly---AsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
Db 488 GTCAATTGGCCAGTGGGGCCACACTCGACCTCGCCACAGTGCTCTCGGTTCGGCTT 547
Qy 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyGlyHisLeuSerVal 187
Db 548 TTGGGTCTGTCTGCGACGAGTGGGATGTTGGCTCAGCACTTTTTCATCACCAGGTC 607
Qy 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 608 TTCAGGACCTTCTGGGGTATCTTTTCGGCCCTCTTGGAGGTGTCGCCAGGCG 667
Qy 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePhe 227
Db 668 TTCTCGTCTCGTGGTGAAGACAGACAACTCACCAGCGCGCCGCCCAAGTCCAC 727
Qy 228 HisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIle 247
Db 728 GCGAGGATCCGACATGACACCCACCTCTGTGTGAGTGGAGTGAG----- 775
Qy 248 GluTyGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 267
Db 776 -----CATGCGTTGGAGATGTTCTCG 796
Qy 268 LeuLeuGlyProProLeuLeuLeuProMetTyPheGlnTyPheGlnIleMetThrMet 287
Db 797 GATGTCGACAGATGAGGAGCTACCGGCTGATGTTGGCGGCTCTCTCTCTCTCTGTC 841
Qy 288 IleValHisLysAsnTrp-----ValAspLeuAlaTrpAla 299
Db 842 GTCTGACACGAGCTGTTTACTTCCCATTTCTCTGTTGGCGGCTCTCTCTCTCTCTGTC 901
Qy 300 ValSerTyTrpIleArgPhePheIleThrTyPheProPheTyGlyLeuGlyAla 319
Db 902 CTCAG---TCCATTCTCTTGTGCTTAACGCTCAGGCCACAAAGCCCTCGGGGCGC 958
Qy 320 LeuLeuPheLeuAsnPheIleArg-----PheLeuGluSerHisTrpPheValTrp--- 336
Db 959 CGTGTGCCATCTCTGTCGAGCAGCTGCTGCTTGGGATGCTG---ACCTGTATC 1015
Qy 336 ----- 336
Db 1016 CTCGCCACCATGTTCTCTGTTCATCAAGATCCGTCACATGCTGTTGTTACTTTTGGTG 1075
Qy 337 -----ValThrGlnMetAsnHisIleValMet 345
Db 1076 TCGCAGCGGTGCGGAAACTGTTGTCGATCGGTGTTCTCGCTCAACCAACACGATG 1135
Qy 346 GluIle-----AspGlnGluAlaTyArgAspTrpPheSerSerGlnLeuThrAla 362
Db 1136 CTTGTGATCTCGAAGGAGGCGGCTCATATGATTTCTTTCACGACGATCATCACG 1195
Qy 363 ThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGln 382
Db 1196 GGTCTGTATGTCACCCCGGCTATTTCGCAACTGTTTTCACGGGTGGATTGAATCATCAG 1255
Qy 383 IleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeu 402

Db 1256 ATCGAGCACCACCTTGTCCCTTCGATGCTCGCCACAACTTTTCAAGATCCAGCTGCT 1315
Qy 403 ValLysSerLeuCyLeuAlaLysHisGlyIleGluTyGlnGluLysProLeuLeuArgAla 422
Db 1316 GTGAGAGCCCTGTGCAAAAGTACATATCGATACCAACACCGGTATGATCGAGGA 1375
Qy 423 LeuLeuAspIleIleArgSerLeuLysLysSerGlyLys 435
Db 1376 ACTGCAGAGGTCTTTAGCGCTGTGAACGAGGTCTCCAAG 1414
RESULT 37
US-08-834-033A-1
; Sequence 1, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUITZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 11-APR-1997
; APPLICATION NUMBER: US/08/834,033A
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-834-033A-1
Alignment Scores:
Pred. No.: 1,51e-43 Length: 1617
Score: 459.00 Matches: 118
Percent Similarity: 43.55% Conservative: 88
Best Local Similarity: 24.95% Mismatches: 183
Query Match: 18.83% Indels: 84
Gaps: 14
US-09-719-601-5 (1-444) x US-08-834-033A-1 (1-1617)
Qy 17 SerValProThrPheSerTrpGluGluIle-----GlnLys 28
Db 86 AGTGTGAGGACGTTTACTCGGCCGAGGTTTGAATGCGGAGCTCTGATGAGGCGAAG 145
Qy 29 HisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyAsnIleThrLys 48
Db 146 AAGGATCCGAGGCGACCCCTTCTTGTGATCATCATCGACAAACAGGTGTACGATGTCGCGAG 205

QY 49 TrpSerIleGlnHisProGlyClyGlnArgValIleGlyHisTyrAlaGlyGluAspAla 68
 Db 206 TTGTCCTCCGATCATCCCGGTGGAAGTGTATCTTCAGCAC--GTTGGCAAGACGCG 262
 QY 69 ThrAspAlaPheArgAlaPheHisProAspLeuGluPheValIleGlyLysPheLeuLysPro 88
 Db 263 ACTGACGCTTTTGACACTTTTCAACCC-----GAGGCTGCTGGGAGACCTTTGCCAAC 316
 QY 89 LeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLys 108
 Db 317 TTTTACGTTGGTGATATT-----GACGAGACGACCGCGATATC---AAGAATGATGAC 367
 QY 109 IleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThr 128
 Db 368 TTTGCGCGCGAGGTCGCGAGCTGCTGCTGTTCCAGTCTCTGTTACTTACTTACGATTCT 427
 QY 129 AsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrp 148
 Db 428 TCAAGGCATCTACACCTTCAAGGTCCTGTTCAACCTCTGCATCTGGGGTTTTCGACG 487
 QY 149 PheThrValPheTyrPheGly---AsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
 Db 488 GTCATTGTGCCAAGTGGGCGCAGACTCGACCTCGCCACAGTCTCTCGGCTGGCTT 547
 QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187
 Db 548 TTGGGTCTGTTCTGGCAGCAGTGGGATGTTGGCTCAGCACTTTTTCATCACCAGTCT 607
 QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
 Db 608 TTCAGACCGCTTTCGGGTGATCTTTTCGGCGCTTCTGGGAGTCTCTGCCAGGC 667
 QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProLeuIlePhe 227
 Db 668 TTCTCGCTCTGCTGGTGGAGGACAGCACACACTCACACCGCCGCCCAACGTCAC 727
 QY 228 HisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIle 247
 Db 728 GGCAGGATCCGACATGACCCACCTCTGTTGACCTGGAGTAC-----775
 QY 248 GluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePhe 267
 Db 776 -----CATCGTTGGAGATGTTCTCG 796
 QY 268 LeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMet 287
 Db 797 GATGTCACAGATGAGGAGCTACCCGATGTGTGCGCTTC-----ATG 841
 QY 288 IleValHisLysAsnTrp-----ValAspLeuAlaTrpAla 299
 Db 842 GTCCTGAACACAGCTGTTTACTTCCCATCTCTCGTTGCGCTCTCTCTCTCTCTGTC 901
 QY 300 ValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyVala 319
 Db 902 CTCACG---TCCATTCTTTTGTCTGCTGCTAACCGTCAAGCCCAAGCCCTCGGGCGG 958
 QY 320 LeuLeuPheLeuAsnPheIleArg-----PheLeuGluSerHisTrpPheValTrp--- 336
 Db 959 CGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1015
 QY 336 -----336
 Db 1016 CTCGCCACCATGTTCTCTGTTTCATCAAGGATCCCGTCAACATGCTGGTGTTCTTTTGGTG 1075
 QY 337 -----ValThrGlnMetAsnHisIleValMet 345
 Db 1076 TCGAGGCGGTGCGGAAACTTGTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1135
 QY 346 GluIle-----AspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAla 362
 Db 1136 CCGTGTGATCTCAAGAGGAGGCGGTGCTGATATGATGATTTCTTCAAGACGATCATCAGC 1195

QY 363 ThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGln 382
 Db 1196 GGTGCGATGTCACCCCGGTCTATTGTCACCACTGTTTCAAGGTTGAACTATCAG 1255
 QY 383 IleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeu 402
 Db 1256 ATCGACACACACTGTTCCCTTCGATGCTCGCCCACTTTTCAAGATCCAGCTGCT 1315
 QY 403 ValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAla 422
 Db 1316 GTCGAGACCTGTGCAAAAAGTACATGTCGATACACACCCGCTATGATCGAGGGA 1375
 QY 423 LeuLeuAspIleIleArgSerLeuLysLysSerGlyLys 435
 Db 1376 ACTGACAGGCTCTTACCGCTGGAACGAGGCTCTCCAAG 1414

RESULT 38
 US-09-363-574-1
 ; Sequence 1, Application US/09363574
 ; Patent No. 6136574
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUITZON, DEBORAH
 ; APPLICANT: MURKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
 ; STREET: 2001 FERRY BUILDING
 ; CITY: SAN FRANCISCO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/363,574
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WARD, MICHAEL R.
 ; REGISTRATION NUMBER: 38,651
 ; REFERENCE/DOCKET NUMBER: CGAB-202 USA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 433-4150
 ; TELEFAX: (415) 433-8716
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1617 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; US-09-363-574-1

Alignment Scores:
 Pred. No.: 1,518-43 Length: 1617
 Score: 459.00 Matches: 118
 Percent Similarity: 43.55% Conservative: 88
 Best Local Similarity: 24.95% Mismatches: 183
 Query Match: 18.83% Indels: 84
 Gaps: 14
 DB: 3

US-09-719-601-5 (1-444) x US-09-363-574-1 (1-1617)
 QY 17 SerValProThrPheSerTrpGluGluIle-----GlnLys 28

Db	86	AGTGTGAGGACGTTTACTCTCGGCGGAGGTTTGAATGCCGAGGCTCTGAATCAGGCGCAAG	145
Qy	29	HisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyraenilleThrLys	48
Db	146	AAGATGCCGAGGACCCCTTCTTGATGATCATCGACAACAGGTGTACGATGCCCGGAG	205
Qy	49	TrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyraenilleGluAspAla	68
Db	206	TTGCTCCCTCATCATCCGGTGAAGTGTGATTTCTCACGCAC---GTTGCAAGGACGGC	262
Qy	69	ThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysPro	88
Db	263	ACTGACGTCCTTTGACACTTTTACCC---GAGCTCTCTGGGAGACTCTTGCCAAC	316
Qy	89	LeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLys	108
Db	317	TTTTACGTTGGTGATATT---GACGAGAGGACCGCATATC---AAGAATGATGAC	367
Qy	109	IleThrGluAspPheArgAlaLeuArgGlyThrAlaGluAspMetAsnLeuPheLysThr	128
Db	368	TTTGGCGCCGAGGTCGCAAGCTGCGTCTGTTCAGGCTCTCTGGTGTACTACGATCT	427
Qy	129	AsnHisValPhePheLeuLeuLeuAlaHisIleAlaLeuGluSerIleAlaTrp	148
Db	428	TCCAAGCATACTACGGCTTCAAGGCTCTCGTCAACCTCTGCATCTGGGTTTGTGACG	487
Qy	149	PheThrValPheTyrrPheGly---AsnGlyTrpIleProThrLeuIleThrAlaPheVal	167
Db	488	GTCATTGTGCCAAGTGGGCGACACTCGACCTCGCCACCTGCTCGGTGGTGGCTT	547
Qy	168	LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrrGlyHisLeuSerVal	187
Db	548	TTGGGCTGTCTCGCAGCAGTCGGATGTTGGCTCACGACTTTTGGCATCACCAGGTC	607
Qy	188	TyrArgLysProLysThrPheAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly	207
Db	608	TTCCAGACACGGTTTCTGGGTGTGATCTTTTGGGCGCTTCTTGGAGGTGCTCCGAGGC	667
Qy	208	AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePhe	227
Db	668	TTCTCGTCCTGCTGGTGAAGGACAGACACACTCACCACGCGCCGCCAACAGTCCAC	727
Qy	228	HisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIle	247
Db	728	GGCAGGATCCGACATTGACACCCACCCCTCTGTTGACCTGGAGTGAG---775	
Qy	248	GluTyrrGlyLysLysLysLysLysTyrrLeuProTyrrAsnHisGlnHisGlyTyrrPhePhe	267
Db	776	-----CATGGTGGAGATGTTCTCG	796
Qy	268	LeuIleGlyProProLeuLeuIleProMetTyrrPheGlnTyrrGlnIleIleMetThrMet	287
Db	797	GATCTCCAGATGAGGACGTGACCCGATGTGGTGGGTTTC-----ATG	841
Qy	288	IleValHisLysAsnTrp-----ValAspLeuAlaTrpAla	299
Db	842	GTCCTGAACAGACCTGGTTTACTTCCCATCTCTCGTTGCGCCCTCTCTCTGGTGC	901
Qy	300	ValSerTyrrIleArgPhePheIleThrTyrrIleProPheTyrrGlyIleLeuGlyVala	319
Db	902	CTCCAG---TCCATTCTTTGTCTGCTGCTCAACGGTCAAGCCACAGCCCTCGGCGCG	958
Qy	320	LeuLeuPheLeuAsnPheIleArg-----PheLeuGluSerHisTrpPheValTrp---	336
Db	959	CGTGTGCCCATCTCGTTGGTCGAGCAGGTGTGGTTCGATGTCACCTGG---ACCTGTGAC	1015
Qy	336	-----336	
Db	1016	CTGGCCACCATGTCCTGTTTCATCAAGGATCCGTCACATGCTGGTGTACTTTTGGTG	1075
Qy	337	-----ValThrGlnMetAsnHisIleValMet	345

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Query Match: 18.83% Indels: 84
DB: 4 Gaps: 14

US-09-719-601-5 (1-444) x US-09-363-526-1 (1-1617)

QY 17 SerValProThrPheSerTrpGluGluLeu-----GlnLys 28
DB 86 AGTGTGAGGACGTTTACTCGGCGGAGGTTTGAATCGGAGGCTCTGAATGAGGCGAAG 145
QY 29 HisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyraAsnIleThrLys 48
DB 146 AAGGATGCCGAGCACCCTTCTTGTATCATCATGACACCAACAGGTGTACCATGTCGCGAG 205
QY 49 TrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyraGlyGluAspAla 68
DB 206 TTGCTCCCTCATCATCCCGGTGAGTGTGATCTTCCAGCAC---GTTGGCAAGGACGC 262
QY 69 ThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysPro 88
DB 263 ACTGACGCTCTTGCACACTTTTCAACCC---GAGGCTGCTTGGGAGACTCTTGGCCAAC 316
QY 89 LeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLys 108
DB 317 TTTTACGTTGCTGATAT-----GACGAGCGACGCGGATATC---AGATGATGATGAC 367
QY 109 IleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThr 128
DB 368 TTTGCGGCGGAGTCCGCAAGTCCGATCTTCTCCAGTCTCTTGGTACTACGATTCT 427
QY 129 AsnHisValPhePheLeuLeuLeuAlaHisIleAlaLeuGluSerIleAlaTrp 148
DB 428 TCCAAGGCATACGCTTCAAGGCTCTGCTTCAACCTTGCATCTGGGCTTGTGACG 487
QY 149 PheThrValPheTyPheGly---AsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
DB 488 GTCATTTGCGCAAGTGGGCGCAGACCTCGACCTCGCCAACTGCTCGGCTGGCTT 547
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrglyHisLeuSerVal 187
DB 548 TTGGGTCTGTTCGGACGAGTGGGATGTTGGCTCAGCAGCTTTTGCATCACCAAGTTC 607
QY 188 TyrglyLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
DB 608 TTCAGGACCGTTCTCGGGGTGATCTTTTCGGCGCTTCTTGGAGGTGCTGCCAGGCG 667
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisIleAlaLysProAsnIlePhe 227
DB 668 TTTCTCGTCTCGTGGTGGAGGACAGACAACTCACCACTCCGCGCCGCCCAACGTCAC 727
QY 228 HisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIle 247
DB 728 GCGGAGATCCGACATGACACCCCTCTGTGACCTGGAGTGAG-----775
QY 248 GluTyrglyLysLysLysLeuLysTyrglyLeuProTyraAsnHisGlnHisGluTyrglyPhe 267
DB 776 -----CATCGTGTGGAGATGTTCTCG 796
QY 268 LeuIleGlyProProLeuLeuIleProMetTyrglyGlnIleMetThrMet 287
DB 797 GATGTCACGATGAGGAGCTGACCCGCGATGTGTGCGGTTTC-----ATG 841
QY 288 IleValHisLysAsnTrp-----ValAspLeuAlaTrpAla 299
DB 842 GTCCTGAACAGACCTGTTTACTTCCCATTCCTCTCGTTTCCCGCTCTCTCTGCTGTC 901
QY 300 ValSerTyrglyLeuArgPhePheIleThrTyrglyProPheTyrglyIleLeuGlyAla 319
DB 902 CTCAG---TCCATTCTTCTGCTGCTTAACGGTCAAGGCGCCCAAGCCCTCGGCGCG 958
QY 320 LeuLeuPheLeuAsnPheIleArg-----PheLeuGluSerHisTrpPheValTrp--- 336
DB 959 CGTGTGCCCATCTCGTGGTGCAGACGCTGTGCGTTGCGATGACACTGG---ACCTGTGATC 1015

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QY 336 -----336
DB 1016 CTCGCCACCATGTTCTGTTTCATCAGGATCCCGTCAACATGCTGGTGTTACTTTTTGGTG 1075
QY 337 -----ValThrGlnMetAsnHisIleValMet 345
DB 1076 TCGCAGCGGTGTGCGGAAACTTGTGGCGATCGTGTTCGCTCAACCAACGCGTATG 1135
QY 346 GluIle-----AspGlnGluAlaTyraArgAspTrpPheSerSerGlnLeuThrAla 362
DB 1136 CCGTGTGATCTCGAAGGAGGCGGTGCTGATGATTTCTTCAGAGCAGATCATCAG 1195
QY 363 ThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGln 382
DB 1196 GGTGCTGATGTCACCGCGGTCTATTTGCCAACTGTTTCCAGGTTCAGGTTGATGAATCAG 1255
QY 383 IleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeu 402
DB 1256 ATCAGACCACTTGTTCCTTCGATCGCTCGCCACCACTTTTCAMAGATCCAGCTGCT 1315
QY 403 ValLysSerLeuCysAlaLysHisGlyIleGluTyrglyGlnLysProLeuLeuArgAla 422
DB 1316 GTCGAGACCTGTGCAAAAAGTACATGTCGATACCAACCGGTATGATCGAGGGA 1375
QY 423 LeuLeuAspIleIleArgSerLeuLysSerGlyLys 435
DB 1376 ACTGAGAGGTCTTTAGCGCTCTGACGAGGTCTCCAAAG 1414

RESULT 40
US-09-330-235-17
; Sequence 17, Application US/09330235
; Patent No. 6459018
; GENERAL INFORMATION:
; APPLICANT: Knutson, Debbie
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
; FILE REFERENCE: MOCO.156.00US
; CURRENT APPLICATION NUMBER: US/09/330,235
; CURRENT FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: 60/089,043
; PRIOR FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 17
; TYPE: DNA
; LENGTH: 1617
; ORGANISM: Mortierella alpina
US-09-330-235-17

Alignment Scores:
Pred. No.: 151e-43 Length: 1617
Score: 459.00 Matches: 118
Percent Similarity: 43.55% Conservative: 88
Best Local Similarity: 24.95% Mismatches: 183
Query Match: 18.83% Indels: 84
DB: 4 Gaps: 14

US-09-719-601-5 (1-444) x US-09-330-235-17 (1-1617)
QY 17 SerValProThrPheSerTrpGluGluLeu-----GlnLys 28
DB 86 AGTGTGAGGACGTTTACTCGGCGGAGGTTTGAATCGGAGGCTCTGAATGAGGCGAAG 145
QY 29 HisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyraAsnIleThrLys 48
DB 146 AAGGATGCCGAGCACCCTTCTTGTATCATCATGACACCAACAGGTGTACCATGTCGCGAG 205
QY 49 TrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyraGlyGluAspAla 68
DB 206 TTGCTCCCTCATCATCCCGGTGAGTGTGATCTTCCAGCAC---GTTGGCAAGGACGC 262
QY 69 ThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysPro 88
DB 263 ACTGACGCTCTTGCACACTTTTCAACCC-----GAGGCTGCTTGGGAGACTCTTGGCCAAC 316

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QY 89 LeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLys 108
Db 317 TTTTACGTTGTGATATT-----GACGAGGACGACCGGATATC---AAGATGATGAC 367
QY 109 IleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThr 128
Db 368 TTTCGGCCGAGGTCCGCAAGCTCGTACCTTTGTCAGTCTCTTTGGTTACTACGATTCT 427
QY 129 AsnHisValPhePheLeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTirp 148
Db 428 TCCAGGCATACTACGCCCTTCAAGTCTCGTTCAACCTTCGATCTCGGGTTTGTGCACG 487
QY 149 PheThrValPheTyrPheGly---AsnGlyTirpIleProThrLeuIleThrAlaPheVal 167
Db 488 GTCATTTGTGGCAAGTGTGGGCGACACCTCGCACCTCGCCACGTCCTCGGCTCGCGCTT 547
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTirpLeuGlnHisAspTyrGlyHisLeuSerVal 187
Db 548 TTGGTCTGTCTGGCAGCATGCGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 607
QY 188 TyrArgLysProLysTirpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 608 TTCCAGGACCGTTTCTGGGGTGTCTTTTCGGCGCTTCTTGGGAGGTGTCTGCCAGGCG 667
QY 208 AlaSerAlaAsnTirpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
Db 668 TTCCTGCTCTGTGTGAAGACAGACACACTCACACGCGCGCGCGCGCGCGCGCGCGCG 727
QY 228 HisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTirpGlnProIle 247
Db 728 GCGGAGGATCCGACATTGACACCCACCTCTGTGTACCTGGAGTGAG-----ATG 775
QY 248 GluTyrGlyLysLysLysLysLysLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePhe 267
Db 776 -----CATGGTTGGAGATGTTCTCG 796
QY 268 LeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMet 287
Db 797 GATGTCGCCAGATGAGGAGTCACCGCATGTGGTGGCTTC-----ATG 841
QY 288 IleValHisLysAsnTirp-----ValAspLeuAlaTirpAla 299
Db 842 GTCTCTGAACACGACCTGTTTACTTCCCACTTCTCGTTTGGCCGCTCTCTCTCTGGTGC 901
QY 300 ValSerTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAla 319
Db 902 CTCCAG---TCCATTCTTTTGTGCTGCTAACGCTAGGCCCAAGCCCTCGGGCGCG 958
QY 320 LeuLeuPheLeuAsnPheIleArg-----PheLeuGluSerHisTirpPheValTirp--- 336
Db 959 CGTGTGCCCATCTCTGTTGGTCGAGCAGCTGTGCTTGGATGTCACCTGG---ACCTGGTAC 1015
QY 336 ----- 336
Db 1016 CTCGCCACCATGTTCTCTGTTTCATCAGGATCCCGTCACATGCTGGTGACTTTTGGTG 1075
QY 337 -----ValThrGlnMetAsnHisIleValMet 345
Db 1076 TCGCAGGGGGTGTGCGGAACCTTGTGGCGATCGTGTCTCGCTCAACCAACGCGTATG 1135
QY 346 GluIle-----AspGlnGluAlaTyrArgAspTirpPheSerSerGlnLeuThrAla 362
Db 1136 CCGTGTGATCTCGAAGGAGGCGGCGTATGGAATTTCTTCAGACGACATCATCAG 1195
QY 363 ThrCysAsnValGluGlnSerPhePheAsnAspTirpPheSerGlyHisLeuAsnPheGln 382
Db 1196 GGTGCTGATGTCCACCGGGTCTATTTCGCAACTGTTTACGGGTGGATTCAACTATCAG 1255
QY 383 IleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeu 402
Db 1256 ATCGAGCACCACTTGTTCCTCTCGATGCTCGCCCAACTTTTCAAGATCCAGCCTGCT 1315
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QY 403 VallysSerLeuCyseAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAla 422
Db 1316 GTCGAGACCTGTGCAAAAAGTACAAATGTCCGATACCAACACCGGTATGATCGAGGGA 1375
QY 423 LeuLeuAspIleIleArgSerLeuLysLysSerGlyLys 435
Db 1376 ACTGACAGAGGTCTTTAGCGCTCTGAACGAGGTCTCCAAG 1414
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Search completed: December 10, 2003, 20:07:32
Job time : 109 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2003, 10:14:26 ; Search time 39 Seconds
(without alignments)
2937.830 Million cell updates/sec

Title: US-09-719-601-5
Perfect score: 2438
Sequence: 1 MKGNGQEGAAAREVSVPT.....DIIRSLKSKGLWLDAYLHK 444

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2425	99.5	444	Q95864	Q95864 homo sapien
2	2190	89.8	444	Q92122	Q92122 rattus norv
3	2189	89.8	444	Q920R9	Q920R9 mus musculus
4	2111	86.6	386	Q96H07	Q96H07 homo sapien
5	2070	84.9	422	Q9H3G3	Q9H3G3 homo sapien
6	1703	69.9	311	Q9Y3X4	Q9Y3X4 homo sapien
7	1687.5	69.2	445	Q9AY64	Q9AY64 sparus aura
8	1668	68.4	454	Q98SW7	Q98SW7 oncorhynch
9	1662	68.2	452	Q9UWM5	Q9UWM5 oncorhynch
10	1653	67.8	454	Q9QGE2	Q9QGE2 salmo salar
11	1642	67.4	454	Q90ZB8	Q90ZB8 oncorhynch
12	1599	65.6	444	Q9DEX6	Q9DEX6 cyprinus ca
13	1564.5	64.2	445	Q90ZB9	Q90ZB9 oreochromis
14	1560.5	64.0	445	Q9Y5Q0	Q9Y5Q0 homo sapien
15	1551.5	63.6	449	Q9JJE7	Q9JJE7 mus musculus
16	1551.5	63.6	449	Q8C4Y5	Q8C4Y5 mus musculus

17	1550.5	63.6	449	11	Q8K1P9	Q8K1P9 rattus norv
18	1545.5	63.4	449	11	Q8CDZ4	Q8CDZ4 mus musculus
19	1516	62.2	444	4	Q60427	Q60427 homo sapien
20	1515	62.1	501	4	Q8NGG0	Q8NGG0 homo sapien
21	1512	62.0	444	4	Q96T10	Q96T10 homo sapien
22	1508	61.9	444	4	Q96T10	Q96T10 homo sapien
23	1508	61.9	444	4	Q9NYX1	Q9NYX1 homo sapien
24	1504	61.7	501	4	Q8NCC7	Q8NCC7 homo sapien
25	1502.5	61.6	444	4	Q9NRP8	Q9NRP8 homo sapien
26	1502	61.6	444	4	Q96SV3	Q96SV3 homo sapien
27	1473	60.4	447	11	Q920R3	Q920R3 rattus norv
28	1471	60.3	447	11	Q920L1	Q920L1 mus musculus
29	1470	60.3	447	11	Q8VC07	Q8VC07 mus musculus
30	1467	60.2	447	11	Q8ROG8	Q8ROG8 mus musculus
31	1459	59.8	447	11	Q9EPV4	Q9EPV4 rattus norv
32	1090.5	44.7	287	11	Q8BZX7	Q8BZX7 mus musculus
33	908	37.2	168	4	Q96SV8	Q96SV8 homo sapien
34	850.5	34.9	352	4	Q60426	Q60426 homo sapien
35	724	29.7	255	11	Q8BV36	Q8BV36 mus musculus
36	651	26.7	189	13	Q8AYC7	Q8AYC7 sparus aura
37	531	21.8	520	10	Q9LEM9	Q9LEM9 ceratodon p
38	517	21.2	483	10	Q9LENO	Q9LENO ceratodon p
39	516.5	21.2	477	10	Q8RXB0	Q8RXB0 phaeodactyl
40	510	20.9	525	10	Q9ZNV2	Q9ZNV2 physcomitri
41	497	20.4	459	10	Q944W4	Q944W4 pythium irr
42	471	19.3	457	3	Q9UVY3	Q9UVY3 mortierella
43	470	19.3	457	3	Q9HEY4	Q9HEY4 mortierella
44	469	19.2	457	3	Q8X173	Q8X173 mortierella
45	467	19.2	446	10	Q9ZTY9	Q9ZTY9 ricinus com

ALIGNMENTS

RESULT 1

Q95864	ID	Q95864	PRELIMINARY;	PRT;	444 AA.
AC	Q95864;				
DT	01-MAY-1999	(TrEMBLrel. 10, Created)			
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)			
DT	01-OCT-2002	(TrEMBLrel. 22, Last annotation update)			
DE	Delta-6 fatty acid desaturase (Fatty acid desaturase 2) (Hypothetical protein FLJ90458).				
GN	FADS2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99085046; PubMed=9867867;				
RA	Cho H.P., Nakamura M.T., Clarke S.D.;				
RT	"Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase.";				
RL	J. Biol. Chem. 274:471-477(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20318619; PubMed=10860662;				
RA	Marquardt A., Stohr H., White K., Weber B.H.F.;				
RT	"cDNA cloning, genomic structure, and chromosomal localization of three members of the human fatty acid desaturase family.";				
RL	Genomics 66:175-183(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Iscgai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu Y., Nakamura Y., Kojima S., Nagahari K., Masubo Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;				
RT	"NEDO human cDNA sequencing project.";				
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.				
DR	EMBL; AF126799; AAD20018.1; -.				

DR EMBL; AF084559; AAG23121.1; --
 DR EMBL; AX074939; BAC11305.1; --
 DR HSP; P00171; IES1.
 DR Genew; HGNC:3575; FADS2.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROMEBS.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
 DR Hypothetical protein; Heme.
 KW Heme.
 SQ SEQUENCE 444 AA; 52259 MW; F65CE58076961A7A CRC64;

Query Match 99.5%; Score 2425; DB 4; Length 444;
 Best Local Similarity 99.5%; Pred. No. 7.1e-209;
 Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGKGGNQGGAAREVSVPTFSWEEIQKNLRTDGLVIDRKVYNTKWSIQHPGQORVI 60
 Db 1 MGKGGNQGGAAREVSVPTFSWEEIQKNLRTDGLVIDRKVYNTKWSIQHPGQORVI 60

QY 61 GHVAGEDATDAFRAFPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTA 120
 Db 61 GHVAGEDATDAFRAFPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTA 120

QY 121 EDNVLKFTNHVFFLLLAHIIAIESIAWFTVFYFGNGWPTLITAFVLATSOAQAGWLQH 180
 Db 121 EDNVLKFTNHVFFLLLAHIIAIESIAWFTVFYFGNGWPTLITAFVLATSOAQAGWLQH 180

QY 181 DYGLSVYRKPKNNHLVHKFVIGHLKGASANNWNRHFQHHAKPNI FHKDPDVMMLHVFV 240
 Db 181 DYGLSVYRKPKNNHLVHKFVIGHLKGASANNWNRHFQHHAKPNI FHKDPDVMMLHVFV 240

QY 241 LGHQPIEYKCKKLKYL PYNHQQEYFFLIGPPLLIIPMYQYQIIMTMIVHKWVDLAWAV 300
 Db 241 LGHQPIEYKCKKLKYL PYNHQQEYFFLIGPPLLIIPMYQYQIIMTMIVHKWVDLAWAV 300

QY 301 SYVIRFFITIPYIGILGALLFNIRFLESHWFWVVTQNNHIVMEIDQAYRDFSSQL 360
 Db 301 SYVIRFFITIPYIGILGALLFNIRFLESHWFWVVTQNNHIVMEIDQAYRDFSSQL 360

QY 361 TATCNVQSFNDFWFSGLNFIQEHHLFPTMPRHNLHKIAPLVKSLCAKHGIEYQEKPLL 420
 Db 361 TATCNVQSFNDFWFSGLNFIQEHHLFPTMPRHNLHKIAPLVKSLCAKHGIEYQEKPLL 420

QY 421 RALLDIIRSLKSGKMLDAYLHK 444
 Db 421 RALLDIIRSLKSGKMLDAYLHK 444

RESULT 2
 Q9Z122 PRELIMINARY; PRT; 444 AA.

AC Q9Z122 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Delta-6 fatty acid desaturase.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley; TIGSUS=Liver;
 RX MEDLINE=99160394; PubMed=10049752;
 RA Aki T., Shimada Y., Inagaki K., Higashimoto H., Kawamoto S.,
 RA Shigeta S., Ono K., Suzuki O.;
 RA "Molecular cloning and functional characterization of rat delta-6
 fatty acid desaturase";
 RL Biochem. Biophys. Res. Commun. 255:575-579 (1999).

CC -! SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AB021980; BAA75496.1; --
 DR HSP; P00171; IES1.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROMEBS.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
 DR Heme.
 KW Heme.
 SQ SEQUENCE 444 AA; 52380 MW; D9AE0C7AE499A1AE CRC64;

Query Match 99.8%; Score 2190; DB 11; Length 444;
 Best Local Similarity 97.8%; Pred. No. 8.2e-188;
 Matches 390; Conservative 26; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGKGGNQGGAAREVSVPTFSWEEIQKNLRTDGLVIDRKVYNTKWSIQHPGQORVI 60
 Db 1 MGKGGNQGGAAREVSVPTFSWEEIQKNLRTDGLVIDRKVYNTKWSIQHPGQORVI 60

QY 61 GHVAGEDATDAFRAFPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTA 120
 Db 61 GHVAGEDATDAFRAFPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTA 120

QY 121 EDNVLKFTNHVFFLLLAHIIAIESIAWFTVFYFGNGWPTLITAFVLATSOAQAGWLQH 180
 Db 121 EDNVLKFTNHVFFLLLAHIIAIESIAWFTVFYFGNGWPTLITAFVLATSOAQAGWLQH 180

QY 181 DYGLSVYRKPKNNHLVHKFVIGHLKGASANNWNRHFQHHAKPNI FHKDPDVMMLHVFV 240
 Db 181 DYGLSVYRKPKNNHLVHKFVIGHLKGASANNWNRHFQHHAKPNI FHKDPDVMMLHVFV 240

QY 241 LGHQPIEYKCKKLKYL PYNHQQEYFFLIGPPLLIIPMYQYQIIMTMIVHKWVDLAWAV 300
 Db 241 LGHQPIEYKCKKLKYL PYNHQQEYFFLIGPPLLIIPMYQYQIIMTMIVHKWVDLAWAV 300

QY 301 SYVIRFFITIPYIGILGALLFNIRFLESHWFWVVTQNNHIVMEIDQAYRDFSSQL 360
 Db 301 SYVIRFFITIPYIGILGALLFNIRFLESHWFWVVTQNNHIVMEIDQAYRDFSSQL 360

QY 361 TATCNVQSFNDFWFSGLNFIQEHHLFPTMPRHNLHKIAPLVKSLCAKHGIEYQEKPLL 420
 Db 361 TATCNVQSFNDFWFSGLNFIQEHHLFPTMPRHNLHKIAPLVKSLCAKHGIEYQEKPLL 420

QY 421 RALLDIIRSLKSGKMLDAYLHK 444
 Db 421 RALLDIIRSLKSGKMLDAYLHK 444

RESULT 3
 Q9Z0R9 PRELIMINARY; PRT; 444 AA.

AC Q9Z0R9 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Delta-6 fatty acid desaturase.
 GN FADS2 OR FADS2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99085046; PubMed=9667967;
 RA Cho H.P., Nakamura M.T., Clarke S.D.;
 RA "Cloning, expression, and nutritional regulation of the mammalian
 Delta-6 desaturase";
 RL J. Biol. Chem. 274:471-477 (1999).
 CC -! SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF126798; AAD20017.1; --


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DR HSP; P00171; 115U.
DR MGD; MGI:1930079; Fads2.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat fam. 2.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 444 AA; 52387 MW; 7615D17024D3B771 CRC64;

Query Match 89.8%; Score 2189; DB 11; Length 444;
Best Local Similarity 87.2%; Pred. No. 1e-187;
Matches 387; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

QY 1 MGKGNQGEAAERVSPTFSWEIOKHNLTDSGLVIDRKVNIITKWSIQHPGGQV 60
DB 1 MGKGNQGEAAERVSPTFSWEIOKHNLTDSGLVIDRKVNIITKWSIQHPGGQV 60
QY 61 GHYAGEDATDAFRAPHPDLEFVGKFLKPLLIIGELAPEPSQDHGKNSKITEDFRALKTA 120
DB 61 GHYAGEDATDAFRAPHPDLEFVGKFLKPLLIIGELAPEPSQDHGKNSKITEDFRALKTA 120
QY 121 EDNLFKTNHVFLLLAHIIALESIAFTVFYFGNGWIPITLITAFVLATSOAAGWLQH 180
DB 121 EDNLFKTNHVFLLLAHIIALESIAFTVFYFGNGWIPITLITAFVLATSOAAGWLQH 180
QY 181 DYGLHSVYRKPKWNHVKFVIGHLKGSANWNNHRHFQHHAKPNI FHKDPDNNMLHVFV 240
DB 181 DYGLHSVYRKPKWNHVKFVIGHLKGSANWNNHRHFQHHAKPNI FHKDPDNNMLHVFV 240
QY 241 LGSEWQIEYGGKKLKYLPYNHOHEYFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300
DB 241 LGSEWQIEYGGKKLKYLPYNHOHEYFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300
QY 301 SYIIRFFITYIPFYGILGALLFLNFIRFLESHWVFWVTQNNHIVMEIDQEAIRDWFSQ 360
DB 301 SYIIRFFITYIPFYGILGALLFLNFIRFLESHWVFWVTQNNHIVMEIDQEAIRDWFSQ 360
QY 361 TATCNVEQSFNDWFSCHLNFOIEH 444
DB 361 TATCNVEQSFNDWFSCHLNFOIEH 444
QY 421 RALLDIIRSLKSGKMLDAYLHK 444
DB 421 RALLDIIRSLKSGKMLDAYLHK 444

RESULT 4
Q96H07 PRELIMINARY; PRT; 386 AA.
ID Q96H07 AC Q96H07;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fatty acid desaturase 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; BC090111; AA090111.1;
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme_1; 1.

Query Match 84.9%; Score 2070; DB 4; Length 422;
Best Local Similarity 96.2%; Pred. No. 4.4e-177;
Matches 380; Conservative 0; Mismatches 5; Indels 10; Gaps 2;

QY 53 HPGQQRVIGHYAGEDAT---DAFRAPHPDLEFVGKFLKPLLIIGELAPEPSQDHGKNSKI 109
DB 35 HPAS-----AGHPITGQDAPRAFPDLEFVGKFLKPLLIIGELAPEPSQDHGKNSKI 87

DR PRINTS; PR00363; CYTOCHROME_B5.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat fam. 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 386 AA; 45524 MW; 2A18FA9CBFBPE432 CRC64;

Query Match 86.6%; Score 2111; DB 4; Length 386;
Best Local Similarity 99.5%; Pred. No. 8.3e-181;
Matches 383; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGKGNQGEAAERVSPTFSWEIOKHNLTDSGLVIDRKVNIITKWSIQHPGGQV 60
DB 1 MGKGNQGEAAERVSPTFSWEIOKHNLTDSGLVIDRKVNIITKWSIQHPGGQV 60
QY 61 GHYAGEDATDAFRAPHPDLEFVGKFLKPLLIIGELAPEPSQDHGKNSKITEDFRALKTA 120
DB 61 GHYAGEDATDAFRAPHPDLEFVGKFLKPLLIIGELAPEPSQDHGKNSKITEDFRALKTA 120
QY 121 EDNLFKTNHVFLLLAHIIALESIAFTVFYFGNGWIPITLITAFVLATSOAAGWLQH 180
DB 121 EDNLFKTNHVFLLLAHIIALESIAFTVFYFGNGWIPITLITAFVLATSOAAGWLQH 180
QY 181 DYGLHSVYRKPKWNHVKFVIGHLKGSANWNNHRHFQHHAKPNI FHKDPDNNMLHVFV 240
DB 181 DYGLHSVYRKPKWNHVKFVIGHLKGSANWNNHRHFQHHAKPNI FHKDPDNNMLHVFV 240
QY 241 LGSEWQIEYGGKKLKYLPYNHOHEYFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300
DB 241 LGSEWQIEYGGKKLKYLPYNHOHEYFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300
QY 301 SYIIRFFITYIPFYGILGALLFLNFIRFLESHWVFWVTQNNHIVMEIDQEAIRDWFSQ 360
DB 301 SYIIRFFITYIPFYGILGALLFLNFIRFLESHWVFWVTQNNHIVMEIDQEAIRDWFSQ 360
QY 361 TATCNVEQSFNDWFSCHLNFOIEH 385
DB 361 TATCNVEQSFNDWFSCHLNFOIEH 385

RESULT 5
Q9H3G3 PRELIMINARY; PRT; 422 AA.
ID Q9H3G3 AC Q9H3G3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P5327.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mesothelium;
RA Zhang J.S.S.; Reddel R.R.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF108658; AAC43192.1;
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA desaturase; 1.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat fam. 2.
KW Heme.
SQ SEQUENCE 422 AA; 49326 MW; A4A7EB76FBF1FFA4 CRC64;

Query Match 84.9%; Score 2070; DB 4; Length 422;
Best Local Similarity 96.2%; Pred. No. 4.4e-177;
Matches 380; Conservative 0; Mismatches 5; Indels 10; Gaps 2;

QY 53 HPGQQRVIGHYAGEDAT---DAFRAPHPDLEFVGKFLKPLLIIGELAPEPSQDHGKNSKI 109
DB 35 HPAS-----AGHPITGQDAPRAFPDLEFVGKFLKPLLIIGELAPEPSQDHGKNSKI 87

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QY 110 TEDFRALRKTAEEDMNLKTNHVFLLLAHIIAIESIAWFTVYFGNGWIPITLITAFVLA 169
Db 88 TEDFRALRKTAEEDMNLKTNHVFLLLAHIIAIESIAWFTVYFGNGWIPITLITAFVLA 147
QY 170 TSOAQAGWLQHDYGHLSVTRKPKNNHVLKFKVIGHLKGSANWNNHRRHFQHHAKNIFHK 229
Db 148 TSOAQAGWLQHDYGHLSVTRKPKNNHVLKFKVIGHLKGSANWNNHRRHFQHHAKNIFHK 207
QY 230 DPVNNMLHVFVLGEWQPIEYGGKKLKYLPYNHGHYFFLLGPPLLIPMYFOYQIIMTMIV 289
Db 208 DPVNNMLHVFVLGEWQPIEYGGKKLKYLPYNHGHYFFLLGPPLLIPMYFOYQIIMTMIV 267
QY 290 HKWVPLAWAVSYIRFFIYIPYIGILGALLFLNFIREFLESWFVWVQMMHIVMEIDQ 349
Db 268 HKWVPLAWAVSYIRFFIYIPYIGILGALLFLNFIREFLESWFVWVQMMHIVMEIDQ 327
QY 350 EAYRDWFSQLTATCNVEQSFNDWFSGLNFOIEHLLPPTWPRNHLKIAPLVKSCLAK 409
Db 328 EAYRDWFSQLTATCNVEQSFNDWFSGLNFOIEHLLPPTWPRNHLKIAPLVKSCLAK 387
QY 410 HGIEYQEKPLLRALLDIIIRSLKSGKWLDAYLHK 444
Db 388 HGIEYQEKPLLRALLDIIIRSLKSGKWLDAYLHK 422

RESULT 6
QY3X4 PRELIMINARY; PRT; 311 AA.
AC QY3X4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE Hypothetical protein (Fragment).
GN DKFZP586C201.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050118; CAB43280.1; -.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 311 AA; 37132 MW; BD9DC62CD2D7F4CD CRC64;

Query Match 69.9%; Score 1703; DB 4; Length 311;
Best Local Similarity 99.3%; Pred. No. 2.3e-144;
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 138 AHIIALESIAWFTVYFGNGWIPITLITAFVLATSOAQAGWLQHDYGHLSVTRKPKNNHLV 197
Db 5 AHIIALESIAWFTVYFGNGWIPITLITAFVLATSOAQAGWLQHDYGHLSVTRKPKNNHLV 64
QY 198 HKFVIGHLKGSANWNNHRRHFQHHAKNIFHKDPVNNMLHVFVLGEWQPIEYGGKKLKYLP 257
Db 65 HKFVIGHLKGSANWNNHRRHFQHHAKNIFHKDPVNNMLHVFVLGEWQPIEYGGKKLKYLP 124
QY 258 PYNHGHYFFLLGPPLLIPMYFOYQIIMTMIVHKNWVDLAWAVSYIRFFIYIPYIGIL 317
Db 125 PYNHGHYFFLLGPPLLIPMYFOYQIIMTMIVHKNWVDLAWAVSYIRFFIYIPYIGIL 184
QY 318 GALLFLNFIREFLESWFVWVQMMHIVMEIDQAYRDWFSQLTATCNVEQSFNDWFSG 377
Db 185 GALLFLNFIREFLESWFVWVQMMHIVMEIDQAYRDWFSQLTATCNVEQSFNDWFSG 244
QY 378 HLNFOIEHLLPPTWPRNHLKIAPLVKSCLAKHGIEYQEKPLLRALLDIIIRSLKSGKWL 437

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Db 245 HLNFOIEHLLPPTWPRNHLKIAPLVKSCLAKHGIEYQEKPLLRALLDIIIRSLKSGKWL 304
QY 438 LDAYLHK 444
Db 305 LDAYLHK 311

RESULT 7
QY3X4 PRELIMINARY; PRT; 445 AA.
AC QY3X4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Putative delta 6-desaturase.
GN FD6D.
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RA Seilliez I., Panzerat S., Kaushik S., Bergot P.;
RL "Cloning, tissue distribution and nutritional regulation of a delta 6-
RL desaturase-like enzyme in gilthead seabream".
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055749; AAL17639.1; -.
SQ SEQUENCE 445 AA; 51820 MW; BOB98E1AF9F6C9AA CRC64;

Query Match 69.2%; Score 1687.5; DB 13; Length 445;
Best Local Similarity 65.1%; Pred. No. 9.1e-143;
Matches 291; Conservative 63; Mismatches 88; Indels 5; Gaps 2;

QY 1 MGKGG---NQEGAAAEVSVPTFSWEIQKHNLRDTSGLVIDRKVNYIKWSIQHPGQ 57
Db 1 MGGGGQLTEPGEPSRRAGV--YTWEEVQSHSRNDQWLVIDRKVNYVTWKAKRHPGGF 58
QY 58 RVIGHYAGEDATDAFRAHPDLEPVGKFLKPLLIGELAPEEPSODHGKNSKITEDFRALR 117
Db 59 RVINHYAGEDATEAFTAFHPDLKFKVQKFLKPLLIGELAAATEPSQDRKNNAVIODFTLR 118
QY 118 KTAEDMNLKTNHVFLLLAHIIAIESIAWFTVYFGNGWIPITLITAFVLATSOAQAGW 177
Db 119 AOAESDGLFRAQPLFFCLHLGHILLLEALAWLIITLWGTSGTWTLTFLISIIATAQOAGW 178
QY 178 LQHDYGHLSVTRKPKNNHVLKFKVIGHLKGSANWNNHRRHFQHHAKNIFHKDPVNNMLH 237
Db 179 LQHDYGHLSVTRKPKNNHVLKFKVIGHLKGSANWNNHRRHFQHHAKNIFHKDPVNNMLH 238
QY 238 VFLGEMQPIEYGGKKLKYLPYNHGHYFFLLGPPLLIPMYFOYQIIMTMIVHKNWVDLA 297
Db 239 IFVLGDTQPEYGIKKIKYLPYHHQHYFLVGPPLIPVYFHTQIIRTWISRDWVDLA 298
QY 298 WAVSYIRFFIYIPYIGILGALLFLNFIREFLESWFVWVQMMHIVMEIDQAYRDWFS 357
Db 299 WMSYLYRLCCYPLVGLFSGVALISFVREFLESWFVWVQMMHLPMDIDHEKHDLT 358
QY 358 SOLTATCNVEQSFNDWFSGLNFOIEHLLPPTWPRNHLKIAPLVKSCLAKHGIEYQEK 417
Db 359 MQLQATCNIEKSVFNDWFSGLNFOIEHLLPPTWPRNHYHLVAFLVHALCEKHGIPYQVK 418
QY 418 PLRLALLDIIIRSLKSGKWLDAYLHK 444
Db 419 TWWQGIIVDIRSLKNSGDLWDLAYLHK 445

RESULT 8
QY3X7 PRELIMINARY; PRT; 454 AA.
AC QY3X7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

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DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Putative delta 6-desaturase.
GN F68P
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Sirisuv S., Yoshizaki G., Kiron V., Takeuchi T., Gen K.;
RC TISSUE=Liver;
RA Seillez I., Panserat S., Kaushik S., Bergot P.;
RT "Cloning, tissue distribution and nutritional regulation of a delta-6-
RT desaturase-like enzyme in rainbow trout.";
RL Comp. Biochem. Physiol. B, Comp. Biochem. 130:83-93(2001).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF301910; AAK26745.1; -.
DR HSSP; P00171; IES1.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme 1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS0255; CYTOCHROME_BS_2; 1.
KW Heme.
SQ SEQUENCE 454 AA; 52398 MW; 18E5D811420D537 CRC64;

Query Match 68.4%; Score 1668; DB 13; Length 454;
Best Local Similarity 64.8%; Pred. No. 5.2e-141;
Matches 294; Conservative 65; Mismatches 89; Indels 10; Gaps 2;

QY 1 MGKGNQGEGA--AREVSV-----TPSWEEIQKHNLRTDGLVIDRKVNITKWS 50
DB 1 MGCGGQQTESSEPVKGDGPDGGRGGSAAVTWEVQKHCHRSQWLVIDREVNIQWAKR 60
QY 51 IOHGGQVGHVAGEDATDAFRAHPDLEFVGKFLKPLLGELAPEPSODHGKNSKIT 110
DB 1 MGCGGQQTESSEPVKGDGPDGGRGGSAAVTWEVQKHCHRSQWLVIDREVNIQWAKR 60
QY 61 KRHPGIRVISHFAGEDATDAFRAHPDNPVFRKFLKPLLGELATTPESODHGKNAVIV 120
DB 111 EDRALRTAEDMNLKTNHVPFLLLAHIIALESIAWFTVFYFGNGWIPFLITAFVLTAT 170
DB 121 QDFQALDRVEREGLRLARPLFFSLYLGHILLLEALGLLWVGTSWSLTLCSLMLAT 180
QY 171 SOAGWLOHDYGHLSVVRKPKWNHVKFVIGHLKGASANNWNRHHPQHAKNI PHKD 230
DB 181 SOSAGWLOHDYGHLSVCKTSNNHVKFVIGHLKGASANNWNRHHPQHAKNPVFSKD 240
QY 231 PDVNNMLHVPVLGEMOPIBYGKKLKYLPYNHCHVEFFLIGPLLPIMYFOYQIIMTVH 290
DB 241 PDVNSLHVPVLGDKQVVEYIGKKLYMPVHHQYFFLIGPLLPVFTTQIFQTFESQ 300
QY 291 KRWDLAWAVSYIRFFITYIPFYIGLALLFLNPIRFLSHFWVVTQMNHIVNEIDOE 350
DB 301 RNVVDLAWAMTYLRFCCYYPFFGFGSVALISFVRFLESHFWVVTQMNHLPWEIDHE 360
QY 351 AYKDFSSQLTATCNVEQSFNDWFSGLNFQIEHLLPFTPRNLHKLIAPLVKSCLAKH 410
DB 361 RHQDWLTQWLSATCNIEQSTFNDWFSGLNFQIEHLLPFTPRNHYHLVAPLALCEKH 420
QY 411 GYEQEKLRLALLDIIRSLKSKGLWLDAYLHK 444
DB 421 GLPYQVKTLOKAIIDVVGSLKSGDLWLDAYLHK 454

RESULT 9
Q8UWMS PRELIMINARY; PRT; 452 AA.
AC Q8UWMS
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)

DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Putative delta 6-desaturase.
GN F68P
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Sirisuv S., Yoshizaki G., Kiron V., Takeuchi T., Gen K.;
RC TISSUE=Liver;
RA Seillez I., Panserat S., Kaushik S., Bergot P.;
RT "Cloning, tissue distribution and nutritional regulation of a delta-6-
RT desaturase-like enzyme in rainbow trout.";
RL Comp. Biochem. Physiol. B, Comp. Biochem. 130:83-93(2001).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AB074149; BAB71963.1; -.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme 1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS0255; CYTOCHROME_BS_2; 1.
KW Heme.
SQ SEQUENCE 452 AA; 52288 MW; 47B1857733E6CAD0 CRC64;

Query Match 68.2%; Score 1662; DB 13; Length 452;
Best Local Similarity 63.9%; Pred. No. 1.8e-140;
Matches 289; Conservative 68; Mismatches 87; Indels 8; Gaps 1;

QY 1 MGKGNQ-----GEGAAAREVSVTPFSWEEIQKHNLRTDGLVIDRKVNITKWSIQ 52
DB 1 MGCGGQQTESSEPVKGDGPDGGRGGSAAVTWEVQKHCHRSQWLVIDREVNIQWAKR 60
QY 53 HPGQVGHVAGEDATDAFRAHPDLEFVGKFLKPLLGELAPEPSODHGKNSKIT 112
DB 61 HPGGIRVISHFAGEDATDAFRAHPDNPVFRKFLKPLLGELATTPESODHGKNAVIGD 120
QY 113 FRALRTAEDMNLKTNHVPFLLLAHIIALESIAWFTVFYFGNGWIPFLITAFVLTAT 172
DB 121 FOALDRVEREGLRLARPLFFSLYLGHILLLEALGLLWVGTSWSLTLCSLMLAT 180
QY 173 AQAGWLOHDYGHLSVVRKPKWNHVKFVIGHLKGASANNWNRHHPQHAKNI PHKD 232
DB 181 SOAGWLOHDYGHLSVCKTSNNHVKFVIGHLKGASANNWNRHHPQHAKNPVFSKD 240
QY 233 VNNMLHVPVLGEMOPIBYGKKLKYLPYNHCHVEFFLIGPLLPIMYFOYQIIMTVHKN 292
DB 241 INSLHVPVLGDKQVVEYIGKKLYMPVHHQYFFLIGPLLPVFTTQIFQTFESQ 300
QY 293 WVDLAWAVSYIRFFITYIPFYIGLALLFLNPIRFLSHFWVVTQMNHIVNEIDOEAY 352
DB 301 WVDLAWAMTYLRFCCYYPFFGFGSVALISFVRFLESHFWVVTQMNHLPWEMDHERH 360
QY 353 RDNFSSQLTATCNVEQSFNDWFSGLNFQIEHLLPFTPRNLHKLIAPLVKSCLAKHGI 412
DB 361 QDWLTQWLSATCNIEQSTFNDWFSGLNFQIEHLLPFTPRNHYHLVAPLALCEKHGI 420
QY 413 EYQEKPLRLALLDIIRSLKSKGLWLDAYLHK 444
DB 421 PYQVKTLOKAIIDVVGSLKSGDLWLDAYLHK 452

RESULT 10
Q8QGE2 PRELIMINARY; PRT; 454 AA.
AC Q8QGE2
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Putative delta-6 fatty acyl desaturase.
GN FADS6.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
SEQUENCE FROM N.A.
RA Hastings N. Jr., Agaba M.K., Tocher D.R., Teale A.J.;
RT "The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and
R Freshwater Teleosts";
R Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF478472; AL82631.1; -.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA_desaturase_1.
DR ProDom; PD000612; Cyt_B5_1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR ProSite; PS0255; CYTOCHROME_B5_2; 1.
DR Heme.
SQ SEQUENCE 454 AA; 52689 MW; DAEC6D815976BDD9 CRC64;
Query Match 67.8%; Score 1653; DB 13; Length 454;
Best Local Similarity 63.4%; Pred. No. 1.2e-139;
Matches 288; Conservative 69; Mismatches 87; Indels 10; Gaps 2;
OY 1 MGKGNQGEA--AREVSVP-----TFSWEEIQKHNLRDGLVIDRKVYNTKWS 50
DB 1 MGCGGQQTESSEPAKGDLPGDGGGSAVYTWEVQRSHRSQDLVDRKVNITQWA 60
OY 51 IOHPGGORVICHVAGEDATDAFAFHPDLEFVCKFLKPLLIGELAPEEPSQDHGKNSKIT 110
DB 61 KRHPGGIRVISHFAGEDATEAFVAFHLEPNFVRKFLKPLLIGELAPTEPSQDHGKNAVL 120
OY 111 EDFRALKTAEDMNLFTKTNHVFLLLIHAIILAESIAWFTVYFGNGWIFTLITAFVLAT 170
DB 121 QDFQALRDHVEREGLLARLFFSVLGHILLLEALGLLWGTWSLTLCSLMLAT 180
OY 171 SOAQAGLQHDYGHLSYVRKPKNNHLVHKFVIGHLKGASANNWNNHRRHFQHHAKPNIFHKD 230
DB 181 SOAQAGLQHDYGHLSYVRKPKNNHLVHKFVIGHLKGASANNWNNHRRHFQHHAKPNIFRKD 240
OY 231 PDVNLHVFVLGWPQIEYCKKLYLPYXNHQHEYFFLIGPPLLI PMYFQYQIIMTVH 290
DB 241 PDINSLFVFLGDTQVPEYGIKKLYMPYHHQYFFLIGPPLLI VPFVFNQIFRTMFSQ 300
OY 291 KNWVDLAWMSYIRPITTYIPFYGILGALLFNFRFLESHWFWVWTONHIVMEIDQE 350
DB 301 RDWVDLAWMSYIRPITTYIPFYGILGALLFNFRFLESHWFWVWTONHIVMEIDHE 360
OY 351 AYRDWFSQLTATCNVQSPFNDFSGHLNFQIEHHLFPTMPRNLHKLAPLVKSLCAKH 410
DB 361 RHQDMLTWQLSATCNISQSTFNDFSGHLNFQIEHHLFPTMPRNLHKLAPLVKSLCEKH 420
OY 411 GIEYQEKPLRALDIIRSLKSKGLWLDAYLHK 444
DB 421 GVPYQVTKLQGMTDVVRSLKSGDLWLDAYLHK 454
RESULT 11
Q90ZE8 PRELIMINARY; PRT; 454 AA.
ID Q90ZE8
AC Q90ZE8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative delta 6-desaturase.
GN FGD6.
OS Oncorhynchus masou (Cherry salmon) (Masu salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8020;
RN [1]
SEQUENCE FROM N.A.
RA Hastings N., Agaba M.K., Tocher D.R., Teale A.J., Sargent J.R.;
RT "The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and
R Freshwater Teleosts";
R Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB070444; BAB63440.1; -.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA_desaturase_1.
DR ProDom; PD000612; Cyt_B5_1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR ProSite; PS0255; CYTOCHROME_B5_2; 1.
DR Heme.
SQ SEQUENCE 454 AA; 52480 MW; 9PAA5E6A7A5CCF76 CRC64;
Query Match 67.4%; Score 1642; DB 13; Length 454;
Best Local Similarity 63.2%; Pred. No. 1.1e-138;
Matches 287; Conservative 70; Mismatches 87; Indels 10; Gaps 2;
OY 1 MGKGNQGEA--AREVSVP-----TFSWEEIQKHNLRDGLVIDRKVYNTKWS 50
DB 1 MGCGGQQTESSEPAKGDLPGDGGGSAVYTWEVQRSHRSQDLVDRKVNITQWA 60
OY 51 IOHPGGORVICHVAGEDATDAFAFHPDLEFVCKFLKPLLIGELAPEEPSQDHGKNSKIT 110
DB 61 KRHPGGIRVISHFAGEDATEAFVAFHLEPNFVRKFLKPLLIGELAPTEPSQDHGKNAVL 120
OY 111 EDFRALKTAEDMNLFTKTNHVFLLLIHAIILAESIAWFTVYFGNGWIFTLITAFVLAT 170
DB 121 QDFQALRDHVEREGLLARLFFSVLGHILLLEALGLLWGTWSLTLCSLMLAT 180
OY 171 SOAQAGLQHDYGHLSYVRKPKNNHLVHKFVIGHLKGASANNWNNHRRHFQHHAKPNIFHKD 230
DB 181 SOAQAGLQHDYGHLSYVRKPKNNHLVHKFVIGHLKGASANNWNNHRRHFQHHAKPNIFSKD 240
OY 231 PDVNLHVFVLGWPQIEYCKKLYLPYXNHQHEYFFLIGPPLLI PMYFQYQIIMTVH 290
DB 241 PDINSLFVFLGDTQVPEYGIKKLYMPYHHQYFFLIGPPLLI VPFVFNQIFRTMFSQ 300
OY 291 KNWVDLAWMSYIRPITTYIPFYGILGALLFNFRFLESHWFWVWTONHIVMEIDQE 350
DB 301 RDWVDLAWMSYIRPITTYIPFYGILGALLFNFRFLESHWFWVWTONHIVMEIDHE 360
OY 351 AYRDWFSQLTATCNVQSPFNDFSGHLNFQIEHHLFPTMPRNLHKLAPLVKSLCAKH 410
DB 361 RHQDMLTWQLSATCNISQSTFNDFSGHLNFQIEHHLFPTMPRNLHKLAPLVKSLCEKH 420
OY 411 GIEYQEKPLRALDIIRSLKSKGLWLDAYLHK 444
DB 421 GVPYQVTKLQGMTDVVRSLKSGDLWLDAYLHK 454
RESULT 12
Q9DEX6 PRELIMINARY; PRT; 444 AA.
ID Q9DEX6
AC Q9DEX6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative delta-6 fatty acyl desaturase.
GN FADS6.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
SEQUENCE FROM N.A.
RA Hastings N., Agaba M.K., Tocher D.R., Teale A.J., Sargent J.R.;
RT "The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and

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RT "cDNA cloning, genomic structure, and chromosomal localization of
 RT three members of the human fatty acid desaturase family.";
 RL Genomics 66:175-183(2000).

[3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF134404; AAD31282.1; -;
 DR EMBL; AF084560; AAG23122.1; -;
 DR EMBL; BC004901; AAH04901.1; -;
 DR HSP; P82291; ICXY.
 DR InterPro; IPR001199; Cy B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme 1; 1.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR ProDom; PD000612; Cy B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 DR PROSITE; PS02555; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 445 AA; 51145 MW; 7840EFG6BE055111D CRC64;

Query Match 64.0%; Score 1560.5; DB 4; Length 445;
 Best Local Similarity 62.3%; Pred. No. 2.2e-131;
 Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;

QY 1 MGKGGNQG--EGNAEREVSVPFSEIEIQKHLNRTDGLVIDRKVNITKSIQHPGQR 58
 DB 1 MGCVGPGGREGPAQGLPTFCMEQIRAHQDPGDKMLVIERVYDISRMAQRHPGGR 60
 QY 59 VIGHYAGE DATAFRAHFDLPBFGVGFLLGELAPPEPSQDGHGKSKITEDFRALRK 118
 DB 61 LIGHGAE DATAFRAHFDLPBFGVGFLLGELAPPEPSQDGHGKSKITEDFRALRK 120
 QY 119 TADNMFLKTNVFFVLLLAHIALESIAFWTFVFGNGWIFTLTAFVLATSOAQGL 178
 DB 121 AEDMKLFDASPTFFAFLLGHILAMEVLAWLLIYLLGPGWPSALAAFTLAISQASWCL 180
 QY 179 QHDYGHLSVYRKPKMNLVHKFVIGHLKGSANWNHRRHFQHKAPNIFPKDPDYNMLHV 238
 DB 181 QHDLGHASIFTKSRNHNVAQRVWGQKGFSAHWNFRHFQHKAPNIFPKDPDVTAPV 240
 QY 239 FLVGEWQPIYGGKKLKYLPYNHQBHYFFLIPPLIPMYFOYQIMTMVHKWVLDLW 298
 DB 241 FLLEGE--SSVEYGGKKERYLPYNQHLYFFLIPPLITLVNFEVENLAYMLVCMQADLLW 299
 QY 299 AVSYVIRFFTYIPFYGILGALLFLNFIREFLSHWFWVVTOMNHVMEIDQAYRDPSS 358
 DB 300 AASFYARFSLVLPFYGVFGVLLFFVAVRVLSHFWFWITQNNHLPKEIGHEKRDVSS 359
 QY 359 QLTATCNVQSFPNDWFSGLNFIQIEHLLFPMPRNLHKLAPLVKSLCAKHGIYQKBP 418
 DB 360 QLAATCNVPSLFTNWFSGHLNFIQIEHLLFPMPRNLHKLAPLVKSLCAKHGLSYEVKP 419
 QY 419 LLRALLDIIRSLKSKGLMLDAYLHK 444
 DB 420 FLTALVDIVRSLSKSGDIWLDAYLHQ 445

RESULT 15

Q9JUE7 PRELIMINARY; PRT; 449 AA.
 ID Q9JUE7
 AC Q9JUE7
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Brain cDNA, clone MNCB-0629, similar to Homo sapiens delta-6 fatty
 DE acid desaturase (CY55RP) mRNA.
 GN FADS3.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RA Osada N.; Kusuda J.; Tanuma R.; Ito A.; Hirata M.; Sugano S.;
 RA Hashimoto K.;
 RT "Isolation of full-length cDNA clones from mouse brain cDNA library
 RL made by oligo-capping method.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AB041560; BAA95044.1; -;
 DR HSP; P04166; IAWP.
 DR MGD; MGI:1928740; Fada3.
 DR InterPro; IPR001199; Cy B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme 1; 1.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR ProDom; PD000612; Cy B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 DR PROSITE; PS02555; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 449 AA; 51497 MW; 6FDB74EC8C07750B CRC64;

Query Match 63.6%; Score 1551.5; DB 11; Length 449;
 Best Local Similarity 61.6%; Pred. No. 1.4e-130;
 Matches 277; Conservative 61; Mismatches 105; Indels 7; Gaps 2;

QY 1 MGKGGNQGEGAAARE-----VSPFSEIEIQKHLNRTDGLVIDRKVNITKSIQHP 54
 DB 1 MGCVGPGGREGPAQGLPTFCMEQIRAHQDPGDKMLVIERVYDISRMAQRHP 60
 QY 55 GGORVIGHYAGE DATAFRAHFDLPBFGVGFLLGELAPPEPSQDGHGKSKITEDFR 114
 DB 61 GGSGLIGHGAE DATAFRAHFDLPBFGVGFLLGELAPPEPSQDGHGKSKITEDFR 120
 QY 115 ALKTAEDNMFLKTNVFFVLLLAHIALESIAFWTFVFGNGWIFTLTAFVLATSOAQ 174
 DB 121 ALRQAEDMKLFDADPTFFAFLLGHILAMEVLAWLLIYLLGPGWSSILAAITLAISQ 180
 QY 175 AGWLQHDYGHLSVYRKPKMNLVHKFVIGHLKGSANWNHRRHFQHKAPNIFPKDPDYN 234
 DB 181 CWCLQHDLGHASIFTKSRNHNVAQRVWGQKGFSAHWNFRHFQHKAPNIFPKDPVT 240
 QY 235 MLHVFLVGEWQPIYGGKKLKYLPYNHQBHYFFLIPPLIPMYFOYQIMTMVHKWV 294
 DB 241 VAPVFLLE--SSVEYGGKKERYLPYNQHLYFFLIPPLITLVNFEVENLAYMLVCMQ 299
 QY 295 DLAWAVSYVIRFFTYIPFYGILGALLFLNFIREFLSHWFWVVTOMNHVMEIDQAYRD 354
 DB 300 DLLWAASFYARFSLVLPFYGVFGVLLFFVAVRVLSHFWFWITQNNHLPKEIGHEKRD 359
 QY 355 WFSQLTATCNVQSFPNDWFSGLNFIQIEHLLFPMPRNLHKLAPLVKSLCAKHGIY 414
 DB 360 WASSQLAATCNVPSLFTNWFSGHLNFIQIEHLLFPMPRNLHKLAPLVKSLCAKHGLHY 419
 QY 415 QEKPLLRALLDIIRSLKSKGLMLDAYLHK 444
 DB 420 EVREFLTALVDIVRSLSKSGDIWLDAYLHQ 449

RESULT 16

Q8C4Y5 PRELIMINARY; PRT; 449 AA.
 ID Q8C4Y5
 AC Q8C4Y5
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fatty acid desaturase 3.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Cerebellum;
EX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK080414; BAC37908.1; -- OCC365378D479989 CRC64;
SQ SEQUENCE 449 AA; 51455 MW; 0CC365378D479989 CRC64;

Query Match 63.6%; Score 1551.5; DB 11; Length 449;
Best Local Similarity 61.6%; Pred. No. 1.4e-130;
Matches 277; Conservative 61; Mismatches 105; Indels 7; Gaps 2;

QY 1 MGKGNQGEAAARE-----VSVPTFSWBIQKHLNLTDSGLVIDSKVYNITKWSIQHP 54
DB 1 MGCVGPGGPGREGAPLPGAPLPIFRWEQIRHDLPGDKWLVIERVYDISRWAQRHP 60

QY 55 GQRVIGHYAGEDATDAFRPHDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFR 114
DB 61 GGSRLIGHGAEADATDAFHAFQDLHFVRKFLKPLLIGELAPEEPSQDGAQAQIEDFR 120

QY 115 ALRKAEDMNLKTNHVPFLLLAHIIALESIAFTVFYFGNGWIPTLITAFVLATSOAQ 174
DB 121 ALRQAEDMKLFEADSTFFALLGHILAMELLAWLIILYLLGPGWSSVLAALILASOAQ 180

QY 175 AGWLQHDYGHLSVYRKPKWNHVKFVGHILKGSANWNNHRRHPOHAKPNIHKPDVYN 234
DB 181 CWCLQHDLGHASIFTKSRWNHVAQFVNGQLKGSFSAHWNFRHPOHAKPNIHKPDVT 240

QY 235 MLHFVFLGEMQPIEVGKKLKYLPYNHCHVEFFLIGPLLPYFQYQIIMTVHKWV 294
DB 241 VAPVFLGE-SSVEYKXKRRYLPYNHCHVEFFLIGPLLPYFQYQIIMTVHKWV 299

QY 295 DLAWAVSYIRFFIYIPFYGILGALLFNIRFLESHFWFVVTQNNHIVMEIDQAYRD 354
DB 300 DLLWAASFSRFFLSYSPFYGATGTLFFAVRVLESFHWFWITQNNHIPKEIGEKHRD 359

QY 355 WFSQLTATCNVQSFNDWFSGLNFOIEHLFPTMPRHNLHKLAPLVKSLCAKHGIEY 414
DB 360 WASSQLAATCNVPSLFDWFSGLNFOIEHLFPTMPRHNRVAVPLVAFKACGHGLHY 419

QY 415 QEKPLLRALLDIIRSLKSGKGLWLDAYLHK 444
DB 420 EVKPFALTALVDIIGSLKSGDIWLDAYLHQ 449

RESULT 17
Q8KLP9 PRELIMINARY; PRT; 449 AA.
AC Q8KLP9;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Putative fatty acid desaturase.
GN FADS3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague Dawley; Tissue=Liver;
RA D'Andrea S., Guillou H., Jan S., Daval S., Rioux V., Legrand P.;
RT "Characterization of a novel putative fatty acid desaturase from
RT rat.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ494720; CAD38527.1; --
DR InterPro; IPR001199; Cyt_B5.

DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme 1; 1.
DR PRINTS; PR00363; CYTOCHROME B5.
DR ProDom; PD000812; Cyt_B5; 1.
DR ProDom; PD001081; FA desat. fam; 2.
KW Heme.
KW PROSITE; PS02555; CYTOCHROME_B5_2; 1.
SQ SEQUENCE 449 AA; 51467 MW; E2E33662095855AB CRC64;

Query Match 63.6%; Score 1550.5; DB 11; Length 449;
Best Local Similarity 61.8%; Pred. No. 1.8e-130;
Matches 278; Conservative 61; Mismatches 104; Indels 7; Gaps 2;

QY 1 MGKGNQGEAAARE-----VSVPTFSWBIQKHLNLTDSGLVIDSKVYNITKWSIQHP 54
DB 1 MGCVGPGGPGREGAPLPGAPLPIFRWEQIRHDLPGDKWLVIERVYDISRWAQRHP 60

QY 55 GQRVIGHYAGEDATDAFRPHDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFR 114
DB 61 GGSRLIGHGAEADATDAFHAFQDLHFVRKFLKPLLIGELAPEEPSQDGAQAQIEDFR 120

QY 115 ALRKAEDMNLKTNHVPFLLLAHIIALESIAFTVFYFGNGWIPTLITAFVLATSOAQ 174
DB 121 ALRQAEDMKLFEADSTFFALLGHILAMELLAWLIILYLLGPGWSSVLAALILASOAQ 180

QY 175 AGWLQHDYGHLSVYRKPKWNHVKFVGHILKGSANWNNHRRHPOHAKPNIHKPDVYN 234
DB 181 CWCLQHDLGHASIFTKSRWNHVAQFVNGQLKGSFSAHWNFRHPOHAKPNIHKPDVT 240

QY 235 MLHFVFLGEMQPIEVGKKLKYLPYNHCHVEFFLIGPLLPYFQYQIIMTVHKWV 294
DB 241 VAPVFLGE-SSVEYKXKRRYLPYNHCHVEFFLIGPLLPYFQYQIIMTVHKWV 299

QY 295 DLAWAVSYIRFFIYIPFYGILGALLFNIRFLESHFWFVVTQNNHIVMEIDQAYRD 354
DB 300 DLLWAASFSRFFLSYSPFYGATGTLFFAVRVLESFHWFWITQNNHIPKEIGEKHRD 359

QY 355 WFSQLTATCNVQSFNDWFSGLNFOIEHLFPTMPRHNLHKLAPLVKSLCAKHGIEY 414
DB 360 WASSQLAATCNVPSLFDWFSGLNFOIEHLFPTMPRHNRVAVPLVAFKACGHGLHY 419

QY 415 QEKPLLRALLDIIRSLKSGKGLWLDAYLHK 444
DB 420 EVKPFALTALVDIIGSLKSGDIWLDAYLHQ 449

RESULT 18
Q8CDZ4 PRELIMINARY; PRT; 449 AA.
AC Q8CDZ4;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Fatty acid desaturase 3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Head;
EX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK029318; BAC26393.1; --
SQ SEQUENCE 449 AA; 51495 MW; 4F0B689C90F22185 CRC64;

Query Match 63.4%; Score 1545.5; DB 11; Length 449;
Best Local Similarity 61.3%; Pred. No. 4.9e-130;

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Matches 276; Conservative 61; Mismatches 106; Indels 7; Gaps 2;

QY 1 MKGKGQSGAARE-----VSVTFSSWEETOKNLRDGLVIDRKVNITKWSIQHP 54
 DB 1 MGVGEPGGPGFREGAPLPIFRWEQIRQDLPGDKWLVIRRVYDISRWAOHRP 60

QY 55 GGVVGHVAGDADTAPAFPHDLEFVGKFKPLLIGELAPEEPSQDHGKNSKITEFR 114
 DB 61 GSRLLGHGADADTAPAFHQLDFVVKFKPLLIGELAPEEPSQDGAQNALIEDFR 120

QY 115 ALRKAEDNVLKFNHVFLLLAHIALESIAFWTFVFGNGWIPTLITAFVLAISOAQ 174
 DB 121 ALRKAEDNVLKFNHVFLLLAHIALESIAFWTFVFGNGWIPTLITAFVLAISOAQ 180

QY 175 AGWLQHDYHLSVYRKPKNLHVHFKVIGHLKAGANWNNHRRHFOHAKPNIFHKDPDVN 234
 DB 181 CWCQLQDLHRAIFYSKRNHVAQFVMOQLGSAHWNFRHFOHAKPNIFHKDPDVN 240

QY 235 MLHVFVLGWPQIEYKCKLKYLPYNNHVEYFFLIGPPLIPYFOYQIIMTVHKNWV 294
 DB 241 VAPVFLGE--SSVEYKCKRRVLPYNNHVEYFFLIGPPLIPYFOYQIIMTVHKNWV 299

QY 295 DLAWAYVYIRFTIYIPVGLGALLFLNFRFLESNFWVVTOMNHVMEIDOEAYRD 354
 DB 300 DLWAAFSYRFLSYSPFGATGTLFLVAVRVLESNFWVVTOMNHVMEIDOEAYRD 359

QY 355 WFSQLTATCNVQSPFNDFWFSGLNFIQIEHLFPTMPRHNLKIAPLVKSICAKHGIEY 414
 DB 360 WASSQLAPTCNVPSLFDWFSGLNFIQIEHLFPTMPRHNLKIAPLVKSICAKHGIEY 419

QY 415 QEKPLARALLDIIRSLKSKGLWLDAYLHK 444
 DB 420 EVKPFUTALVDIIGSLKSGDIWLDAYLHQ 449

RESULT 19

O60427 PRELIMINARY; PRT; 444 AA.

ID O60427 AC O60427; 1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE BC269730.2 (Hypothetical protein) (Fatty acid desaturase 1).
 GN DKFZP762M2311 OR FADS1.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCready P.M., Coleman M., Skowronski E., Adamson A.W.,
 RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
 RA Danganan L., Poundstone P., Christensen M., Amico-Keller G.,
 RA Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G.,
 RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
 RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
 RA Kobayashi A., Olsen A.S., Carrano A.V.,
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RA Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20318619; PubMed=10860662;
 RA Marquardt A., Schor H., White K., Weber B.H.F.;
 RT "cDNA cloning, genomic structure, and chromosomal localization of
 RT three members of the human fatty acid desaturase family."
 RL Genomics 66:175-183(2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DB EMBL; AC004770; AAC23397.1; --

Query Match 62.2%; Score 1516; DB 4; Length 444;
 Best Local Similarity 62.0%; Pred. No. 2.1e-127;
 Matches 272; Conservative 62; Mismatches 99; Indels 6; Gaps 3;

QY 11 AARESVSVPT---PSWEEIOKLNLRDGLVIDRKVNITKWSIQHPGQORVIGHYAGED 67
 DB 7 AATAAQGPPTPRYFTTWDEVAQRSGCBERWLVIDRKVNISEFTRRHPGGSRVISHYAGD 66

QY 68 ATDAFAFHDPLEFVGKFKPLLIGELAPEEPSQDHGKNSKITEFRALRKTAEADNLFK 127
 DB 67 ATDFVAFHINKGLVKKYNNLLIGELSPQSPFETKKNELTDEFRELATVERMGLMK 126

QY 128 TNHVFFLLLAHIALESIAFWTFVFGNGWIPTLITAFVLAISOAQAGWLQHDYHLSV 187
 DB 127 ANHVFFLLYLLHLLDGAALWLTWVFGTSFLPFLCAVLLSAVQAQAGWLQHDYHLSV 186

QY 188 YRKPKNNLHVHFKVIGHLKAGANWNNHRRHFOHAKPNIFHKDPDVNMLH--VFVLGEWQ 245
 DB 187 FSTSKNNLHVHFKVIGHLKAGAPASWNNHMFQHAKPNCERKDPDINN-HPFFALGKIL 245

QY 246 PIYKCKKLYLPYNNHVEYFFLIGPPLIPYFOYQIIMTVHKNWDLAWAVYYIR 305
 DB 246 SVELGKQKKYMPYNNHVEYFFLIGPPLIPYFOYQIIMTVHKNWDLAWAVYYIR 305

QY 306 PFITYIPFYGLGALLFLNFRFLESNFWVVTOMNHVMEIDOEAYRDWFSQLTATCN 365
 DB 306 FFLTYVFLGKAPLGLFFVIRFLESNFWVVTOMNHVMEIDOEAYRDWFSQLTATCN 365

QY 366 VEQSFNDFWFSGLNFIQIEHLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPLARALLD 425
 DB 366 VHKSAFNDFWFSGLNFIQIEHLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPLARALLD 425

QY 426 IIRSLKSKGLWLDAYLHK 444
 DB 426 IIRSLKSKGLWLDAYLHQ 444

RESULT 20
 ID Q8NCGO PRELIMINARY; PRT; 501 AA.
 AC Q8NCGO; 2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein FLJ90273.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
 RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.


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RESULT 22
Q96139 PRELIMINARY; PR7; 444 AA.
AC Q96139;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Patty acid desaturase 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Eute
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homin
OC NCBI_TaxId=9606;
RN [1]
RC SEQUENCE FROM N.A.
RA Straussberg R.;
PL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1-SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; BC007846; AAH07846.1; -.
DR InterPro; IPR001199; Cyt.B5.
DR InterPro; IPR005804; FA_Desat.fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme 1; 1.

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DR PRINTS; PR00363; CYTOCHROMEBS.
DR ProDom; PD000612; Cyt B5; 1.
DR ProSITE; PS001081; FA_desat_fam; 2.
DR ProSITE; PS00255; CYTOCHROME_B5_2; 1.
DR Heme.
SQ SEQUENCE 444 AA; 51954 MW; 2888BA9346A8A8A CRC64;

Query Match      61.9%; Score 1508; DB 4; Length 444;
Best Local Similarity 61.7%; Pred. No. 1.1e-126;
Matches 271; Conservative 62; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEEIQKNLRTDGLVIDRKVYNITKWSIOHPGQGVIGHYAGED 67
DB 7 AAETAAGQPTPRYFTDWEVAQSGCEERWLVIDRKVYNISEFTRRHPGGSRVISHYAGQD 66
QY 68 ATDAFAFPDLDFGVCKFLPKLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNMLFK 127
DB 67 ATDPFVAFHINKGLVKYNNLSLIGELSPQSFPTKNEKLTDFEFLRATVERMGLMK 126
QY 128 TNHVFLLLAHIALESIAFTVYFGNGWPTLTITAPVLATSOAQAGWLQHDYGHLSV 187
DB 127 ANHVFLLYLLHLLDGAAMLTLWVFGTSFLLCAVLLSAVQAQAGWLQHDYGHLSV 186
QY 188 YRKPKNHLVHKFVIGHLKASANNWHRHFQHHAKENIFHKDPDYNMLH--VFVLGEWQ 245
DB 187 FSTSKNNHLHFFVIGHLKGPASANNWHRHFQHHAKENIFHKDPDYNMLH--VFVLGEWQ 245
QY 246 PIEYGGKKLYLPYNHQHEFFYFLIGPPLIPYFQYQIIMTVIHKWVDLAWAVSYIR 305
DB 246 SVELGQKKKYPYNNHQHYFFLIGPPLIPYFQYQIIMTVIHKWVDLAWAVSYIR 305
QY 306 FFITYPFYIGLALLFLNFIRESHFVFWVQNNHIVNEIDQEAAYRDFSSQLTATCN 365
DB 306 FFITYPFYIGLALLFLNFIRESHFVFWVQNNHIVNEIDQEAAYRDFSSQLTATCN 365
QY 366 VEGSFNDFSGHNFQIEHLLFPTPRNLHKIAPLVKSLCAKHGIEYQEKPLRALLD 425
DB 366 VHSKAFNDFSGHNFQIEHLLFPTPRNLHKIAPLVKSLCAKHGIEYQEKPLRALLD 425
QY 426 IIRSLKSKGLWLDAYLHK 444
DB 426 IIRSLKSKGLWLDAYLHK 444

RESULT 24
Q8NCC7 PRELIMINARY; PRT; 501 AA.
AC Q8NCC7, 2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90338.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RA "NDO human cDNA sequencing project.";
RT Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AK074819; BAC11229.1;
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.

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DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
KW Hypothetical protein; Heme.
SQ SEQUENCE 501 AA; 57827 MW; C729B0DA3C54053C CRC64;

Query Match
Best Local Similarity 61.7%; Score 1504; DB 4; Length 501;
Matches 270; Conservative 63; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAERVSVP---FSWEEIQKHLRTDGLVIDRKYNTKWSIQHFGQORVIGHYAGED 67
DQ 64 AAEATAAQGTPRYFTWDEVAQSGCEERWLVIDRKYNISFTRRHGGSRVISHYAGD 123
QY 68 ATDAFRAPDLEFVGKFLKPLIGELAPEPSQDHGKSKITDFRALRKTAEADNMLFK 127
DQ 124 ATDPFVAHINKGLVKYKYNLSLIGELSEPSQSFETPKNKELTDFRELRAIVERMGLMK 183
QY 128 TNHVFLLLAHIIALESIAWTFVYFGNGWIPITLITAFVLATSOAQAGWLQHDYGHLSV 187
DQ 184 ANHVFFLLYLLHLLDGAWLTLWVFGTSFLPFLLCVLLSAVQAQAGWLQHDYGHLSV 243
QY 188 YRKPKNHLVHKFVCHLKGASANNWNRHFOHAKPNIFHKPDVNMH--VFVLGEWQ 245
DQ 244 FTSKWNHLHHRFVCHLKGASANNWNRHFOHAKPNIFHKPDVNMH--VFVLGEWQ 302
QY 246 PIEYGGKKLYLPYNHGEYFPLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAVSYVIR 305
DQ 303 SVELGKQKKYFYNHGEYFPLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAVSYVIR 362
QY 306 PFTIIPFVIGLLENFIRFLESHWVWVVTQNNHIVMEIDQAYRDWFSSQLTATCN 365
DQ 363 FLLTVPVLLGLKAFGLFVIRFLESHWVWVVTQNNHIVMEIDQAYRDWFSSQLTATCN 422
QY 366 VEQSFNDFWFSHNLFOIEHLFPMPRNHLKIAPLVKSICAKHGIEYQKPLRLALD 425
DQ 423 VKKSAFNDWFSHNLFOIEHLFPMPRNHLKIAPLVKSICAKHGIEYQKPLRLALD 482
QY 426 IIRSLKSGKGLWLDAYLHK 444
DQ 483 IIRSLKSGKGLWLDAYLHK 501

RESULT 25
Q9NRP8 PRELIMINARY; PRT; 444 AA.
AC Q9NRP8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Delta-5 desaturase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20069725; PubMed=10601301;
RA Cho H.P., Nakamura M., Clarke S.D.;
RT "Cloning, expression, and fatty acid regulation of the human delta-5
RT desaturase."
RL J. Biol. Chem. 274:37335-37339(1999).
RC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF199596; AAF29378.1; -.
DR HSSP; P04166; 1BSM.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme 1; 1.
DR PRINTS; PR00363; CYTOCHROME B5.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat. fam; 2.
DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 444 AA; 51980 MW; 78D476EB107891B2 CRC64;

Query Match
Best Local Similarity 62.4%; Score 1502.5; DB 4; Length 444;
Matches 266; Conservative 62; Mismatches 95; Indels 3; Gaps 2;

QY 21 FSWEEIQKHLRTDGLVIDRKYNTKWSIQHFGQORVIGHYAGEDATDAFRAPDLE 80
DQ 20 FTWDEVAQSGCEERWLVIDRKYNTSEFTRRHGGSRVISHYAGQDATDPFVAPHINKG 79
QY 81 FVGKFLKPLIGELAPEPSQDHGKSKITDFRALRKTAEADNMLFKTHVFPFLLLAH 140
DQ 80 LVKYNWNSLLIGELSEPSQSFETPKNKELTDFRELRAIVERMGLMKANHVFPFLLLH 139
QY 141 IALESIAWTFVYFGNGWIPITLITAFVLATSOAQAGWLQHDYGHLSVYRKPKNHLVHKF 200
DQ 140 LLDGAWLTLWVFGTSFLPFLLCVLLSAVQAQAGWLQHDYGHLSVYRKPKNHLVHKF 199
QY 201 VIGHLKGASANNWNRHFOHAKPNIFHKPDVNMH--VFVLGEWQPIYGGKKLYLP 258
DQ 200 VIGHLKGASANNWNRHFOHAKPNIFHKPDVNMH--VFVLGEWQPIYGGKKLYLP 258
QY 259 YNHQHEYFPLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAVSYVIRFITYIPFYGILG 318
DQ 259 YNHQHEYFPLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAVSYVIRFITYIPFYGILG 318
QY 319 ALLFNLPIRFLSHWVWVVTQNNHIVMEIDQAYRDWFSSQLTATCNVQSFNDFWFSGH 378
DQ 319 FLGLFPIRFLSHWVWVVTQNNHIVMEIDQAYRDWFSSQLTATCNVQSFNDFWFSGH 378
QY 379 LNFQIEHLFPMPRNHLKIAPLVKSICAKHGIEYQKPLRLALDIFRSKKSGKWL 438
DQ 379 LNFQIEHLFPMPRNHLKIAPLVKSICAKHGIEYQKPLRLALDIFRSKKSGKWL 438
QY 439 DAYLHK 444
DQ 439 DAYLHK 444

RESULT 26
Q96SV3 PRELIMINARY; PRT; 444 AA.
AC Q96SV3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ14616.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Yamanabe S., Kimura Y., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakanatsu A., Nakamura Y., Nagahara K., Masuho Y.,
RA Ninomiya K., Iwanaga T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AK027522; BAB55173.1; -.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme 1; 1.
DR PRINTS; PR00363; CYTOCHROME B5.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat. fam; 2.
DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
KW Hypothetical protein; Heme.
SQ SEQUENCE 444 AA; 51934 MW; 4BF7046AE343058B CRC64;
```

Query Match 61.6%; Score 1502; DB 4; Length 444;
 Best Local Similarity 61.7%; Pred. No. 3.9e-126;
 Matches 271; Conservative 62; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAEREVSPT---FSWEEIQKHLRTDGLVIDRKVYNITKWSIQHPGGQORVIGHYAGED 67
 DB 7 AAEATAAGGTPPYFTWDEVAQSGCEERWLVIDRKVYNISEFTRRHPGGSRVISHYAGOD 66

QY 68 ATDAFAFHPDLEFVCKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEEDMNLFK 127
 DB 67 ATDPFVAFHINKLVKYNLSLIGELSPQSFSEFTKNEKLTDBFRELRATVERMGLMK 126

QY 128 THNVFLLLAHIALESIAFWFVFGNGWPTLITAFVLATSAQAQWLOHGYCHLSV 187
 DB 127 ANHVFFLLVLLHLLDGAWLTLWVGTSFLPFLCVALLSAVQAQWLOHDFGLSV 186

QY 188 YRPKPNHLVHKVIGHLKGASANNVHRHFOHAKPNIFHKDPDNNMLH--VFVLGEWQ 245
 DB 187 FSTSKVNLHLHFEVIGHLKGASANNVHRHFOHAKPNIFHKDPDNNMLH--HPFFALGKIL 245

QY 246 PIEYGGKKLYLPYNHGHYFFLIGPPLIPMYFOYQIIMTVHKWVDLAWAVSYIR 305
 DB 246 SVELGQKKKYPYNHGHYFFLIGPPLIPMYFOYQIIMTVHKWVDLAWAVSYIR 305

QY 306 FETTYIPFGILGALLFLNFIRLESHWFWVTQNNHIVMEIDQAYRDWFSQATCN 365
 DB 306 FELTYVPLGLKAFGLFTVRELESNFWFWVTQNNHIVMEIDQAYRDWFSQATCN 365

QY 366 VEGSFNDWFSGLNFQIEHLEPPTPRNHLKIAPLVKSACAKGIEYQEXPLLRALID 425
 DB 366 VHSASFNDWFSGLNFQIEHLEPPTPRNHLKIAPLVKSACAKGIEYQEXPLLRALID 425

QY 426 IIRSLKSGKMLWDAYLHK 444
 DB 426 IIRSLKSGKMLWDAYLHQ 444

RESULT 27
 Q920R3 PRELIMINARY; PRT; 447 AA.

AC Q920R3
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Delta-5 fatty acid desaturase.
 GN DSD.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RC TISSUE=Liver;
 RP SEQUENCE FROM N.A.
 RA Ingaki K., Aki T., Shimada Y., Kawamoto S., Shigeta S., Ono K.,
 RA Suzuki O.;
 RT "Cloning and expression of rat liver delta-5 fatty acid desaturase."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AB052085.1; -!
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 DR PROSITE; PS02555; CYTOCHROME_B5_2; 1.
 KW Heme
 SQ SEQUENCE 447 AA; 52482 MW; 764D7D7C9AA3F7BE CRC64;

Query Match 60.4%; Score 1473; DB 11; Length 447;
 Best Local Similarity 61.8%; Pred. No. 1.5e-123;

Matches 264; Conservative 59; Mismatches 100; Indels 4; Gaps 3;

QY 21 PSWEEI-QKHLRTDGLVIDRKVYNITKWSIQHPGGQORVIGHYAGEDATDAFRAHPDL 79
 DB 22 FTWEEVAQSGRGRKRWLVIDRKVYNISDFSRHPGGSRVISHYAGQDAIDFVAHINK 81

QY 80 EFVKGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEEDMNLFKTNHVPFLLLAH 139
 DB 82 GLVRKYNLSLIGELAPEEPSPEPTKNAKLTDBFRELRATVERMGLMKANHLFFFLYLLH 141

QY 140 IIALESIAFWFVFGNGWPTLITAFVLATSAQAQWLOHGYCHLSVYRKPKNHLVHK 199
 DB 142 ILLDVAAWLTLWVGTSFLPFLCVALLSAVQAQWLOHDFGLSVFSTWTNHLVHH 201

QY 200 FVIGHLKGASANNVHRHFOHAKPNIFHKDPDNNMLH--VFVLGEWQPIEYGGKKLYL 257
 DB 202 FVIGHLKGASANNVHRHFOHAKPNIFHKDPDNNMLH--HPLFFALGKVLSELGKKEKKCHM 260

QY 258 PYNHGHYFFLIGPPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFEITVIFVGL 317
 DB 261 PYNHGHYFFLIGPPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFEITVIFVGL 320

QY 318 GALLFLNFIRLESHWFWVTQNNHIVMEIDQAYRDWFSQATCNVEQSFNDWFSG 377
 DB 321 GLCLCFIVRLESNFWFWVTQNNHIVMEIDQAYRDWFSQATCNVEQSFNDWFSG 380

QY 378 HLNFQIEHLEPPTPRNHLKIAPLVKSACAKGIEYQEXPLLRALIDIRSLKSGKMLW 437
 DB 381 HLNFQIEHLEPPTPRNHLKIAPLVKSACAKGIEYQEXPLLRALIDIRSLKSGKMLW 440

QY 438 LDAYLHK 444
 DB 441 LDAYLHQ 447

RESULT 28
 Q920L1 PRELIMINARY; PRT; 447 AA.

AC Q920L1
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Delta-5 desaturase.
 GN 0710001003RIK OR DSD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6; TISSUE=Liver;
 RA Matsuzaka T., Shimano H.;
 RT "Dual gene regulation of mouse delta-5 and -6 desaturases by SREBP-1
 and PPAR alpha."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AB072976; BAB68984.1; -!
 DR EMBL; AK083959; BAC39079.1; -!
 DR MGD; MGI:1923517; 0710001003RIK.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROME B5.

```

DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat_fam; 2.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 447 AA; 52323 MW; 1C69B61DF919A009 CRC64;

Query Match      60.3%; Score 1471; DB 11; Length 447;
Best Local Similarity 61.6%; Pred. No. 2.3e-123;
Matches 263; Conservative 62; Mismatches 98; Indels 4; Gaps 3;

QY 21 FSWEBI-QKHNLRITDGLVIDRKVYNITKWSIQHPGQGVIGHYAGEDATDAFRAHPDL 79
DB 22 FTWEVQAQSGREKRWLVDRKVNISDFSRHPGGSRVISHYAGQDATDFFVAFHINK 81
QY 80 ETVGFLKPLLLIGELAPEPSODHGKNSKITEDFALRKTAEADMLFKTNHVFLLLLAH 139
DB 82 GLVRKYNMSSLIGELAPEPSPTKKNKALTDEFRELRAATVERMGLMKANHLFFLVYLLH 141
QY 140 IIALESIAWTFVYFGNGWIPITLITAFVLATSOAAGWLQHDYGHLSVYRKPKNHLVHK 199
DB 142 ILLLDVAWLTIWIFGTSLVFPCVALLSTVQAAGWLQHDYGHLSVFGTSTWNHLHH 201
QY 200 FVIGHLKASANNWNRHFQHEAKNI PHKDPDVNMLH--VFVLGEWQPIEYGGKKLYL 257
DB 202 FVIGHLKAPASANNWNRHFQHEAKNCFRKPDPINN-HPLFFALGKVLPELGRKKCKM 260
QY 258 PYNHOHEYFELIGPPLIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFITYIPFYGIL 317
DB 261 PYNHQKHYFELIGPPLIPMYFOYQIIMTMVHKWVDLAWMLSFYARIFFTYMPLLGLK 320
QY 318 GALLFLNFIRESLHFWVMTQNMHIVMEIDQEAAYRDWFSQLTATCNVEQSFENDWFSG 377
DB 321 GFLGFFIVRPLESNWVMTQNMHIVMEIDHNRVDVWVSTQLQATCNVHQSFAFNWFSG 380
QY 378 HLNFOIEHLPPTMPRHNLKIAPLVKSIAKHGIEYOEKPLLRALLDITRSLKSKGLW 437
DB 381 HLNFOIEHLPPTMPRHNYHKVAPLVQSLCAKYGKIESKPLLTAFADIVYSLKESGLW 440
QY 438 LDAYLHK 444
DB 441 LDAYLHQ 447

RESULT 29
Q8VC07
ID Q8VC07 PRELIMINARY; PRT; 447 AA.
AC Q8VC07;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 52.3 kDa protein.
GN 0710001003RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue=Kidney;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; BC022139; AAH26831.1; -.
DR EMBL; BC026831; AAH26831.1; -.
DR MGD; MGI:1923517; 0710001003RIK.
DR InterPro; IPR001199; Cyt B5.
DR ProDom; PD000612; Cyt B5; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR Pfam; PF00487; FA_desaturase; 1.

DR ProDom; PD00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR ProDom; PD000612; Cyt B5; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Hypothetical protein; Heme.
SQ SEQUENCE 447 AA; 52337 MW; FOAFCCAL2919B8B2 CRC64;

Query Match      60.3%; Score 1470; DB 11; Length 447;
Best Local Similarity 61.4%; Pred. No. 2.9e-123;
Matches 262; Conservative 63; Mismatches 98; Indels 4; Gaps 3;

QY 21 FSWEBI-QKHNLRITDGLVIDRKVYNITKWSIQHPGQGVIGHYAGEDATDAFRAHPDL 79
DB 22 FTWEVQAQSGREKRWLVDRKVNISDFSRHPGGSRVISHYAGQDATDFFVAFHINK 81
QY 80 ETVGFLKPLLLIGELAPEPSODHGKNSKITEDFALRKTAEADMLFKTNHVFLLLLAH 139
DB 82 GLVRKYNMSSLIGELAPEPSPTKKNKALTDEFRELRAATVERMGLMKANHLFFLVYLLH 141
QY 140 IIALESIAWTFVYFGNGWIPITLITAFVLATSOAAGWLQHDYGHLSVYRKPKNHLVHK 199
DB 142 ILLLDVAWLTIWIFGTSLVFPCVALLSTVQAAGWLQHDYGHLSVFGTSTWNHLHH 201
QY 200 FVIGHLKASANNWNRHFQHEAKNI PHKDPDVNMLH--VFVLGEWQPIEYGGKKLYL 257
DB 202 FVIGHLKAPASANNWNRHFQHEAKNCFRKPDPINN-HPLFFALGKVLPELGRKKCKM 260
QY 258 PYNHOHEYFELIGPPLIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFITYIPFYGIL 317
DB 261 PYNHQKHYFELIGPPLIPMYFOYQIIMTMVHKWVDLAWMLSFYARIFFTYMPLLGLK 320
QY 318 GALLFLNFIRESLHFWVMTQNMHIVMEIDQEAAYRDWFSQLTATCNVEQSFENDWFSG 377
DB 321 GFLGFFIVRPLESNWVMTQNMHIVMEIDHNRVDVWVSTQLQATCNVHQSFAFNWFSG 380
QY 378 HLNFOIEHLPPTMPRHNLKIAPLVKSIAKHGIEYOEKPLLRALLDITRSLKSKGLW 437
DB 381 HLNFOIEHLPPTMPRHNYHKVAPLVQSLCAKYGKIESKPLLTAFADIVYSLKESGLW 440
QY 438 LDAYLHK 444
DB 441 LDAYLHQ 447

RESULT 30
Q8ROG8
ID Q8ROG8 PRELIMINARY; PRT; 447 AA.
AC Q8ROG8;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical 52.4 kDa protein.
GN 0710001003RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; BC026848; AAH26848.1; -.
DR MGD; MGI:1923517; 0710001003RIK.
DR InterPro; IPR001199; Cyt B5.
DR ProDom; PD000612; Cyt B5; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR Pfam; PF00487; FA_desaturase; 1.

```



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Db 61 QHAKPNCRKDPDINM-HPLFFALGKVLPELVGREKKHMPYNHQHKYFFELGIPGALLP 119
Qy 277 MYFQIIMTMVHKNNVDLAWAVSYIRFFITVIPPYIGILGALLFLNFRFLESHWFW 336
Db 120 LYFQWYIFVQKKNVDLAWLSFYARIFFTYMPLGLGKGFGLFFVIRFLESHWFW 179
Qy 337 VTQNHVWEIDQAYRWFSQLTATCNVQSFNDWFSQHLNFIQIEHLLFPTMPRHNL 396
Db 180 VTQNHVWEIDQAYRWFSQLTATCNVQSFNDWFSQHLNFIQIEHLLFPTMPRHNL 239
Qy 397 HKIAPLVKSLCAKHGIEQEPFLRALDIIRSLKSKGLWLDAYLHK 444
Db 240 HKVAPLVKSLCAKHGIEQEPFLRALDIIRSLKSKGLWLDAYLHQ 287

RESULT 33
Q96SV8
ID Q96SV8 PRELIMINARY; PRT; 168 AA.
AC Q96SV8
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ14607.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Nagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.
RT "NEO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027513; BAB55167.1; -.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 168 AA; 20218 MW; 4EE3991624210E12 CRC64;

Query Match 37.2%; Score 908; DB 4; Length 168;
Best Local Similarity 98.8%; Pred. No. 1.9e-73;
Matches 166; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 277 MYFQIIMTMVHKNNVDLAWAVSYIRFFITVIPPYIGILGALLFLNFRFLESHWFW 336
Db 1 MYFQIIMTMVHKNNVDLAWAVSYIRFFITVIPPYIGILGALLFLNFRFLESHWFW 60
Qy 337 VTQNHVWEIDQAYRWFSQLTATCNVQSFNDWFSQHLNFIQIEHLLFPTMPRHNL 396
Db 61 VTQNHVWEIDQAYRWFSQLTATCNVQSFNDWFSQHLNFIQIEHLLFPTMPRHNL 120
Qy 397 HKIAPLVKSLCAKHGIEQEPFLRALDIIRSLKSKGLWLDAYLHK 444
Db 121 HKIAPLVKSLCAKHGIEQEPFLRALDIIRSLKSKGLWLDAYLHK 168

RESULT 34
O60426
ID O60426 PRELIMINARY; PRT; 352 AA.
AC O60426
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Coleman M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomey M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a human BAC containing the FEN1 DNA repair
gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004770; AAC23396.1; -.
DR Genew; HGNC:3576; FADS3.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
FT NON TER 1_1
SQ SEQUENCE 352 AA; 39851 MW; 488341D5A1672399 CRC64;

Query Match 34.9%; Score 850.5; DB 4; Length 352;
Best Local Similarity 61.4%; Pred. No. 7.1e-68;
Matches 151; Conservative 35; Mismatches 59; Indels 1; Gaps 1;

Qy 70 DAFRAPHDLFVFGKFLKPLLIGELAPEPSQDHGKNSKITDFRALRKTAEDMNLFTKN 129
Db 1 DAFRAPHDLNFRKFLQLLIGELAPEPSQDGLNLAQLVEDFRALHQAEDMKLFDS 60
Qy 130 HVFFLLLLAHITALESIATFTVYFGNGWIPILITAFVLATSOAQAGWLOHGYHLSVTR 189
Db 61 PTFFAFLLGHILAMEVLAWLIIYLLPGWVPSALAAFTLAISQAQSWCLQDHLGHASIFK 120
Qy 190 KPKWNLVHKFVIGHLKGSANWNNHRHPQHAKNIPHKDPVNMHLHVFVLGEQPIEY 249
Db 121 KSWNHVAQKFMVQGLKGSANWNNHRHPQHAKNIPHKDPVNTVAPVFLIGE-SSVEY 179
Qy 250 GKKGKLYLPYNHGHYFFLIGPPLIIPYFYQYQYQYQYQYQYQYQYQYQYQYQYQY 309
Db 180 GKKGKLYLPYNHGHYFFLIGPPLIIPYFYQYQYQYQYQYQYQYQYQYQYQYQY 239
Qy 310 YIPFYG 315
Db 240 YIPFYG 245

RESULT 35
Q8BV36
ID Q8BV36 PRELIMINARY; PRT; 255 AA.
AC Q8BV36
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Delta-5 desaturase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK080706; BAC37985.1; -.
SQ SEQUENCE 255 AA; 29221 MW; 345E537DC5AF741B CRC64;
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(1)
RN  SEQUENCE FROM N.A.
RC  STRAIN=wt3; TISSUE=Protonemata;
RX  MEDLINE=20307617; PubMed=10848999;
RA  Sperling P., Lee M., Girke R., Zaehring U., Stymne S., Heinz E.;
RT  "A bifunctional delta 6-fatty acyl acetylase/desaturase from the
RT  moss Ceratodon purpureus. A new member of the cytochrome b5
RT  superfamily.";
RL  Eur. J. Biochem. 267:3801-3811(2000).
CC  -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR  EMBL: AJ250734; CAB94992.1; -.
DR  HSSP: P04166; 1BSM.
DR  InterPro: IPR001199; Cyt_B5.
DR  Pfam: PF00487; FA desaturase; 1.
DR  Pfam: PF00173; heme_1; 1.
DR  ProDom: PD000612; Cyt_B5; 1.
DR  ProDom: PD001081; FA desat. fam; 2.
DR  PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW  Heme.
SQ  SEQUENCE 483 AA; 54857 MW; C451D042169AB1C2 CRC64;

Query Match      21.2%; Score 517; DB 10; Length 483;
Best Local Similarity 30.5%; Pred. No. 8.4e-38;
Matches 140; Conservative 85; Mismatches 176; Indels 58; Gaps 18;

Qy  3 KGGNGEGAAAREV---SVPTSEWEEIOKHLRTDGLVIDRKVYNITKMSIQHPGQGV 59
Db  42 QGKTAGQTLRQSVQDKKPGTYSLADVASHDRPGDCWNVKVKYDISRFADDPFGG-TV 100
Qy  60 IGHVAGEDATDAFRAHFDLEFVGKFLPLLIIGELAPEEPSQDHGKSKITDPRLAKRT 119
Db  101 ISTYGRGTDVFATFHPAAM--KQNDYVIGDLAREEPLDE-----LLKYRDMRAE 152
Qy  120 AEDMNLPTNHNHVFLLLAHIALESIAWTFVFGNGWIPTLTITAFVLATSOAQAGWLQ 179
Db  153 FVREGLFSSKAWFLLQTLNAAFAASIAICYDKSYW-AIVLSASIMGLFVQCCGWL 211
Qy  180 HDYGHLSVYRKPKNHLVHKVIGHL-----KGASANNHHRHFQHKAKNIFHK----- 229
Db  212 HDFLHQVFE---NRTANSP-FGLFGNCVLGFSVSWRTKNIHTAPNECDEQITPL 266
Qy  230 DPVNMHLHVFVLGEWQ-----PIYGGKKLKYLPYNHQHEYFFLIGPPLIPMY----- 278
Db  267 DEDIDTLPIIA---WSKEILATVE-SKRLIRVLQVQH-----YMLPLLFMARYSWTFGS 317
Qy  279 ----FOYQIIMTM-IVHKQWVDLAWAVSYIRFTITVYFYGILGALLFLNFIREFLESHW 333
Db  318 LLFTFNPDLSTKGLIEKGTAFHYAFWFSWAAFIH--LP--GVAXPLAWMVATLVAGLL 373
Qy  334 FVWVTQNMHIVMEIDQAYRDWFSQTLATCNVQSPFNDFWFSGLHNFQIEHHLFPTMPR 393
Db  374 LGFVFTLSHGKGVYNES-KDFVRAQVITTRTKRGWENDFWFTGLOTLQIEHHLFPTMPR 432
Qy  394 HNLKHIAPLVKSLCKHGIEQKPELRLALDIIIRSLKK 432
Db  433 HNPXIAPEQVEALCKKHGLEVDNVSVGASVAVVYKALKE 471

RESULT 39
Q8RXB0 PRELIMINARY; PRT; 477 AA.
ID Q8RXB0
AC Q8RXB0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Delta 6 fatty acid desaturase D6.
GN D6
OS Phaeodactylum tricornutum.
OC Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
OC Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
OX NCBI_TaxID=2850;
RN (1)

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RP  SEQUENCE FROM N.A.
RC  STRAIN=UTEX 646;
RA  Donergue F., Ierchl J., Zaehring U., Heinz E.;
RT  "Cloning and functional characterization of Phaeodactylum tricornutum
RT  front-end desaturases involved in eicosapentaenoic acid
RT  biosynthesis.";
RL  Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC  -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR  EMBL: AV082393; AAL92563.1; -.
DR  InterPro: IPR001199; Cyt_B5.
DR  Pfam: PF00487; FA desaturase; 1.
DR  Pfam: PF00173; heme_1; 1.
DR  ProDom: PD000612; Cyt_B5; 1.
DR  ProDom: PD001081; FA desat. fam; 1.
DR  PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW  Heme.
SQ  SEQUENCE 477 AA; 53452 MW; 2A4B8E30F8BDF99F CRC64;

Query Match      21.2%; Score 516.5; DB 10; Length 477;
Best Local Similarity 29.3%; Pred. No. 9.2e-38;
Matches 146; Conservative 75; Mismatches 170; Indels 107; Gaps 20;

Qy  1 MKGGG---NQEGGAAREVSVPTSEWEEIOKHLRTDGLVIDRKVYNITKMSIQHPG 56
Db  1 MKGGGARASKGSTARK-----ISWQEVKTHASPEDAWIHSNKVYDVSNWH-EHPGG 53
Qy  57 QRVIGHAGEDATDAFRAHFDLEFVGKFLPLLIIGELAPE-----EPSQDHGKSKITE 111
Db  54 AVIFTH-AGDDMTDIFAAHAPGSG---SLMKKFLYIGELLPETTGKPEQ-----IAPEK 104
Qy  112 DFRALKTAEDMNLKTNHVFLLLAHIALESIAWTFVFGNGWIPTLTITAFVLAT 171
Db  105 GYRDLRSKLIIMGMFKSNKWFYVYKLSNMATWAAACALVFYSDRFVW-HLASAVMLGTF 163
Qy  172 QOAGQWLOHDYGHLSVYRKPKNHLVHKVIGHLKGASANNHHRHFQHKAKNIF----- 227
Db  164 FQSGWLAHDFLHQVFTKRKHGDLGLFWGNLMQGVSVQWKNKNGHHAHPNLCSSA 223
Qy  228 ---HKDPVNMHLHVFVLGEWQIEY-----OKKK--LKYPYNHQHEYFFLIGPPLIP 276
Db  224 VAQDGDPTDITMPLAWSQQASYRELQADGKDSGLVKFMIRNQSIFYF-----PILLLA 279
Qy  277 MV-----FOYQIIMTM-IVHKQWVDLAWAVSYIRF 306
Db  280 RLSWLNESFKAFGLGAASENAAELKAGLOYPLEKAGILLHYAW--MLTVSGFGF 337
Qy  307 FTIYIPFY-----GILGALLFLNFIREFLESHWVWVQNMHIV-EIDQAYRDWFS 357
Db  338 SFAYTAFYELTATASCGFLLAIVF-----GLGHNGMATYNADARPDEWK 381
Qy  358 SOLTATCNVE-----QSPFNDFWFSGLHNFQIEHHLFPTMPRNLKHIAPLVKSLCKHG 412
Db  382 LQVTTTRNTGTHGHPQAPVDFWFCGGLQVQVDDHLLFPSPRNLAKTHALVESPFCKEWG 441
Qy  413 EYQKPELRLALDIIIRSL 430
Db  442 QYHEADLVGDTMVELHHL 459

RESULT 40
Q9ZNNW2 PRELIMINARY; PRT; 525 AA.
ID Q9ZNNW2
AC Q9ZNNW2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DELTA6-acyl-lipid desaturase.
GN DES6.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2003, 16:22:14 ; Search time 280 seconds
(without alignments)
4280.537 Million cell updates/sec

Title: US-09-719-601-5

Perfect score: 2438

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Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV-xlh

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-DB=N_Geneseq_19Jun03 -QMT=rasap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2438	100.0	3184	21	AAZ48247 Human oxidoreducta
2	2425	99.5	1335	22	AAD19403 Human delta-6-desa
3	2425	99.5	3083	22	AAK94346 Human full-length
4	2425	99.3	3106	21	AAK76019 Human ORFX ORF1574
5	2425	99.5	4089	21	AAA90953 Human fatty acid d
6	2190	89.8	1335	22	AAI66599 Rat fatty acid des
7	2186	89.7	1335	22	AAD19402 Rat delta-6-desatu
8	2068.5	84.8	2825	22	AAK94377 Human full-length
9	1935	79.4	2257	19	AAV63643 Contig 253538a enc
10	1935	79.4	2257	20	AAK00910 Human desaturase g
11	1935	79.4	2257	20	AAV82642 Contig 253538a enc
12	1935	79.4	2257	21	AAA49939 Human delta-5-desa
13	1935	79.4	2257	21	AAA09453 Human contig 2535
14	1935	79.4	2257	21	AAA14594 Nucleotide sequenc
15	1935	79.4	2257	24	ABS71826 Human delta5-desat
16	1935	79.4	2257	24	ABS76713 Human desaturase c
17	1703	69.9	2621	24	ABT10758 Human breast c
18	1669	68.5	1575	24	ABT90108 Human polynucleoti
19	1668	68.4	2588	22	AAK94786 Human full-length
20	1646	67.5	1843	19	AAV63642 Contig 2535 encodi
21	1646	67.5	1843	20	AAV80099 Human desaturase g
22	1646	67.5	1843	20	AAV82641 Contig 2535 encodi
23	1646	67.5	1843	21	AAA49938 Human delta-5-desa
24	1646	67.5	1843	21	AAA09452 Human contig DNA e
25	1646	67.5	1843	21	AAK14593 Nucleotide sequenc
26	1646	67.5	1843	24	ABS71825 Human delta5-desat
27	1646	67.5	1843	24	ABS76712 Human desaturase c
28	1594	65.4	1474	21	AAF21845 Human breast and o
29	1560.5	64.0	1700	21	AAZ93706 CYB5RP fatty acid
30	1560.5	64.0	1757	25	AAK93651 cDNA encoding huma
31	1560.5	64.0	1757	21	AAA90954 Human fatty acid d
32	1560.5	64.0	1772	22	AAK99727 Human protein enco
C 33	1516	62.2	1972	24	AAK35347 Human cDNA encodin
C 34	1516	62.2	4203	21	AAA90955 Human fatty acid d
35	1516	62.2	4205	21	AAA90952 Human fatty acid d
36	1515	62.1	1928	25	AAK93652 cDNA encoding huma
37	1512	62.0	2236	22	AAK94234 Human full-length
38	1512	62.0	1856	22	AAH15766 Human cDNA sequenc
39	1508	61.9	1335	21	AAK49322 Human delta-5-desa
40	1508	61.9	1335	22	AAK25236 Nucleotide sequenc
41	1508	61.9	1335	24	ABS71819 Human delta5-desat
42	1508	61.9	1335	24	ABS76706 Human cDNA encodin
43	1504.5	61.7	2614	21	AAK76207 Human ORFX ORF1762
44	1504.5	61.7	2629	22	AAK99666 Human protein enco
45	1504	61.7	2080	22	AAK94270 Human full-length

ALIGNMENTS

RESULT 1	
AAZ48247	
ID	AAZ48247 standard; cDNA; 3184 BP.
XX	
XX	AAZ48247;
AC	
XX	
DT	28-MAR-2000 (first entry)
XX	
DE	Human oxidoreductase protein (HORP)-5 encoding cDNA (clone 008879).
XX	
KW	Human oxidoreductase protein; HORP; neurological; autoimmune; cancer;
KW	reproductive; cell proliferative disorder; vesicle trafficking;
KW	endocrine disorder; ss.
XX	
OS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers

DB:	US-09-719-601-5 (1-444) x AAD19403 (1-1335)	Gaps:	0
QY	1 MetGlyLysGlyGlyAsnGlnGlyGluGluValAlaGluArgGluValSerValProThr	20	
DB	1 ATGGGGAAGGGAGGGAGACCAGGGGGGCGGGGGCGCCGCGCGAGGTTGTCGGTCCAC	60	
QY	21 PheSerTyrGluGluGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp	40	
DB	61 TTCAGCTGGGAGAGATTCAGAACATAACCTGCGCACCGACAGAGTGGCTGGTCATTGAC	120	
QY	41 ArgLysValTyrAsnIleThrLysTyrSerIleGlnHisProGlyGlyGlnArgValIle	60	
DB	121 CGCAAGGTTTAAACATCACCAGATGGTTCATCCAGACCCCGGGGGCCAGCGGTTCATC	180	
QY	61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu	80	
DB	181 GGGCACTACGCTGGAGAAGATGCAACGATGCTTCGCGCCTTCACACCTGACCTGGAA	240	
QY	81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer	100	
DB	241 TTCGTGGGCAAGTTCCTTGAACCCCTCTGATTGGTGAAGTGGCCCGGAGGAGCCGAGC	300	
QY	101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla	120	
DB	301 CAGGACCAAGGCAAGACTCAAGATCACTGAGGACTTCGGGCGCTTGAGGAAGACGGCT	360	
QY	121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle	140	
DB	361 GAGGACATGAACCTGTTCAAGACCAACCGTGTTCCTCTCTCTCTCTCTCTCTCTCTCT	420	
QY	141 IleAlaLeuGluSerIleAlaTyrPheThrValPheTyrPheGlyAsnGlyTyrIlePro	160	
DB	421 ATCGCCCTGGAGAGCATTCATGGTTCACTGTCTTTTCTTTTCTTTTCTTTTCTTTTCT	480	
QY	161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTyrLeuGlnHis	180	
DB	481 ACCCTCATCAGGGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGT	540	
QY	181 AspTyrGlyHisLeuSerValTyrArgLysProLysTyrAsnHisLeuValHisLysPhe	200	
DB	541 GATTATGCCACCTGTCTGTCTCAGAAACCCCAAGTGGAGAACACCTTGTCTTGTCTTGT	600	
QY	201 ValIleGlyHisLeuLysGlyValSerAlaAsnTyrTrpAsnHisArgHisPheGlnHis	220	
DB	601 GTCAITGGCCACTTAAAGGGTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGT	660	
QY	221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal	240	
DB	661 CACGCAAGCCTTAAACATCTTCCACAGGATCCCGATGTGAACATGCTGCGACGTGTGTGT	720	
QY	241 LeuGlyGluTyrGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLys	260	
DB	721 CTGGGCGAATGGCGCCATCGAGTACGCAAGAGAGAGTGAATACCTGCTTGTCTTGT	780	
QY	261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuLeuProMetTyrPheGln	280	
DB	781 CACCAGACAGAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	840	
QY	281 TyrGlnIleIleMetThrMetIleValHisLysAsnTyrValAspLeuAlaTyrAlaVal	300	
DB	841 TACAGATCATCATGACCATGATGCTCCATAGAACTGGGTGAGCTGGGCTGGGCGGTC	900	
QY	301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyLeuGlyAlaLeu	320	
DB	901 AGCTACTACATCCGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	960	
QY	321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTyrPheValTyrValThrGlnMet	340	
DB	961 CTTTTCCTCAACTTCATCAGGTTCTCTGGAGAGCCACTGGTGTGTGGGGTCACACAGATG	1020	
QY	341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTyrPheSerSerGlnLeu	360	

RESULT 2

AAD19403

ID AAD19403 standard; DNA; 1335 BP.

XX

AAD19403;

18-DEC-2001 (first entry)

XX

Human delta-6-desaturase (hD6D-1) coding region.

XX

Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema; mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection; gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome; endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome; cardiovascular disease; Crohn's disease; congenital liver disease; schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer; arterial hypertension; atherosclerosis; chronic inflammatory disorder; autoimmune disorder; hypercholesterolaemia; atopic disorder; hD6D-1; gene therapy; human; ds.

XX

Homo sapiens.

OS

XX

Key Location/Qualifiers

FT 1..1335

FT /*tag= a

FT /product= "Human D6D-1 protein"

XX

WO200170993-A2.

XX

27-SEP-2001.

XX

26-MAR-2001; 2001WO-CA00398.

XX

24-MAR-2000; 2000CA-2301158.

XX

(SCOT-) SCOTIA HOLDINGS PLC.

PA

XX

Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;

PI

XX

WPI; 2001-611507/70.

DR

XX

P-PSDB; AAE11083.

XX

Nucleic acid encoding delta-6-desaturase gene useful for treating atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome, gastrointestinal disorders, viral infections and post viral fatigue -

PT

XX

Example 4; Fig 4; 164pp; English.

PS

XX

The invention relates to polynucleotides that control delta-6-desaturase genes (D6D) and methods useful for identifying compounds which inhibit or promote the activity of mammalian D6D. Compounds which modulate D6D gene segments are useful for treating lipid metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome, gastrointestinal disorders, viral infections, cystic fibrosis, pre-menstrual syndrome, endometriosis, Crohn's disease, alcoholism, Alzheimer's syndrome, cardiovascular disease, Crohn's disease, cancer, congenital liver disease, schizophrenia, diabetes and diabetic complications including diabetic neuropathy, nephropathy and retinopathy. Compounds of the invention are also useful for inhibiting progressive and acute disorders such as arterial hypertension, atherosclerosis, chronic inflammatory and autoimmune disorders, hypercholesterolaemia and other atopic disorders. D6D genes are useful in gene therapy. The present sequence is human delta-6-desaturase (hD6D-1) coding region.

XX

SQ Sequence 1335 BP; 307 A; 405 C; 336 G; 287 T; 0 other;

Alignment Scores:

Pred. No.:	2,21e-257	Length:	1335
Score:	2425.00	Matches:	442
Percent Similarity:	99.55%	Conservative:	0
Best Local Similarity:	99.55%	Mismatches:	2
Query Match:	99.47%	Indels:	0

DB 1021 AATCATCGTCATGGAGATTGACAGAGAGCCCTACCGTGACTGGTTTCAGTAGCCAGCTG 1080
 QY 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
 DB 1081 ACAGCCACTGCAACGTCAGAGCAGTCCCTTCTTCAACGACTGGTTTCAGTAGCCAGCTTAAC 1140
 QY 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
 DB 1141 TTCAGATGAGCACCACCTCTTCCCCACCATGCCCGCCGACCACTTACCAAGATCGCC 1200
 QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
 DB 1201 CGCTGGTGAAGTCTCTATGTGGCAAGCATGGCATTTGAATACCAAGAGAGCCGCTACTG 1260
 QY 421 ArgAlaLeuLeuAspIleAlaArgSerLeuLysLysSerGlyLysLeuTyrLeuAspAla 440
 DB 1261 AGGGCCCTGCTGGACATCATCAGGTCCCTGGAAGTCTGGGAAGCTGTGGCTGGACGCC 1320
 QY 441 TyrLeuHisLys 444
 DB 1321 TACCTTCACAA 1332

RESULT 3
 AAK94346
 ID AAK94346 standard; cDNA; 3083 BP.

AC AAK94346;

DT 06-NOV-2001 (first entry)

DE Human full-length cDNA, SEQ ID NO: 3049.

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.

XX EP1130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-0114089.

XX 08-JUL-1999; 99JP-0194486.

XX 11-JAN-2000; 2000JP-0118774.

XX 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

XX P-PSDB; AAK93425.

XX 830 Primers useful for synthesizing full length cDNA clones and their

XX use in genetic manipulation -

XX Claim 8; SEQ ID NO 3049; 1380pp + sequence listing; English.

XX The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5' and 3'-ends of the cDNA
 CC molecules have been determined. Primers for synthesizing the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is a full length
 CC human cDNA of the invention.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from BPO.

SQ Sequence 3083 BP; 615 A; 937 C; 884 G; 647 T; 0 other;

Alignment Scores:

Pred. No.: 7,78e-257 Length: 3083
 Score: 2425.00 Matches: 442
 Percent Similarity: 99.55% Conservative: 0
 Best Local Similarity: 99.55% Mismatches: 2
 Query Match: 99.47% Indels: 0
 DB: 22 Gaps: 0

US-09-719-601-5 (1-444) x AAK94346 (1-3083)

QY 1 MetGlyLysGlyLysAsnGlnGlyGluAlaAlaGluArgGluValSerValProThr 20
 DB 91 ATGGGGAAGGAGGAAACAGGGCGAGGGGGCGCGAGCGAGGTGTGCGTGGCCACC 150
 QY 21 PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
 DB 151 TTCAGCTGGGAGAGATTCCGAAGCATTAACCTGCCACCGACAGGTGGTGGTCAATTGAC 210
 QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
 DB 211 CGCAAGGTTTACAACATCACCAATGGTCCATCCAGCACCCCGGGGGCGCGAGGTCATC 270
 QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
 DB 271 GGGCACTACGCTGGAGAGATCAACGGATGCTTCGGCGCTTCACCTGACTGGAA 330
 QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100
 DB 331 TTCGTGGCAAGTTCCTTGAACCCCTGCTGATTGGTGAATGGCCCGGAGAGCCAGC 390
 QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
 DB 391 CAGGCCACGGCAAGAACTCAAGATCACTAGGACTTCCGGGCCCTTGGAGAGACGGCT 450
 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
 DB 451 GAGGACATGAACCTGTTCAAGCAACCAACCGTGTCTCTCTCTCTCTCTCTCTCTCT 510
 QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160
 DB 511 ATCGCCCTGGAGAGCATTCATGGTTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 570
 QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
 DB 571 ACCTCATACAGCCCTTGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 630
 QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200
 DB 631 GATTATGGCCACCTGTGTCTACAGAAACCCCAAGTGAACCCACCTTGTCCACAAATTC 690
 QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
 DB 691 GTATTGGCCACTTAAGGGTGTCTGTCCAACTGTGTGGATCATCGCCATTCATTCAG 750
 QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
 DB 751 CAGCCCAAGCCTAACATCTTCCAAAGGATCCCGATGTGAACATGTGTCAGCTGTGTGT 810
 QY 241 LeuGlyLysTrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLys 260
 DB 811 CTGGCGGAAATGGGAGCCCATTCAGTAGTCGGCAGAGAGAGCTGAATACCTGCCCTACAT 870
 QY 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
 DB 871 CACCAGCAGCAATATCTTCTCTGATTGGCGCCGCTGCTCATCCCATGTATTTCCAG 930
 QY 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
 DB 931 TACCAGATCATCATGACCATGATCGTCCATGAAGACTGGGTGGACCTGGCGCTGGCGCTC 990
 QY 301 SerTyrTrpIleArgPhePheIleThrTyrIleProPheTyrGlyLysLeuGlyAlaLeu 320


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Db 181 GGACACTATTCCGGAGAGAGATGCTACGGATGCCTTCCTCGCTCCACCTGGACCTGGAT 240
Qy 81 PheValGlyLysPheLeuLysProLeuLeuLeuGlyGlyLeuAlaProGluGluProSer 100
Db 241 TTCGTGGGCAAGTCTTTGAAGCCCTGCTGATTGCTGAGCTGGCCCGAGAGAGCCGAGC 300
Qy 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
Db 301 CTGGACCGGGCAAAAGCTCTCAGATCACCGAGACTTCAGGGCCCTGAAGAGACTGCT 360
Qy 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
Db 361 GAGCAGATGAACCTTTTCAAAACCAACACCTGTTCTTCTTCCTCTGTCCTCCACATC 420
Qy 141 IleAlaLeuGluSerIleAlaThrPheThrValPheThrPheGlyAsnGlyTrpIlePro 160
Db 421 ATCGTCAATGGAAGATCGCTGGTTCATCTCTGCTACTTCGGCAATGGCTGATTCCTC 480
Qy 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
Db 481 ACCGTCAATCAGGCTGTTGCTCTGCTACCTCCAGGCCCAAGCTGGATGGCTACAACAT 540
Qy 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200
Db 541 GATTATGGCCACCTTTCTGTCTAAGAATAATCCATATGGAACCAATTTGTCACCAATTT 600
Qy 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
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Qy 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
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Qy 241 LeuGlyGluTrpGlnProIleGlyTrpGlyLysLysLysLeuLysTyrTrpTyrAsn 260
Db 721 CTTGAGAGTGGCACCCCTCGAGTATGGCAGAGAGAGCTGAATATCTGCCCTCAACAC 780
Qy 261 HisGlnHisGluTyrPhePheLeuLeuGlyProProLeuLeuIleProMetTyrPheGln 280
Db 781 CACCAGCATGAATACTTCTTCGTATGATCGAGACCCGCTGCTCATCCCTATGATCTCCAG 840
Qy 281 TyrGlnIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
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Qy 301 SerTyrTyrIleArgPheIleThrTyrIleProPheTyrGlyLeuLeuGlyAlaLeu 320
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Qy 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
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Qy 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
Db 1021 AACCACATTTGTCAGAGATTGATCTTGATCACTACCGGAGCTGGTTCAGCAGCCAGCTG 1080
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Qy 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
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Qy 441 TyrLeuHisLys 444
Db 1321 TACCTCCACAA 1332
RESULT 7
AAD19402
ID AAD19402 standard, DNA; 1335 BP.
XX AAD19402;
AC AAD19402;
XX 18-DEC-2001 (first entry)
XX Rat delta-6-desaturase (rD6D-1) coding region.
DE
XX Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema;
KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;
KW gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;
KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;
KW cardiovascular disease; Crohn's disease; congenital liver disease;
KW schizophrenia; diabetic neuropathy; nephropathy; cancer;
KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;
KW autoimmune disorder; hypercholesterolaemia; atopic disorder; rD6D-1;
KW gene therapy; rat; ds.
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XX 26-MAR-2001; 2001WO-CA00398.
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XX 24-MAR-2000; 2000CA-2301158.
XX
XX (SCOT-) SCOTIA HOLDINGS PLC.
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XX Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;
XX WPI; 2001-611507/70.
XX P-PSDB; AAEL1081.
XX
XX Nucleic acid encoding delta-6-desaturase gene useful for treating
XX atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,
XX gastrointestinal disorders, viral infections and post viral fatigue -
XX
XX Example 3; Fig 3; 164pp; English.
XX
XX The invention relates to polynucleotides that control delta-6
XX desaturase genes (D6D) and methods useful for identifying compounds
XX which inhibit or promote the activity of mammalian D6D. Compounds
XX which modulate D6D gene segments are useful for treating lipid
XX metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid
XX arthritis, Sjogren's syndrome, gastrointestinal disorders, viral
XX infections and post viral fatigue, pre-menstrual syndrome,
XX endometriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,
XX cardiovascular disease, Crohn's disease, cancer, congenital liver
XX disease, schizophrenia, diabetes and diabetic complications including
XX diabetic neuropathy, nephropathy and retinopathy. Compounds of the
XX invention are also useful for inhibiting progressive and acute
XX disorders such as arterial hypertension, atherosclerosis, chronic
XX inflammatory and autoimmune disorders, hypercholesterolaemia and
XX other atopic disorders. D6D genes are useful in gene therapy. The
XX present sequence is rat delta-6-desaturase (rD6D-1) coding region.
XX
XX Sequence 1335 BP; 311 A; 396 C; 326 G; 302 T; 0 other;
```

Alignment Scores:

```

Pred. No.:      5,3e-231      Length:      1335
Score:          2186.00      Matches:      389
Percent Similarity: 93.47%      Conservative: 26
Best Local Similarity: 87.61%      Mismatches: 29
Query Match:      89.66%      Indels:      0
DB:              22          Gaps:        0

US-09-719-601-5 (1-444) x AAD19402 (1-1335)

QY 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20
   |||
Db 1 ATGGGGAGGAGGAGTAACAGAGGAGAGGGAGCAGCTCCAGGTCCTCGATGCCACC 60
   |||

QY 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
   |||
Db 61 TTCCCGCTGGGAGGAGATTGAGAAGACACACCTCGCGACCGCCGCGTGGCTGTCATCGAC 120
   |||

QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
   |||
Db 121 CGCAAGGTCTACAGTTACCAATGGTCCAGCGGACCCAGGGGGGACCGGTGTCTATC 180
   |||

QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
   |||
Db 181 GGACACTATTTCGGAGAGATCTACGGATGCTTCGGTGCCTTCCACCTCGACCTGGAT 240
   |||

QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluProSer 100
   |||
Db 241 TTCGTGGGCAAGTCTTGAAGCCCTCTGCTGATGTGTGAGCTGGCCCGGAGAGGCCACG 300
   |||

QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
   |||
Db 301 CTGGACCGGGGCAAAAGCTCTCAGATCACCAGAGGACTTCAGGGCCCTGAAGAGACTGCT 360
   |||

QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
   |||
Db 361 GAGGACATGAACCTTTCAAACCAACCACTGTTCTTCTTCTCTCTCTCTCTCTCTCTCT 420
   |||

QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160
   |||
Db 421 ATCGTCATGGAAGCATCGCTGGTTCATCTCTCTGTAATCTCGCAATGGCTGGATTCCT 480
   |||

QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
   |||
Db 481 ACCGTATCACGGCTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
   |||

QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200
   |||
Db 541 GATTATGGCCACTTCTCTCTATAGAAATCCATATGGAACCACTTGTCCCAAGTTT 600
   |||

QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
   |||
Db 601 GTCAATGGCCACTTAAAGGGTCCCTCCGCCAACTGGTGGAAACCATTCGACATTTCCAGCAC 660
   |||

QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
   |||
Db 661 CATGGAGAGCCCAACATCTTCCAAAGGACCCCGGACATAAAGAGCCTCGACGTGTTGGCC 720
   |||

QY 241 LeuGlyGluTrpGlnProIleGlyLysLysLysLeuLysTyrLeuProTyrAsn 260
   |||
Db 721 CTTGGAGAGTGGCAGCCCTCGAGTATGGCAAGAGAGAGCTGAATATCTGCCCTACAAC 780
   |||

QY 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
   |||
Db 781 CACCAAGCATGAATCTTCTCTGATCGGACCCAGCCGCTGCTCATCTCTATCTACTTCAG 840
   |||

QY 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
   |||
Db 841 TACCAAGATCATCATGACCATGATGACCCAGAGACTGGTGGACTTGGCTGGGCCATC 900
   |||

QY 301 SerTyrTrpIleArgPhePheIleThrTrpIleProPheTyrGlyIleLeuGlyAlaLeu 320
   |||
Db 901 AGCTACTATGCACTTCTCTTACACCTATATCCCTTCTATGGCATCTTGGGAGCCCTG 960
   |||

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QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
   |||
Db 961 GTTTTCTCAACTTTATCAGTTCTCTGGAGAGCCACTGGTTTGTGTGGGTACACAGATG 1020
   |||

QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerGlnLeu 360
   |||
Db 1021 AACCACTTGTCAATGAGATTGATCTTGTATCACTACCGGAGCTGGTTCAGCAGCCAGCTG 1080
   |||

QY 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
   |||
Db 1081 GCAGCCACCTGCAATGTGGAGCAGTCTTCTTCAATGACTGGTTTCAGCGGACCTCAAT 1140
   |||

QY 381 PheGlnIleGluHisIleLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
   |||
Db 1141 TTCAGATTGAGCACCACCTCTTCCCACTATGCCCAGACACAACTTGCACAGATTGCC 1200
   |||

QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
   |||
Db 1201 CCACTGGTGAAGTCTCTCTGGCCCAAGCATGGCATTAATACAGAGAGCCGCTGCTG 1260
   |||

QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
   |||
Db 1261 AGGCGCCTGCTCGACATTGTGAGTTTCATGAAGAGCTCTGGGAGCTGTGGTGGATGCC 1320
   |||

QY 441 TyrLeuHisLys 444
   |||
Db 1321 TACCTCCACAA 1332
   |||

RESULT 8
AAK94377
ID AAK94377 standard; cDNA; 2825 BP.
XX
AC AAK94377;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human full-length cDNA, SEQ ID NO: 3111.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
XX
PR 11-JAN-2000; 2000JP-0118774.
XX
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Osa T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
XX
DR P-PSDB; AAM93456.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 3111; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping

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CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is a full length
 CC human cDNA of the invention. The present sequence is a full length
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.

XX Sequence 2825 BP; 562 A; 868 C; 778 G; 617 T; 0 other;

Alignment Scores:

Pred. No.: 1,538-217 Length: 2825
 Score: 2068.50 Matches: 378
 Percent Similarity: 99.44% Conservations: 0
 Best Local Similarity: 99.44% Mismatches: 3
 Query Match: 84.84% Indels: 3
 DB: 22 Gaps: 1

US-09-719-601-5 (1-444) x AAK94377 (1-2825)

QY 64 AlaGlyGluAspAlaThr-----AspAlaPheArgAlaPheHisProAspLeuGlu 80
 DB 7 GCAGGACACCCCAATCACCGGGCAACAGGATGCTTCCGCGCTTCCACCTGACCTGGAA 66
 QY 81 PheValGlyLysPheLeuLysProLeuLeuGlyGluLeuAlaProGluGluProSer 100
 DB 67 TTCGTGGGCAAGTCTTGAACCCCTGCTGATTGTGTAAGTGGCCCGGAGAGCCGAGC 126
 QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
 DB 127 CAGGACACCGGCAAGAACTCAAGATCACTGAGGACTTCCGGGCTTCCGAGGAGAGCGCT 186
 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
 DB 187 GAGGACATGAACCTGTTCAAGACCAACACAGTGTTCTTCTCTCTCTCTCTCTCTCTCTCT 246
 QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheThrGlyAsnGlyTrpIlePro 160
 DB 247 ATCGCCCTGGAGGATTCATGATGCTACTGCTTTTACTTGGCAATGGCTGGATTCCT 306
 QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
 DB 307 ACCCTCATCAGCGCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 366
 QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200
 DB 367 GATTATGGCCACCTGCTCTCTACAGAAACCAAGTGAACCACTTGTCCACAAATTC 426
 QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
 DB 427 GTCAATTGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGAATCATCGCCACTTCCAGCAC 486
 QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
 DB 487 CACGCCAACCTTAACATCTTCCACAGGATCCGATGTGAACATCTGCACGTGTTCCT 546
 QY 241 LeuGlyGluTrpGlnProIleGluTrpGlyLysLysLysLysLysLysLysLysLysLys 260
 DB 547 CTGGGCGAATGGCAGCCCATCAGTACGCGCAAGAAAGAGTGAATATCTGCTGCTGCTGCT 606
 QY 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
 DB 607 CACCAGCAGATATCTTCTCTGATTGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 666
 QY 281 TyrGlnIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
 DB 667 TACCAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 726
 QY 301 SerTyrTyrIleArgPheIleThrTrpIleProPheThrGlyIleLeuGlyAlaLeu 320
 DB 727 AGCTACTATCCGGTCTTCTACACCTACATACCTCTTCTACGCAATCTTGGAGCCCTC 786
 QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
 DB 787 CTTTCTCTCACTTCACTGAGTTCCTGGAGAGCCACTGCTGCTGCTGCTGCTGCTGCTGCTG 846

QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTrpArgAspTrpPheSerSerGlnLeu 360
 DB 847 AATCATCATGTCATGAGATTGACACGAGGAGGCTACCGTACTGCTTCACTAGTACCGCTG 906
 QY 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
 DB 907 ACAGCCACCTGCAACGTGGAGCAGTCCTTCTTCAACGACTGGTTCAGTGGACACCTTAAC 966
 QY 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
 DB 967 TTCCAGATTGAGCACCACCTTCTTCCACCATGCCCCCGCACAACTTACACAAATCGCC 1026
 QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
 DB 1027 CCGCTGCTGAAGTCTCTATGTCGCAAGCATGCAATACCCAGGAGAGCGCTACTG 1086
 QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
 DB 1087 AGGCCCCCTGCTGGACATCATCAGTCCCTGAAGAAGTCTGGGAAGCTGTGGCTGGACGCC 1146
 QY 441 TyrLeuHisLys 444
 DB 1147 TACCTTCAAAA 1158
 RESULT 9
 AAV63643
 ID AAV63643 standard; cDNA; 2257 BP.
 XX AC AAV63643;
 XX 15-FEB-1999 (first entry)
 DT Contig 253538a encoding a human desaturase enzyme.
 XX Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome; human;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.
 XX Homo sapiens.
 OS WC9846763-A1.
 FN 22-OCT-1998.
 PD 10-APR-1998; 98WO-US07126.
 PF 11-APR-1997; 97US-0834655.
 PR (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PA Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
 PI Thurmond J;
 DR WPI; 1998-594582/50.
 DR P-PSDB; AAW84156.
 XX New isolated fatty acid desaturase enzymes - used for the production
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 PT compositions, nutritional compositions, cosmetics or animal feed
 XX Example 12; Pages 117-118; 165pp; English.
 XX The present sequence encodes a human desaturase enzyme. The sequence was
 CC identified based on homology between human cDNA sequences and Mortierella
 CC alpina desaturase gene sequences. The specification describes methods for
 CC desaturating a fatty acid and for producing a desaturated fatty acid by
 CC expressing increased levels of a desaturase. The enzyme can be used for
 CC desaturating fatty acids. The enzyme can be used to produce

CC polyunsaturated fatty acids, which can be used for treating malnutrition,
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The
 CC polyunsaturated fatty acids can be used for treating e.g. restenosis
 CC after angioplasty, inflammation, rheumatoid arthritis, asthma, They
 CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They
 CC can also be used to inhibit platelet aggregation, cause vasodilation,
 CC lower cholesterol levels, inhibit proliferation of vessel wall smooth
 CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
 CC and other side effects caused by non-steroidal anti-inflammatory drugs,
 CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
 CC encephalomyelitis and chronic fatigue after viral infections, treat
 CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
 CC inflammatory skin disorders.

XX .
 SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Alignment Scores:

Pred. No.: 5,92e-203 Length: 2257
 Score: 1935.00 Matches: 352
 Percent Similarity: 88.84% Conservative: 30
 Best Local Similarity: 81.86% Mismatches: 44
 Query Match: 79.37% Indels: 4
 DB: 19 Gaps: 2

US-09-719-601-5 (1-444) x AAV63643 (1-2257)

QY 19 ProThr-----PheSerTrpGluGluGluGlnLysHisAsnLeuArgThrAspSer 35
 DB 7 CCTACCCCGCGCTACTTTCATCTGGGAGAGGTGCGCCAGCGCTCAGGGTGGAGGCGG 66
 QY 36 GlyLeuValIleAspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGly 55
 DB 67 TGGCTAGTATCGACCGTAAAGTGTACACATCAGCGAGTTACCCCGCGCATCCAGGG 126
 QY 56 GlyGlnArgValIleGlyHisTyAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
 DB 127 GCGTCCCGGTCATCAGCACATACCGCGGCGAGGTCCACGATCCCTTTGTGGCCTTC 186
 QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95
 DB 187 CATATCAACAGGCGCTTGTGAAGAGTATATGAACTCTCTCCCTGATGGAGAACTGCT 246
 QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115
 DB 247 CCAGAGCAGCCAGCTTTGAGCCACCAAGAAATAGAGCTGACAGATGATGTTCCGGGAG 306
 QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135
 DB 307 CTGGGGCCACAGTGGAGCGGATGGGCTCATGAAGGCCAACCATGTCCTTCTTCCTGCTG 366
 QY 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyPheGly 155
 DB 367 TACCTGTGTGCACATCTTGTCTGATGGTGTGCGCTGCGCTGCTCACCCTTTGGTCTTTGGG 426
 QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln 174
 DB 427 ACGTCTTTTGGCCTTCTCTCTGTCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
 QY 175 AlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerValTrpArgLysProLysTrpAsn 194
 DB 487 GCTGGATGGCTGCACATGATTATGGCCACTGTCTCTCTACAGAAACCCAGTGGAAAC 546
 QY 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsn 214
 DB 547 CACCTTGTCCACAAATTCGTCAATGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAAT 606
 QY 215 HisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234
 DB 607 CATGCCACTTCCAGACCCAGCCAGCCTTAACATCTTCCACAGAGATCCCGATGTGAAC 666
 QY 235 MetLeuHisValPheValLeuGlyGluTrpGlnProIleGlyTrpLysLysLysLeu 254
 DB 667 ATGCTGACGCTGTTGTTCTGGGGGAATGGCAGGCCATCGAGTACGCGCAAGAGAGCTG 726

QY 255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProLeuLeu 274
 DB 727 AAATACCTGCGCTCAATCAATCAGCAGCAAGAACTTCTTCTGATGGGCGCGCTGCTC 786
 QY 275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294
 DB 787 ATCCCATGATTTCCAGTACCAGATCATCATGACCATGATCGTCCATTAAGAACTGGGTG 846
 QY 295 AspLeuAlaTrpAlaValSerTyrTyrIleArgPheIleThrTyrIleProPheTyr 314
 DB 847 GACCTGGCGCTGGCGCTGAGCTACTACATCCGGTTCCTTCATCACCTATATCCCTTTCAC 906
 QY 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334
 DB 907 GGCATCTCTGGGAGCCCTCTTCTTCTCAACTTCATCATGGTCTCTGGAGACCATGGT 966
 QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyArgAsp 354
 DB 967 GTGTGGGTCCACAGATGAATCATCATCTGATGGAGATTGACAGGAGGCGCTACCGTCA 1026
 QY 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374
 DB 1027 TGGTTCACTAGCCACCTGCAGCCACCTGCAACGTGGAGCAGTCTCTTTCACAGACTGG 1086
 QY 375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHis 394
 DB 1087 TTCAGTGGAGCACCTTAACTTCCAGATTGAGCACCACCTCTTCCCAACCATGCCCGGAC 1146
 QY 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
 DB 1147 AACTTACACAGATCGCCCGCTGCTGAGTCTATGTGCAAGCATGGCATTTGAATAC 1206
 QY 415 GlnGluLysProLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGly 434
 DB 1207 CAGGAGAAAGCCCTACTCAGGCGCCCTGCTGGACATCATCAGTCTCCTGAAGAAGTCTGG 1266
 QY 435 LysLeuTrpLeuAspAlaTyIleHisLys 444
 DB 1267 AAGCTGTGGTGGAGCGCTTACCTTCCACAA 1296
 RESULT 10
 AAX00910
 ID AAX00910 standard; DNA; 2257 BP.
 XX
 AC AAX00910;
 XX
 DT 26-MAR-1999 (first entry)
 XX
 DE Human desaturase gene contig 253538a.
 XX
 KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUPA; oil;
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed; human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS
 FT 1..2256
 FT /*tag= a
 FT /note= "contains internal stop codons"
 XX
 PN W09846764-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 10-APR-1998; 98WO-US07421.
 XX
 PR 24-OCT-1997; 97US-0956985.
 PR 11-APR-1997; 97US-0833610.

PR 11-APR-1997; 97US-0834033.
 PR 11-APR-1997; 97US-0834655.
 XX (ABBO) ABBOTT LAB.
 PA (CALU) CALGENE LLC.
 XX Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
 PI Thurmond J;
 XX WPI. 1999-080739/07.
 DR P-PSDB; AAW95514.
 XX Nucleic acid construct able to express fatty acid desaturase in
 PT plants - useful in human or animal nutrition, as cosmetics and
 PT therapeutically, e.g. for restenosis, cancer and diabetes
 XX Claim 48; Page 161-162; 210pp; English.
 XX The invention relates to a nucleic acid construct that contains at least
 CC one of the nucleotide sequences (AAW00889 to AAW00891) encoding
 CC Mortierella alpina delta 6, delta 12 and delta 5 desaturases (AAW95504 to
 CC AAW95506) respectively, coupled to an expression control sequence
 CC functional in plants. Recombinant plant cells containing at least one DNA
 CC encoding a M. alpina fatty acid desaturase (FAD), can be used for the
 CC production of polyunsaturated fatty acid (PUFA), these recombinant cells
 CC or plants containing them are used to produce oils such as linoleic
 CC acid, arachidonic acid, gamma-linolenic acid, dihomogamma-linolenic
 CC acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils
 CC are used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
 CC dietary supplements or substitutes, for use in humans or animals; (iii)
 CC for treating disorders associated with inadequate consumption or
 CC production of PUFA (or their metabolites such as prostaglandins), e.g.
 CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics,
 CC and (v) as animal feeds. Fragments of the DNA are used as probes to
 CC isolate related coding sequences. Recombinant plants can produce high
 CC yields of PUFA, since new pathways can be created and unwanted ones
 CC suppressed. Plants can be engineered to express oils of particular PUFA
 CC composition, e.g. one similar to that in human milk, and product recovery
 CC is simpler than with e.g. fish. Sequences AAW00904-910 represent DNA
 CC sequences of various contigs of human desaturase genes which are similar
 CC to the M. alpina desaturase sequences.
 XX SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Alignment Scores:
 Pred. No.: 5,92e-203 Length: 2257
 Score: 1935.00 Matches: 352
 Percent Similarity: 88.84% Conservative: 30
 Best Local Similarity: 81.86% Mismatches: 44
 Query Match: 79.37% Indels: 4
 DB: 20 Gaps: 2

US-09-719-601-5 (1-444) x AAW00910 (1-2257)

QY 19 ProThr-----PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSer 35
 DB 7 CCTACCCCGCGCTACTTCACTCGGAGGAGTGGCCCGAGCTCAGCGTGGCGAGGCGG 66
 QY 36 GlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGly 55
 DB 67 TGGCTAGTGTGACCCGTAGGTGTACACATCAGCGAGTTCACCCCGCGGATCCAGG 126
 QY 56 GlyGlnArgValIleGlyHisIleValAlaGlyGluAspAlaThrAspAlaPhe 75
 DB 127 GGCTCCCGGGTCATCAGCCACTACCGCGGCGAGATGCCAGGATCCCTTTGGGCTTC 186
 QY 76 HisProAspLeuGluPheValGlyLysPheLysProLeuLeuIleGlyGluLeuAla 95
 DB 187 CACATCAACAGGCGCTTGTGAAGAGTATATGAATCTCTCTGTGATGGAGACTGTCT 246
 QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115

DB 247 CCAGAGCAGCCCGAGCTTTGAGCCCAAGCAATGAAGAGCTGACAGATGAGTCCGGGAG 306
 QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135
 DB 307 CTGCGGGCCACAGTGGAGCGGATGGGCTCATGAAGGCCACCATGTCTCTTCTCTGCTG 366
 QY 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGly 155
 DB 367 TACCTGCTGCACATCTTGTCTGTGGTGTGGAGCTGCTCACCTTTGGGTCTTTGGG 426
 QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln 174
 DB 427 AGCTCCCTTTTGGCCCTCTCTCTGTGGGTGCTGCTCAGTGCAGTTCAGAGGCCCA 486
 QY 175 AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194
 DB 487 GCTGGATGGCTGCAACATGATTATGCCACCTGTCTGTACAGAAACCCCAAGTGAAC 546
 QY 195 HisLeuValHisLysPheValIleGlyHisLeuValGlyValAsnAlaAsnTrpTrpAsn 214
 DB 547 CACCTTGTCCACAAATTCGTATTCGCTTAAAGGTGCTCTGCCAATCTGTGGTGAAT 606
 QY 215 HisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234
 DB 607 CATCGCCACTTCCAGCACCCAGCCCAAGCCTAACTTCTCCCAAGGATCCCGATGTGAAC 666
 QY 235 MetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTrpGlyLysLysLeu 254
 DB 667 ATCTGCAGCTGTGTGTCTGGCGAATGGAGCCCATCGATACGGCAGAGAGAGCTG 726
 QY 255 LysTrpLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProLeuLeu 274
 DB 727 AATACCTGCTTACAAATCACCAGCAGCAATACTTCTCTGATTGGCGCGCTGCTC 786
 QY 275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294
 DB 787 ATCCCATGATTTCCAGTACCAGATCATCATGATCATGATCATGATCATGATCATGAT 846
 QY 295 AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314
 DB 847 GACCTGGCGCTGGCGCTGCTACTACTACTCGGTCTTCTCATCACCTACATCCCTTTCTAC 906
 QY 315 GlyLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334
 DB 907 GGCACTCTGGAGCGCTCTCTTTCCTCACTTCACTGAGTTCCTGAGAGCCACTGGTTT 966
 QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAsp 354
 DB 967 GTGTGGTTCACACAGATGAATCATCTCATGGAGATTGACCCAGAGGCTTACCGTGAC 1026
 QY 355 TrpPheSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374
 DB 1027 TGGTTCAGTAGCCAGCTGACGCCACCTGCAACGTGGAGCAGTCTTCTTCAACGACTGG 1086
 QY 375 PheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThrMetProArgHis 394
 DB 1087 TTCACTGGACACCTTAATCTCCAGATTGAGCACCACTCTTCTCCCAACCATGCCCGGCAC 1146
 QY 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
 DB 1147 AACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGTCATTTGAATAC 1206
 QY 415 GlnGluLysProLeuLeuArgAlaLeuAspIleIleArgSerLeuLysLysSerGly 434
 DB 1207 CAGGAGAACCGCTTACTGAGGGCCCTGCTGGACATCATCAGTCTCTTCTGAGAGTCTGGG 1266
 QY 435 LysLeuTrpLeuAspAlaTyrLeuHisLys 444
 DB 1267 AAGCTGTGGTGGAGCGCTTACCTTACAAA 1296

RESULT 11
 AAW82642
 ID AAW82642 standard; DNA; 2257 BP.

QY 395 AnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleLeuTyr 414
 DB 1147 AACTTACACAAATCGCCCGCTGTGAAGTCTCTATGTGCCAAGCATGGCATTAATAC 1206
 QY 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGly 434
 DB 1207 CAGGAGACCCCTACTAGGCGCCCTGTGGACATCATCAGTCCCTGAAGAAGTCTGGG 1266
 QY 435 LysLeuTrpLeuAspAlaTyrLeuHisLys 444
 DB 1267 AAGCTGTGGCTGGACGCTTACCTTACAAA 1296

RESULT 12

ID AAA49939 standard; cDNA; 2257 BP.

XX AAA49939;

DT 10-OCT-2000 (first entry)

XX Human delta-5-desaturase-related contig 253538A.

DE Delta-5-desaturase; human; polyunsaturated fatty acid;
 KW arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;
 KW docosahexaenoic acid; nutrition; feedstuff; ss.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FT 1..1299
 FT CDS /*tag= a

XX WO200040705-A2.

XX 13-JUL-2000.

XX 29-DEC-1999; 99WO-US311163.

XX 08-JAN-1999; 99US-0227613.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Leonard AEY, Huang Y, Parker-Barnes JW;

XX WPI; 2000-465975/40.

XX P-PSDB; AA195446.

XX New polypeptide useful for preparation of nutritional supplements based
 PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids
 PT at carbon 5 -
 XX Example 1; Fig 8; 127pp; English.

XX The present sequence is that of contig 253538A, a contig produced
 CC from overlapping contigs 2535 (see AAA49938) and 384933 (see
 CC AAA49936), which were isolated from the Incyte Lifeseq database on
 CC the basis of homology to Mortierella alpina delta-5-desaturase and
 CC delta-6-desaturase cDNA sequences. The contig includes a partial
 CC open reading frame that aligns with M. alpina delta-5- and
 CC delta-6-desaturase sequences. The contig was utilised in the
 CC isolation of cDNA (see AAA49932) encoding human delta-5-desaturase
 CC (see AA195445). Delta-5-desaturase catalyzes the conversion of
 CC dihydro-gamma-linolenic acid to arachidonic acid and of 20:4n-3 to
 CC eicosapentaenoic acid. Recombinant enzyme, expressed in prokaryotic
 CC or eukaryotic hosts using the isolated human delta-5-desaturase
 CC cDNA, can be used in the production of polyunsaturated fatty acids
 CC that may be added to nutritional, veterinary and pharmaceutical
 CC compositions.

XX Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Alignment Scores:

Pred. No.: 5.92e-203 Length: 2257

Score: 1935.00 Matches: 352
 Percent Similarity: 88.84% Conservative: 30
 Best Local Similarity: 81.86% Mismatches: 44
 Query Match: 79.37% Indels: 4
 DB: 21 Gaps: 2

US-09-719-601-5 (1-444) x AAA49939 (1-2257)

QY 19 ProThr-----PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSer 35
 DB 7 CCTACCCCGCGCTACTTCCCTGGGACGAGGTGCCGCCAGCGTCCAGGTGGCAGGAGCGG 66
 QY 36 GlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGly 55
 DB 67 TGGCTAGTGTATCGACCGTAACTAGGTGTAAACATCAGCGAGTTACCCCGCGCATCCAGGG 126
 QY 56 GlyGluArgValIleGlyHisTyrAlaGlyLysAlaThrAspAlaPheArgAlaPhe 75
 DB 127 GGCTCCCGGCTCATCAGCCACTACGCGCGGCGAGGATGCCAGGATCCCTTTGGGCGCTTC 186
 QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyLeuAla 95
 DB 187 CACATCAACAAGGCGCTTGTGAAGAAGTATATGAATCTCTCTCTGATTGGAGAACTGTCT 246
 QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115
 DB 247 CCAGAGCAGCCGCTTTGAGCCCAACCAAGAGCTGACAGATGATTCGCGGAG 306
 QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135
 DB 307 CTGGGCGCACAGTGGAGCGGATGGGGCTCATGAAGGCCAACCATGTCTTCTTCCTGCTG 366
 QY 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGly 155
 DB 367 TACCTGTGTGCATCTTGTCTGTGGATGGTGCAGCGCTGGCTACCCTTGGGCTTTGGG 426
 QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln 174
 DB 427 ACCTCCTTTTGGCCCTTCTCTCTGTGGGTGTGTCTCAGTGCAGTTCAGCAGGCGCCAA 486
 QY 175 AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194
 DB 487 GCTGGATGGCTGCAACATGATTATGGCCACTGTCTCTACAGAAACCCCAAGTGGAAC 546
 QY 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsn 214
 DB 547 CACCTTGTCCACAAATTCGTTCATTGGCCACTTAAAGGGTGCCTCTGCAACTGGTGAAT 606
 QY 215 HisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234
 DB 607 CATGCCCACTTCCAGCACCGCCCAAGCCTTAACATCTTCCACAGGATCCCGATGTGAAC 666
 QY 235 MetLeuHisValPheValLeuGlyGluTrpIleProIleMetThrMetIleValHisLysLysLeu 254
 DB 667 ATGTGTCAGGTGTGTGTCTGGCGAATGGCAGGCCATCGAGTACGGCAAGAGAGCTG 726
 QY 255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeu 274
 DB 727 AAATACCTGGCCCTCAATCACAGCAGCAATCTTCTTCGATTTGGCCGCCCTGCTC 786
 QY 275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294
 DB 787 ATCCCATGTATTTCAGTACCAGATCATCATGACCATGATCGTCCATAGAACTGGGTG 846
 QY 295 AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314
 DB 847 GACCTGGGCTGGCGCGTACATCCGGTTCCTTCATCAGGTTCTTCACCTACATCCCTTTCTAC 906
 QY 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334
 DB 907 GGCATCTCTGGGAGCGCTCTTCTTCTCACTTCATCAGGTTCTTCAGGAGCCACTGGTTT 966
 QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAsp 354

Db 967 GTGTGGGTACACAGATCAATCATCTGTCATGGAGATTGACGAGGCGCTACCGTGAC 1026
 QY 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374
 Db 1027 TGGTTTCATGACGCTGACGACCACTGCAACGTGGAGCAGTCTCTTCTTCAACGACTGG 1086
 QY 375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHis 394
 Db 1087 TTCAGTGACACCTTAATCTCCAGATTGAGCACCACCTCTTCCCAACCATGCCCGGCAC 1146
 QY 395 AsnLeuHisLeuIleAlaProLeuValIleSerLeuCysAlaLeuHisGlyIleGluTyr 414
 Db 1147 AACCTTACACAGATGCCCGCTGTGGAGTCTCTATGTGCCAGCATGGCAATTGAATAC 1206
 QY 415 GlnGluYsProLeuLeuArgAlaLeuLeuAspIleLeuArgSerLeuLeuYsSerGly 434
 Db 1207 CAGGAGAAGCGCTACTGAGGCGCTGCTGCACATCATCAGTCCCTGAGAGTCTGGG 1266
 QY 435 LysLeuTrpLeuAspAlaTyrLeuHisLys 444
 Db 1267 AAGCTGTGGCTGGACGCTACCTTACAAA 1296
 RESULT 13
 ID AAA09453 standard; DNA; 2257 BP.
 AC AAA09453;
 XX
 DT 10-AUG-2000 (first entry)
 DE Human contig 2535 DNA encoding desaturase homologue.
 KW delta-6 desaturase; gamma-linolenic acid; biosynthesis;
 KW transgenic insect cell; polyunsaturated long chain fatty acid;
 KW antiinflammatory; antirheumatic; antiasthmatic; antipsoriatic;
 KW osteopathic; cytostatic; antidiabetic; dermatological; gynecological;
 KW anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;
 KW antiaggregant; vasotropic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 1..2256
 FT /*tag= a
 FT /transl_except= (pos:1297..1299, aa:Xaa)
 FT /transl_except= (pos:1375..1377, aa:Xaa)
 FT /transl_except= (pos:1785..1788, aa:Xaa)
 FT /transl_except= (pos:1885..1887, aa:Xaa)
 FT /transl_except= (pos:1963..1965, aa:Xaa)
 FT /transl_except= (pos:2017..2019, aa:Xaa)
 FT /transl_except= (pos:2062..2064, aa:Xaa)
 FT /note= "Xaa not defined"
 XX
 PN WO200020602-A2.
 XX
 PD 13-APR-2000.
 XX
 PF 29-SEP-1999; 99WO-US22686.
 XX
 PR 05-OCT-1998; 98US-0103110.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Mukerji P, Huang Y, Parker-barnes JM, Das T;
 XX
 DR WPI; 2000-328935/28.
 DR P-PSDB; AA92618.
 XX
 PT Novel transgenic insect cells comprising a nucleotide sequences which
 PT encode delta-6-desaturase or delta-12- desaturase, useful for producing
 PT poly-unsaturated long chain fatty acids, e.g. arachidonic acid
 XX

PS
 XX
 CC AAA09447-52 are human DNA sequences identified based on homology to
 CC Mortierella alpina delta-5 and delta-6 desaturase genes. The human
 CC DNA's were aligned based on areas of homology to form a contig.
 CC Consensus sequences were assembled. A contig, 2511785 overlaps with
 CC contig 3506132, and this new contig was called 2535 (AAA09453).
 CC The fatty acid desaturases are able to catalyse the conversion of oleic
 CC acid to linoleic acid, linoleic acid to gamma-linolenic acid or of
 CC alpha-linolenic acid to stearidonic acid. Transgenic insect cells
 CC comprising a nucleotide sequence which encodes a polypeptide comprising
 CC residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6
 CC desaturase (AA92599), or comprising delta-12 desaturase (AA92600) are
 CC claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated
 CC from the recombinant insect cells are also claimed. Production of
 CC polyunsaturated long chain fatty acids (PUFAs) in insect cells has many
 CC advantages, as insect cells have greatly simplified lipid compositions,
 CC are not subject to external variable fluctuations, and can easily be
 CC maintained and manipulated. The oils are used in pharmaceutical
 CC compositions, infant formulas, dietary supplements or substitutes, and
 CC cosmetics (all claimed). The PUFA supplements have antiinflammatory,
 CC antirheumatic, antiasthmatic, antipsoriatic, osteopathic, cytostatic,
 CC antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,
 CC hypotensive, nephrotropic, vasodilator, antiaggregant and vasotropic
 CC activity.
 XX
 SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;
 Alignment Scores:
 Pred. No.: 5.92e-203 Length: 2257
 Score: 1935.00 Matches: 352
 Percent Similarity: 88.84% Conservative: 30
 Best Local Similarity: 81.86% Mismatches: 44
 Query Match: 79.37% Indels: 4
 DB: 21 Gaps: 2
 US-09-719-601-5 (1-444) x AAA09453 (1-2257)
 QY 19 ProThr-----PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSer 35
 Db 7 CTTACCCCGCGCTTCTTACCTGGGAGAGGTGGCCCGCTCAGGGTGGCGAGGCGG 66
 QY 36 GlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGly 55
 Db 67 TGGCTAGTATCGACCGTAAAGTGTACAAATCATCAGCGAGTTCACCCCGCGGATCCAGG 126
 QY 56 GlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
 Db 127 GGCTCCCGGGTCAATGACCACTACCGCGGCGAGGATGCCACCGATCCCTTTGTGGCTTC 186
 QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95
 Db 187 CACATCAACAAGGGCGCTTGTGAAGAAGTATATGAACCTCTCTCTGATTGGAGACTGTCT 246
 QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115
 Db 247 CCAGAGCAGCCCGCTTTGAGCCCAAGATTAAGAGCTGACAGATGATGTTCCGGAG 306
 QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135
 Db 307 CTGGGGCCACAGCTGGAGCGGATGGGGCTCATGAGGCCAACCATGTCTTCTCTCTG 366
 QY 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGly 155
 Db 367 TACCTGCTGCACATCTTGTCTGGATGGTGGAGCTGCTCACCCTTGGGTCTTTGGG 426
 QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln 174
 Db 427 ACCTCTTTTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 486
 QY 175 AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194
 Db 487 GCTGGATGGCTGCAACATGATTATGCCACCTGTCTGTCTACAGAAAACCCCAAGTGAAC 546

QY 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsn 214
 Db 547 CACCTGTGTCACAAATTCGTCATTGGCCACCTTAAGGGTGCCTTCGCAACTGTGGAAAT 606
 QY 215 HisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234
 Db 607 CATGCCCACTTCCAGCACCGCCAGAGCTTAACATCTTCCCAAGGATCCCGATGTGAAC 666
 QY 235 MetLeuHisValPheValLeuGlyLysTrpGlnProlIleGlyLysLysLeu 254
 Db 667 ATGCTGCACGTGTGTGTCGGCAATGGCAGCCCATCGAGTACGGCAAGAAAGCTG 726
 QY 255 LysTrpLeuProTrpAsnHisGlnHisGluTrpPhePheLeuIleGlyProProLeuLeu 274
 Db 727 AATATACCTGCCCTACAAATCACAGACAGATACCTTCTTCCTGATTTGGCCGCGCTGCTC 786
 QY 275 IleProMetTrpPheGlnTrpGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294
 Db 787 ATCCCACTGATTTTCAGTACCATCATCATGACCATGCTGCTCAATGAAGAACTGGGTG 846
 QY 295 AspLeuAlaTrpAlaValSerTrpTrpIleArgPhePheIleThrTrpIleProPheTrp 314
 Db 847 GACCTGGCCCTGGCGGTGAGTCTACATCCGTTCTTCATCACCTATCCCTTTCTAC 906
 QY 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPhelIleArgPheLeuGluSerHisTrpPhe 334
 Db 907 GGCATCCTGGAGCCCTCTTTCCTCAACTTCATCAGGTTCTCTGGAGAGCCACTGGTGT 966
 QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTrpArgAsp 354
 Db 967 GTGTGGGTACACAGATGAATCACATCGTCATGGAGATGACACAGAGGCTACCGTGAC 1026
 QY 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374
 Db 1027 TGTTTCAGTAGGAGCTGACAGCCACCTGCAACGTTGGAGCACTCTTCTTCAACGACTGG 1086
 QY 375 PheSerGlyHisLeuAsnPhelGlnIleGluHisLeuPheProThrMetProArgHis 394
 Db 1087 TTCAGTGGACACCTTAACCTTCAGATTGAGCACCTCTTCCACCATGCCCCGGCAC 1146
 QY 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTrp 414
 Db 1147 AACTTACACAGATCCCGCGCTGGTGAAGTCTCTATGTGCAAGCATGCGCATTAATAC 1206
 QY 415 GlnGlyLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGly 434
 Db 1207 CAGGAGAAGCCGCTACTGAGGCGCCCTGCTGGACATCATCAGTTCCTTGAAGAAGTCTGG 1266
 QY 435 LysLeuTrpLeuAspAlaTrpLeuHisLys 444
 Db 1267 AAGCTGTGGTGGACGCTACCTTTCACAA 1296
 RESULT 14
 AAA14594
 ID AAA14594 standard; DNA; 2257 BP.
 XX
 AC AAA14594;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Nucleotide sequence of a contig of a human desaturase enzyme.
 XX
 KW Deltas-desaturase; poly-unsaturated long chain fatty acid; PUFA;
 KW arachidonic acid; infant formula; dietary supplement; dietary substitute;
 KW cosmetic; stress; metabolic disorder; gastrointestinal difficulty;
 KW malabsorption; restenosis; angioplasty; inflammation; kidney stone;
 KW rheumatoid arthritis; asthma; psoriasis; osteoporosis; tract stone;
 KW cancer; cachexia; diabetes; eczema; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder;
 KW blood score; platelet aggregation; vasodilatation;
 KW gastro-intestinal bleeding; ss.

XX Homo sapiens.
 XX WO200020603-A1.
 XX 13-APR-2000.
 XX 29-SEP-1999; 99WO-US22692.
 XX 05-OCT-1998; 98US-0103109.
 XX (ABBO) ABBOTT LAB.
 XX Mukerji P, Huang Y, Parker-Barnes JH, Das T;
 XX WPI; 2000-364599/31.
 XX P-PSDB; AAY84703.
 XX Novel transgenic insect cell with modified delta-5-desaturase
 XX production, useful for altering fatty acid biosynthesis -
 XX Example 9; Page 148-149; 161pp; English.
 XX AAA14588-94 represent contigs of a human desaturase. The specification
 XX describes a Mortierella alpina delta5-desaturase. The protein is
 XX involved in the biosynthesis of poly-unsaturated long chain fatty
 XX acids (PUFAs). The polynucleotide is to produce PUFAs, especially
 XX arachidonic acid. The oils produced by the invention are used in
 XX pharmaceutical compositions, infant formulas, dietary supplements,
 XX used to treat normal individuals temporality exposed to stress, or
 XX individuals having specialized needs due to chronic or acute diseases
 XX (e.g. metabolic disorders such as gastrointestinal difficulties and/or
 XX malabsorption, and other disorders such as restenosis after angioplasty,
 XX symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis,
 XX osteoporosis, kidney stones, tract stones, cancer, cachexia associated
 XX with cancer, diabetes, eczema, endometriosis, premenstrual syndrome,
 XX myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis,
 XX acute respiratory syndrome, hypertension, inflammatory skin disorders,
 XX as well as reduce blood score, inhibit platelet aggregation, cause
 XX vasodilatation, inhibit proliferation of vessel wall smooth muscle and
 XX fibrous tissue, prevent or reduce gastro-intestinal bleeding, and for
 XX geriatric treatments).
 XX Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;
 SQ
 Alignment Scores:
 Pred. NO.: 5.92e-203 Length: 2257
 Score: 1935.00 Matches: 352
 Percent Similarity: 88.84% Conservative: 30
 Best Local Similarity: 81.86% Mismatches: 44
 Query Match: 79.37% Indels: 4
 Ds: 21 Gaps: 2
 US-09-719-601-5 (1-444) x AAA14594 (1-2257)
 QY 19 ProThr-----PheSerTrpGluGluIleGlnLysHisLeuArgThrAspSer 35
 Db 7 CCTACCCCGCGCTACTTCACTGGGACGAGGTGCCCGACGCTCAGGGTCCGAGGACGG 66
 QY 36 GlyLeuValIleAspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGly 55
 Db 67 TGGTGTGTGTGTCACCGTACAGTGTACATCAGCGAGTTCACCGCGCATCCAGGG 126
 QY 56 GlyGlnArgValIleGlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
 Db 127 GGCTCCCGGGTCACTCAGCCACTAGCGCGGCGAGGATCCCGGATCCCTTTGTGGCCTTC 186
 QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95
 Db 187 CACATCAACAAGGGCTTGTGAAGAGTATATGACTCTCTCTGATGGAGAACTGTCT 246
 QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115

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Db 247 CCAGAGCAGCCAGCTTTGAGCCACCAAGATATAAGAGCTGACAGATGAGTTCCGGGAG 306
Qy 116 LeuArgLysThrAlaGluAspValLeuPheLeuThrAsnHisValPhePheLeuLeu 135
Db 307 CTGCGGGCCACAGTGGAGCGGATGGGCTCATGAAGGCCAACCATGCTCTTCTCTGCTG 366
Qy 136 LeuLeuAlaHisIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGly 155
Db 367 TACCTGTGTCACATCTTGCTGTGATGGTGCAGCTGGCTCACCTTTGGTCTTTGGG 426
Qy 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGluAlaGln 174
Db 427 AGCTCCTTTTTCCTCTCTGCTGTGGGTGCTCAGTGCAGTTCAGCAGGCCCA 486
Qy 175 AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194
Db 487 GTGGATGGCTGCACATGATTATGGCCACCTGTCTGTACAGAAACCCCAAGTGGAC 546
Qy 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpAsn 214
Db 547 CACCTTGTCCACAAATTCGTATTGGCCACTTAAGGGTGCCTCTGCCAAGTGGGAAT 606
Qy 215 HisArgHisPheGlnHisIleAlaLysProAsnIlePheHisLysAspProAspValAsn 234
Db 607 CATCGCCACTTCCAGCACACCCAGCCCTAACATCTTCCACAGGATCCCGATGTGAAC 666
Qy 235 MetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeu 254
Db 667 ATGCTGCAGCTGTTTGTCTGGCGCAATGGCAGCCCATCGAGTACGGCAAGAGCTG 726
Qy 255 LysTyrLeuProTyrAsnHisGlnHisIleGlyTyrPhePheLeuIleGlyProProLeuLeu 274
Db 727 AAATACCTCGCCCTACAAATCACAGCAGCAATACTTCTTCTGATGGGCCCGCTGCTC 786
Qy 275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294
Db 787 ATCCCATGATTTTCCAGTACCAAGATCATCATGACCATGATCGTCCATAAGTCTGGTG 846
Qy 295 AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314
Db 847 GACCTGGCTGGCGCGTCACTACTACATCCGGTTCTTCACTACATCATCCCTTTCTAC 906
Qy 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334
Db 907 GCATCTCTGGAGCCCTCTTCTTCTCACTTCACTCAGTTTCTGGAGAGCACTGGTTT 966
Qy 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAsp 354
Db 967 GTGTGGGTCAACAGATGAATCACATCGTCATGGAGATTGACAGGAGGCCCTACCGTGAC 1026
Qy 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPheAsnAspTrp 374
Db 1027 TGGTTTCAGTAGCCAGCTGACAGCCACCTGCAACGTGGAGCAGTCTCTTCAACAGATCG 1086
Qy 375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHis 394
Db 1087 TTCAGTGAGCACCTTAATTCAGATTGAGCACCACTCTTCCCAACATGCCCGGCAC 1146
Qy 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
Db 1147 AACTTACACAGATGCCCGCTGGTGAAGTCTCTATGTGCAAGCATGGCAATGAATAC 1206
Qy 415 GlnGluLysProLeuLeuArgAlaLeuAspIleIleArgSerLeuLysLysSerGly 434
Db 1207 CAGGAGAGCCGCTACTGAGGCCCTGCTGGACATCATCAGTCTCTTGAAGATCTTGGG 1266
Qy 435 LysLeuTrpLeuAspAlaTyrIleuHisLys 444
Db 1267 AAGCTGTGGCTGGAGCCCTACCTTCCACAAA 1296

```

RESULT 15
ABS71826

ID ABS71826 standard; DNA; 2257 BP.
 XX
 AC ABS71826;
 XX
 DT 02-DEC-2002 (first entry)
 XX
 XX Human deltas-desaturase gene #8.
 DE
 XX Human; deltas-desaturase; polyunsaturated fatty acid; DGLA;
 KW dihomo-gamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;
 KW eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX US6432684-B1.
 PN
 XX 13-AUG-2002.
 PD
 XX 08-JAN-1999; 99US-0227613.
 PF
 XX 11-APR-1997; 97US-0833610.
 PR
 PR 10-APR-1998; 98WO-US07422.
 XX
 XX (ABBO) ABBOTT LAB.
 PA
 XX Mukerji P, Leonard AB, Huang Y, Das T;
 PI WPI; 2002-689761/74.
 DR
 XX
 XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing
 PT the conversion of dihomo-gamma-linolenic acid to arachidonic acid and
 PT in the conversion of 20:4n-3 to eicosapentaenoic acid -
 XX
 PS Example 1; Figure 8; 88bp; English.
 CC The invention relates to an isolated human deltas-desaturase nucleotide
 CC sequence (I) which desaturates polyunsaturated fatty acids at
 CC carbon 5. The nucleotide sequence (I) may be used in the recombinant
 CC production of vectors and host cells for the production of deltas-
 CC desaturase. Deltas-desaturase may be utilised in the conversion of
 CC dihomo-gamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the
 CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA Or
 CC polyunsaturated fatty acids produced from it may be added to
 CC pharmaceutical compositions, nutritional compositions, animal feeds, as
 CC well as other products such as cosmetics. ABS71819-ABS71854
 CC represent human deltas-desaturase coding sequences and PCR primers of
 CC the invention.
 XX
 SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Alignment Scores:
 Pred. No.: 5,92e-203 Length: 2257
 Score: 1935.00 Matches: 352
 Percent Similarity: 88.84% Conservative: 30
 Best Local Similarity: 81.86% Mismatches: 44
 Query Match: 79.37% Indels: 4
 DB: 24 Gaps: 2

US-09-719-601-5 (1-444) x ABS71826 (1-2257)

Qy 19 ProThr-----PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSer 35
 Db 7 CCTACCCCGGCTACTTCACTGGCAGCGAGTGGCCAGCGCTCAGGTGGCAGGCGG 66
 Qy 36 GlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGly 55
 Db 67 TGCTAGTATCAGCGTAAAGGTGTACACATCAGCAGGTTCACCCCGCGCATCCAGG 126
 Qy 56 GlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
 Db 127 GGCTCCCGGGTTCATCAGCCACTACCGCGGCGAGGATGCCACGATCCCTTTGTGGCTTC 186

CC topical ointments. The PUFAs produced by this method are useful in
 CC producing pharmaceutical compositions for treating rough or aging skin,
 CC injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,
 CC asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,
 CC cachexia associated with cancer, diabetes, eczema, AIDS, multiple
 CC sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting
 CC platelet aggregation, inducing vasodilation, reducing cholesterol
 CC levels, inhibiting proliferation of fibrous tissue, treating
 CC endometriosis, and myalgic cephalomyelitis. The gene for delta5
 CC desaturase is located on chromosome 11q12. The present sequence
 CC is a partial cDNA for a human delta5 desaturase.

XX Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Alignment Scores:

Pred. No.: 5.92e-203 Length: 2257
 Score: 1935.00 Matches: 352
 Percent Similarity: 88.84% Conservative: 30
 Best Local Similarity: 81.86% Mismatches: 44
 Query Match: 79.37% Indels: 4
 DB: 24 Gaps: 2

US-09-719-601-5 (1-444) x ABS76713 (1-2257)

QY 19 ProThr-----PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSer 35
 DB 7 CCTACCCCGCGCTACTTCCCTGGGACGAGTGCCCGACGCGCTCAGGGTCGGAGCGG 66
 QY 36 GlyLeuValIleAspArgLysValIleThrLysTrpSerIleGlnHisProGly 55
 DB 67 TGGTGTAGTATGACCGCTAAGGTGTACAAATCATCAGGAGTTCACCCGCGCATCCAGG 126
 QY 56 GlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
 DB 127 GGCTCCCGGGTCATCAGCCATCAGCCGGGAGAGTCCCGGATCCCTTTGTGGCCTTC 186
 QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95
 DB 187 CATCAACAAAGGCGCTTGTGAAGAGTATATGAACCTCTCTCTGATTGGAGACTGTCT 246
 QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115
 DB 247 CCAGAGCAGCCCGCTTTGGCCCAACCAAGAAATAAAGAGCTGACAGATGATTCGCGGAG 306
 QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135
 DB 307 CTGCGGCGCAGTGGAGCGAGTGGGCTCATGAAGCCCAACCATGCTCTTCTTCTGCTG 366
 QY 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGly 155
 DB 367 TACCTGTGTCACATCTTCTGCTGATGTCAGCTGGCTCACCCTTTGGTCTTTGGG 426
 QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln 174
 DB 427 AGCTCTTTTGGCCCTTCTCTCTGTCGGTGTGCTCAGTCAGTTCAGAGGCCCA 486
 QY 175 AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194
 DB 487 GCTGGATGGCTGCAACATGATTATGGCCACCTGCTGTCTACAGAAAACCAAGTGAAC 546
 QY 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsn 214
 DB 547 CACCTTGTCACAAATTCGTATTGGCCACCTTAAGGGTGGCTCTGCCAACTGGTGAAT 606
 QY 215 HisArgHisPheGlnHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234
 DB 607 CATGCCACTTCCAGCACCAGCCAGCGCTAACATCTTCCACAGGATCCCGATGTGAAC 666
 QY 235 MetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeu 254
 DB 667 ATGCTGACAGTGTGTGTTCTGGCGGAATGGGACCCCATCGAGTACGGCAAGAGACTG 726
 QY 255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeu 274

DB 727 AAATACCTGGCCCTCAATCACCAGCAGCAATACTTCTTCTGATTGGCGCGCTGCTC 786
 QY 275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294
 DB 787 ATCCCCCATGTATTTCCAGTACCAGATCATCATGACCATGATCGTCCATPAAGAACTGGGTG 846
 QY 295 AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314
 DB 847 GACCTGGCTGGCGCTCAGCTACTACATCCGGTTCTTTCATCACCTACATCCCTTCTAC 906
 QY 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334
 DB 907 GGCATCCTGGGAGCCCTCTTCTTCTCAACTTCATCAGGTTCTCTGGAGAGCCACTGGTTT 966
 QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAsp 354
 DB 967 GTGTGGGTACACAGATGAATCATCATCTCATGGAGATTGACGAGGCGCTACCGTGAC 1026
 QY 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374
 DB 1027 TGGTTTCAGTAGCCAGCTGACAGCCACCTGCAACGTCGAGCAGTCTCTTCTCAACGACTGG 1086
 QY 375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHis 394
 DB 1087 TTCAGTGGACACTTAATCTTCAGATTGAGCACCACTTCTTCCCACCATGCGCATTCGAATAC 1146
 QY 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
 DB 1147 AACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTCGAATAC 1206
 QY 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGly 434
 DB 1207 CAGGAGAACCCCTACTGAGGGCCCTGCTGGACATCATCAGTCTCCCTGAAGAAGTCTGGG 1266
 QY 435 LysLeuTrpLeuAspAlaTyrLeuHisLys 444
 DB 1267 AAGCTGTGCTGGACGCTTACCTTCACAAA 1296

RESULT 17
 ABT10758
 ID ABT10758 standard; cDNA; 2621 BP.
 XX
 AC ABT10758;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human breast cancer associated coding sequence SEQ ID NO: 892.
 XX
 KW Human; breast specific gene; breast cancer; differential expression;
 KW cytostatic; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200259271-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 25-JAN-2002; 2002WO-US02176.
 XX
 PR 25-JAN-2001; 2001US-263757P.
 PR 25-APR-2001; 2001US-286090P.
 PR 23-MAY-2001; 2001US-292517P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Orr MS, Nation M, Diggins JC, Zeng W;
 XX
 DR WPI; 2002-674803/72.
 XX
 PT Diagnosing breast cancer in a patient comprises detecting the level of
 PT gene expression in cell or tissue samples, where a differential gene
 PT expression is indicative of breast cancer -

Qy	138	AlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGly	151
Db	14	GCCCAATCATCGCCCTGGAGAGCATTCATGGTTCACCTGCTCTTTTACTTTTGGCAATGCG	73
Qy	158	TpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrp	177
Db	74	TGGATTCCTACCCCTCATCAGGCCCTTGTCCTTGCTACCTCTCAGGCCCAAGCTGGATGG	133
Qy	178	LeuGlnHisAspTyrGlyHisLeuSerValTyrArgIysProLysTrpAsnHisLeuVal	197
Db	134	CTGCAACATGATTATGGCCACCTGCTGCTCTACAGAAACCCCAAGTGGAAACCACTTGTC	193
Qy	198	HisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHis	217
Db	194	CACAAATTGTCATTGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGGATCATCGCCAC	253
Qy	218	PheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHis	237
Db	254	TTCCAGCACACGCCAAGCCTAACCATCTTCCACAGGATCCCGATGTGAACATGCTGCAC	313
Qy	238	ValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeu	257
Db	314	GTGTTTGTTCGGCGGAATGGCAGGCCATTCGAGTACGGCAAGAGAGAGCTGAATACCTG	373
Qy	258	ProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMet	277
Db	374	CCCTACAATCACCCAGCACGAATACTTCTTCTCGATTGGCGCGCGCTGCTCATCCCATG	433
Qy	278	TyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAla	297
Db	434	TATTTCCAGTACCAGATCATCATGACCATGTCGTCCATAAGAACTGGGTGGACCTGGCC	493
Qy	298	TrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyLeu	317
Db	494	TGGCCGCTCAGCTACTACATCCGGTTCCTTCATCACCTACATCCCTTTCTACGGCATCCTG	553
Qy	318	GlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVal	337
Db	554	GGAGCCCTCCCTTTTCTCTCACTTCATCAGGTTCTTCTGGAGAGCCACTGGTTGTGTGGGTC	613
Qy	338	ThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSer	355

CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 1575 BP; 313 A; 500 C; 386 G; 368 T; 8 other;

Alignment Scores:

Pred. No.: 7,91e-174 Length: 1575
 Score: 1669.00 Matches: 298
 Percent Similarity: 99.67% Conservative: 0
 Best Local Similarity: 99.67% Mismatches: 1
 Query Match: 68.46% Indels: 0
 DB: 24 Gaps: 0

US-09-719-601-5 (1-444) x ABL90108 (1-1575)

QY 146 IleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAla 165
 DB 3 ATTGCATGGTTCACGTCTTTTACTTTGGCAATGGCTGATTCCTACCTCATCAGGCC 62
 QY 166 PheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeu 185
 DB 63 TTTGTCTGTGTACCTCTCAGGCCCAAGCTGKATGGCTGCAACATGATTATGGCCACCTG 122
 QY 186 SerValTyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeu 205
 DB 123 TCTGTCTACAGAAACCCCAAGTGGACCACTTGTCCACAAATTCGTCATTTGGCCACTTA 182
 QY 206 LysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsn 225
 DB 183 AAGGGTGGCTCTGCCAACTGGTGGGAATCATCGCCACTTCCAGCACCAAGCCCAAGCTAAC 242
 QY 226 IlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlyTrpGln 245
 DB 243 AITCTCCACAGAGATCCCGATGTGAATGTCGACGTTGTGTCTGGGCGAATGGCAG 302
 QY 246 ProfileGlyTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGlyTyr 265
 DB 303 CCCATCGAGTACGGCAAGAAGCTGAATACCTGGCTCACTACATCACCAGCAGCAATAC 362
 QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleMet 285
 DB 363 TTTCTTCCTGATGGGCGCGCTGCTCATCCCATGTTATTCAGTACCATCATCATG 422
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg 305
 DB 423 ACCATGATGTCCTCAATAAGAACTGGTGGACCTGGCGCTGGCGCTCAGCTACTACATCGG 482
 QY 306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
 DB 483 TTTCTTCATCACCATACCTCTTCACGGCATCTCGGAGGCCCTCTTTCTCAACTTC 542
 QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
 DB 543 ATCAGGTTCCTGGAGGCCACTGTTGTGTGGGTACACAGATGAATCATCATGTCATG 602
 QY 346 GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
 DB 603 GAGATTGACAGAGGCGCTTACCGTACCTGGTTCAGTAGCCAGCTGACAGCCACCTGCAAC 662
 QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
 DB 663 GTGGAGCAGTCTCTTTCACAGCATGTTTCAGTGGACACCTTAATCTTCAGATTGAGCAG 722
 QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
 DB 723 CACCTCTCCCAACCATGCGCCGGCACAACTTACACAAGATCGCCCGCTGGTGAAGTCT 782
 QY 406 LeuCysAlaLysHisGlyIleGlyTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425

Db 783 CTATGTGCCAAGCATGGCATTCGAATACCAGGAGAGCGCTACTGAGGGCCCTGCTGGAC 842
 QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
 Db 843 ATCATCAGTCCCTGGAAGAAGTCTGGGAAGCTGTGGTGGACGCTACCTTACCAA 899

RESULT 19

AAK94786
 ID AAK94786 standard; cDNA; 2558 BP.
 XX
 AC AAK94786;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human full-length cDNA, SEQ ID NO: 3894.
 XX
 KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
 XX
 OS Homo sapiens.
 PN EP1130094-A2.
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114089.
 XX
 PR 08-JUL-1999; 99JP-0194486.
 PR 11-JAN-2000; 2000JP-0118774.
 PR 02-MAY-2000; 2000JP-0183765.
 XX
 PA (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI; 2001-524255/58.
 DR P-PSDB; AAM93830.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX
 PS Claim 8; SEQ ID NO 3894; 1380pp + sequence listing; English.
 XX

CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 CC molecules have been determined. Primers for synthesising the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is a full length
 CC human cDNA of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from BPO.

XX Sequence 2558 BP; 502 A; 777 C; 710 G; 569 T; 0 other;

Alignment Scores:

Pred. No.: 2.12e-173 Length: 2558
 Score: 1668.00 Matches: 297
 Percent Similarity: 99.67% Conservative: 1
 Best Local Similarity: 99.33% Mismatches: 1
 Query Match: 68.42% Indels: 0
 DB: 22 Gaps: 0

US-09-719-601-5 (1-444) x AAK94786 (1-2558)

QY 146 IleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAla 165
 Db 1 ATTGCATGGTTCACGTCTTTTACTTTGGCAATGGCTGATTCCTACCTCATCAGGCC 60

QY 166 PheValLeuAlaThrSerGlnhlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeu 185
 DB 61 TTTGTGCTTGTACCTCTCAGGCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTG 120
 QY 186 SerValTyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeu 205
 DB 121 TCTGTCTACAGAAACCCCAAGTGAACACCTTGTCCACAAATTCATCATTTGGCCACTTA 180
 QY 206 LysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsn 225
 DB 181 AAGGGTGCTCTGCCAACTGGTGAATCATGCCACTTCCAGCACCCAGCCCAAGCCTAAC 240
 QY 226 IlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGln 245
 DB 241 ATCTTCCACAGGATCCCGATGTGAACATGCTGCACGTGTGTCTGGGGGAATGGCAG 300
 QY 246 ProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys 265
 DB 301 CCCATCGAGTACGGCAAGGAAGCTGAAATACCTGCCCTACAAATCACCCAGCAGCAATAC 360
 QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMet 285
 DB 361 TTCTTCTGATGGGGCGCGCTGTCTATCCCATGTATTTCCAGTACCATCATCATG 420
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg 305
 DB 421 ACCATGATGTCATTAAGAACTGGGTGGACCTGGCTGGCGCTCAGCTACTACATCCGG 480
 QY 306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
 DB 481 TTCTTCTATCACCTACATCCCTTTCTACGGCATCTGGGAGCCCTCTTTCTCTCACTTC 540
 QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
 DB 541 ATCAGGTTCCTGGAGAGCCACTGTTTGTGTGGTCCACACAGATGAATCACATGCTCATG 600
 QY 346 GluIleAspGlnIleAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
 DB 601 GAGATTGACAGAGAGCCCTACCTGTACTGTTCAGTAGCAGTACACCCACCTGGCAAC 660
 QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
 DB 661 GTGGAGCAGTCTCTTCAACGACTGTTTCAGTGGACACCTTAACCTCCAGATTGAGCAC 720
 QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
 DB 721 CACCTCTTCCCAACCATGCCCGGCACAACTTACACAGATCGCCCGCTGTGTGAAGTCT 780
 QY 406 LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
 DB 781 CTATGTGCCAAGCATGGCATTGATACCGGGGAGCGCCCTACTGAGGGCCCTGCTGGAC 840
 QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
 DB 841 ATCATCAGTCTCCTGAAGAAGTCTGGGAAGCTGTGGAGCTGTGGACCTTACCTTACAAA 897
 RESULT 20
 AAV63642
 ID AAV63642 standard; cDNA; 1843 BP.
 XX
 AC AAV63642;
 XX
 DT 15-FEB-1999 (first entry)
 XX
 DE Contig 2535 encoding a human desaturase enzyme.
 XX
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome; human;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.

OS Homo sapiens.
 XX
 PN W09846763-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 10-APR-1998; 98WO-US07126.
 XX
 PR 11-APR-1997; 97US-0834655.
 XX
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 XX
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmond J;
 XX
 DR WPI: 1998-594592/50.
 DR P-PSDB; AAW841155.
 XX
 PT New isolated fatty acid desaturase enzymes - used for the production
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 PT compositions, nutritional compositions, cosmetics or animal feed
 XX
 PS Example 12; Pages 116-117; 165pp; English.

XX The present sequence encodes a human desaturase enzyme. The sequence was
 CC identified based on homology between human cDNA sequences and Mortierella
 CC alpina desaturase gene sequences. The specification describes methods for
 CC desaturating a fatty acid and for producing a desaturated fatty acid by
 CC expressing increased levels of a desaturase. The enzyme can be used for
 CC desaturating fatty acids. The enzyme can be used to produce
 CC polyunsaturated fatty acids, which can be used for treating malnutrition,
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The
 CC polyunsaturated fatty acids can be used for treating e.g. restenosis
 CC after angioplasty, inflammation, rheumatoid arthritis, asthma,
 CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They
 CC can also be used to inhibit platelet aggregation, cause vasodilation,
 CC lower cholesterol levels, inhibit proliferation of vessel wall smooth
 CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
 CC and other side effects caused by non-steroidal anti-inflammatory drugs,
 CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
 CC encephalomyelitis and chronic fatigue after viral infections, treat
 CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
 CC inflammatory skin disorders.

XX Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Alignment Scores:

Align. No.: 3,46e-171 Length: 1843
 Score: 1646.00 Matches: 294
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 67.51% Indels: 0
 DB: 19 Gaps: 0

US-09-719-601-5 (1-444) x AAV63642 (1-1843)

QY 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170
 DB 1 GTCCTTTTACTTGGCAATGGCTGGATTCCTACCTCATCAGGCTTTGTCTTGCTTACC 60
 QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
 DB 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTCTCAGAAAA 120
 QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
 DB 121 CCCAAGTGGAAACCACTTGTCCCAAAATTCGTATTGGCCACTTAAGGGTGGCTCTGCC 180
 QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
 DB 191 AACTGGTGGAAATCATCGCACTTCCAGCAGCACCCAGGCTTAACATCTTCCCAAGGAT 240

QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250
 Db 241 CCCGATGTAACATCTCTCAGCTGTTTCTTGGCGAATGGCAGCCATCGATACGGC 300
 QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
 Db 301 AAGAAAGAGCTGAATACCTGCGCTTACCAATCACCAGCAGCAATATCTTCTCTGATGGG 360
 QY 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
 Db 361 CGCGCGCTGCTCATCCCATGATTTCCAGTACCAAGATCATGACCATCATCGTCCAT 420
 QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
 Db 421 AAGAACTGGTGGACCTGGCGCTGGCGCTAGCTACTACATCGCTTCTTCATCACCTAC 480
 QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
 Db 481 ATCCCTTTCTACGGCATCTGGAGCCCTCTTTCTCAACTTCATCAGGTTCTCTGGAG 540
 QY 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
 Db 541 AGCCACTGGTTGTGGGTACACAGATGAATCATCATCGTATGGAGATTGACCGAG 600
 QY 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
 Db 601 GCTACCGCTGACTGTTTCTAGTACGAGCTGACAGCCACTGCAACGCTGGAGCAGTCTCTC 660
 QY 371 PheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThr 390
 Db 661 TTCACGACTGTTTCTAGTGGACACTTAACTTCAGATTGAGCACCCTCTTCCACC 720
 QY 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410
 Db 721 ATGCCCGCGCACAACTTACACAGATGCGCGCTGGTGAAGTCTCTATGTGCCAAGCAT 780
 QY 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430
 Db 781 GGCATTGAATACAGAGAGAGCGCTACTAGGCGCCCTGCTGGACATCATCAGTCTCTG 840
 QY 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
 Db 841 AAGAAAGTCTGGGAAGCTGTGGTGGAGCGCTACCTTCAAAA 882

RESULT 21
 AAX00909 standard; DNA; 1843 BP.
 XX AC AAX00909;
 XX DT 26-MAR-1999 (first entry)
 XX DE Human desaturase gene contig 2535.
 XX KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW stearidonic acid; eicosapentaenoic acid; main nutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed; human; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT 1..1842
 XX CDS /*tag= a
 XX FT /*note= "contains internal stop codons"
 XX FN W09846764-A1.
 XX PD 22-OCT-1998.
 XX PF 10-APR-1998; 98WO-US07421.

XX 24-OCT-1997; 97US-0958985.
 PR 11-APR-1997; 97US-0833610.
 PR 11-APR-1997; 97US-0834033.
 PR 11-APR-1997; 97US-0834655.
 XX (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 XX Chaudhary S, Huang Y, Knutzon D, Leonard AS, Mukerji P;
 PI Thurmond J;
 XX WPI; 1999-080739/07.
 DR P-PSDB; AAW95513.
 XX Nucleic acid construct able to express fatty acid desaturase in
 PT plants - useful in human or animal nutrition, as cosmetics and
 FT therapeutically, e.g. for restenosis, cancer and diabetes
 XX Claim 48; Page 160-161; 210pp; English.
 XX The invention relates to a nucleic acid construct that contains at least
 CC one of the nucleotide sequences (AA00889 to AAX00891) encoding
 CC Mortierella alpina delta 6, delta 12 and delta 5 desaturases (AAW95504 to
 CC AAW95506) respectively, coupled to an expression control sequence
 CC functioning in plants. Recombinant plant cells containing at least one DNA
 CC encoding a M. alpina fatty acid desaturase (FAD), can be used for the
 CC production of polyunsaturated fatty acid (PUFA). These recombinant cells
 CC or plants containing them are used to produce oils such as linoleic
 CC acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic
 CC acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils
 CC are used: (i) to treat malnutrition; (ii) in infant feeding formulas; or
 CC dietary supplements or substitutes, for use in humans or animals; (iii)
 CC for treating disorders associated with inadequate consumption or
 CC production of PUFA (or their metabolites such as prostaglandins), e.g.
 CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics,
 CC and (v) as animal feeds. Fragments of the DNA are used as probes to
 CC isolate related coding sequences. Recombinant plants can produce high
 CC yields of PUFA, since new pathways can be created and unwanted ones
 CC suppressed. Plants can be engineered to express oils of particular PUFA
 CC composition, e.g. one similar to that in human milk, and product recovery
 CC is simpler than with e.g. fish. Sequences AAX00904-910 represent DNA
 CC sequences of various contigs of human desaturase genes which are similar
 CC to the M. alpina desaturase sequences.
 XX SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Alignment Scores:
 Pred. No.: 3,46e-171 Length: 1843
 Score: 1646.00 Matches: 294
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 67.51% Indels: 0
 DB: 20 Gaps: 0
 US-09-719-601-5 (1-444) x AAX00909 (1-1843)
 QY 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170
 Db 1 GTCTTTTACTTTGGCAATGGCTGGATTCTTACCTCATCAGCGCTTTGCTTGTCTAC 60
 QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
 Db 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGCTGTCTACAGAAA 120
 QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
 Db 121 CCCAAGTGGAAACCACTTGTCCCAAAATTCGTATTGGCCACTTAAGGTGCTCTGCC 180
 QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
 Db 181 AACTGGTGGATCATCGCCACTTCCAGCACCACCGCAAGCTTAACATCTTCCACAGGAT 240

QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250
 DB 241 CCCGATGTAACATGCTGCACGTGTTGTTCTGGCGAATGGACCCCATCGATGACGC 300
 QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
 DB 301 AAGAAGAGCTGAATACCTGCGCTTACAAATCACCAGCAGCAATATCTTCTGATGGG 360
 QY 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
 DB 361 CGCGCGCTGCTCATCCCATGATTTCAGTACCAAGATCATGACCATGATGCTCAT 420
 QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
 DB 421 AAGAACTGGGTGGACCTGCGCTGGCGGCGTACGACTACTACATCCGTTCTTCATCACCTAC 480
 QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
 DB 481 ATCCCTTTCTACGGCATCTCTGGAGCCCTCTTTCTCACTTCTCATCAGGTTCCTGGAG 540
 QY 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
 DB 541 AGCCACTGTTTGTGGTCTCACAGATGATCATGCTCATGGAGATTGACCCAGGAG 600
 QY 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
 DB 601 GCCTACCGTGACTGGTTCTAGTAGCCAGCTGACAGCCACCTGCAACGTTGGAGCGTCTTC 660
 QY 371 PheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThr 390
 DB 661 TTCACGACTGGTTCTAGTGACACCTTAATCTCCAGATTGACACCACTCTTCCCCACC 720
 QY 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410
 DB 721 ATGCCCCGGCACAACTTACACAGATGCGCCGCTGCTGAGTCTCTATGTCGCAAGCAT 780
 QY 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430
 DB 781 GGCAATGAATACAGGAGAGCGCTACTGAGGGCCCTGCTGGACATCATCAGTCCCTG 840
 QY 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
 DB 841 AAGAAGTCTGGAGAGCTGTGGCTGGAGCGCTACCTTACAAA 882
 RESULT 22
 AAV82641
 ID AAV82641 standard; DNA; 1843 BP.
 AC
 XX AAV82641;
 XX
 DT 11-FEB-1999 (first entry)
 XX
 DE Contig 2535 encoding a desaturase enzyme.
 XX
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.
 OS Homo sapiens.
 XX
 PN WO9846765-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 10-APR-1998; 98WO-US07422.
 XX
 PR 11-APR-1997; 97US-0833610.
 XX
 PA (ABBO) ABBOTT LAB.

(CALJ) CALGENE LLC.

PA
 XX Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
 PI Thurmond J;
 XX

XX WPI; 1999-009334/01.
 DR P-PSDB; AAW85134.
 DR

XX New nucleic acid encoding deltas and other desaturase enzymes -
 PT useful in production of oils of increased arachidonic acid content,
 PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
 XX
 PS Claim 86; Pages 110-111; 153pp; English.

XX The present sequence encodes a human desaturase enzyme. The enzyme
 CC sequence is used in the methods of the invention. The specification
 CC describes methods for desaturating a fatty acid and for producing a
 CC desaturated fatty acid by expressing increased levels of a desaturase.
 CC The enzyme can be used for desaturating fatty acids. The enzyme can be
 CC used to produce polyunsaturated fatty acids, which can be used for
 CC treating malnutrition, in pharmaceutical compositions, in cosmetics or
 CC in animal feed. The polyunsaturated fatty acids can be used for treating
 CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,
 CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.
 CC They can also be used to inhibit platelet aggregation, cause
 CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
 CC wall smooth muscle and fibrous tissue, reduce or prevent
 CC gastro-intestinal bleeding and other side effects caused by non-steroidal
 CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual
 CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after
 CC viral infections, treat AIDS, multiple sclerosis, acute respiratory
 CC syndrome, hypertension and inflammatory skin disorders.

SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Alignment Scores:

Pred. No.: 3,46e-171 Length: 1843
 Score: 1646.00 Matches: 294
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 67.51% Indels: 0
 DB: 20 Gaps: 0

US-09-719-601-5 (1-444) x AAV82641 (1-1843)

QY 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170
 DB 1 GTCCTTTACTTTGGCAATGGCTGGATTCTTACCTCATCAGCGCTTGTCTTGTCTTACC 60
 QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
 DB 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 120
 QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
 DB 121 CCCAAGTGGACACCACTTGTCCACAAATTCGTCTATTGGCCACTTAAAGGGTGGCTCTGCC 180
 QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisLysAlaLysProAsnIlePheHisLysAsp 230
 DB 181 AACTGGTGAATCATCGCCACTTCCAGCACCCACCAAGCTTAACATCTTCCCAAGGAT 240
 QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250
 DB 241 CCCGATGTGAACATGCTGTCACGTGTTGTTCTGGCGAATGGACGCCCATCGAGTCGGC 300
 QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
 DB 301 AAGAAGAGCTGAATACCTGCGCTTACAAATCACCAGCAGCAATATCTTCTCTGATGGG 360
 QY 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
 DB 361 CGCGCGCTGCTCATCCCATGATTTCAGTACCAAGATCATGACCATGATGCTCAT 420

QY 231 LysAsnTrpValAspLeuAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
 DB 421 AAGAACTGGGAGGACCTGGCGCTGAGTACTACATCCCGTTCTTCAATCACCCTAC 480
 QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
 DB 481 ATCCCTTTCTACGGCATCCTGGAGCCCTCTTCTCTCAACTTCATCAGGTTCTCTGGAG 540
 QY 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
 DB 541 AGCCACTGGTTGTGGGTGCACAGATGAATCACATCGTCATGGAGATGACAGGAG 600
 QY 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
 DB 601 GCCTACCGTACTGTTTCTAGTACGAGTGCAGCCACCTGCAACAGTGGAGCAGTCTCTTC 660
 QY 371 PheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThr 390
 DB 661 TTCAACGACTGGTTTCTAGTGGACACCTTAACCTTCAGATTTGAGCACCTCTTCCCCACC 720
 QY 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410
 DB 721 ATGCCCGCGCACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCGCAAGCAT 780
 QY 411 GlyIleGluTyrGlnGluIleProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430
 DB 781 GGCATTGAATACCGAGAGACCGCTACTGAGGCCCTGCTGGACATCATCAGTCCCTG 840
 QY 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
 DB 841 AAGAACTGTGGAGACTGTGGTGCAGCCCTACCTTACAAA 882

RESULT 23
 AAA49938
 ID AAA49938 standard; cDNA; 1843 BP.
 AC AAA49938;
 XX
 DT 10-OCT-2000 (first entry)
 DE Human delta-5-desaturase-related contig 2535.
 XX
 KW Delta-5-desaturase; human; polyunsaturated fatty acid;
 KW arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;
 KW docosahexaenoic acid; nutrition; feedstuff; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 1..885
 FT /*tag= a
 FT
 XX
 PN WO200040705-A2.
 XX
 PD 13-JUL-2000.
 XX
 PF 29-DEC-1999; 99WO-US31163.
 XX
 PR 08-JAN-1999; 99US-0227613.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Mukerji P, Leonard AEY, Huang Y, Parker-Barnes JM;
 XX
 DR WPI; 2000-465975/40.
 DR P-PSDB; AAY95448.
 XX
 XX New polypeptide useful for preparation of nutritional supplements based
 PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids
 PT at carbon 5 -
 XX
 PS Example 1; Fig 7; 127pp; English.
 XX

CC The present sequence is that of contig 2535, a contig produced
 CC from overlapping contigs 2511785 (see AAA49937) and 3506132 (see
 CC AAA49938), which were isolated from the Incyte Lifeseg database on
 CC the basis of homology to Mortierella alpina delta-5-desaturase and
 CC delta-6-desaturase cDNA sequences. The contig includes a partial
 CC open reading frame. It overlaps with another isolated contig,
 CC 3854933 (see AAA49936), creating a final contig, 253538a (see
 CC AAA49939), that contains a partial open reading frame which aligns
 CC with M. alpina delta-5 and delta-6-desaturase sequences. The
 CC contig was utilised in the isolation of cDNA (see AAA49932) encoding
 CC human delta-5-desaturase (see AAY95445). Delta-5-desaturase
 CC catalyzes the conversion of dihomogamma-linolenic acid to
 CC arachidonic acid and of 20:4n-3 to eicosapentaenoic acid.
 CC Recombinant enzyme, expressed in prokaryotic or eukaryotic hosts
 CC using the isolated human delta-5-desaturase cDNA, can be used in
 CC the production of polyunsaturated fatty acids that may be added to
 CC nutritional, veterinary and pharmaceutical compositions.
 XX
 SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Alignment Scores:
 Pred. No.: 3,46e-171 Length: 1843
 Score: 1646.00 Matches: 294
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 67.51% Indels: 0
 DB: 21 Gaps: 0

US-09-719-601-5 (1-444) x AAA49938 (1-1843)

QY 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170
 DB 1 GTCCTTTTACTTTGGCAATGCGTGGATTCTACCTCTCATCAGCGCTTGTCTCTGCTTACC 60
 QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
 DB 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACTCTCTGTCTACAGAAA 120
 QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
 DB 121 CCNAGTGGAAACCACTTGTCCACAAATTCGATTGGCCACTTAAGGGTGCCCTCTGCC 180
 QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
 DB 181 AACTGGTGAATCATCGCCACTTCCAGCACCAACGCAAGCTTAACATCTTCCACAAGGAT 240
 QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250
 DB 241 CCGATGTGAACATGCTGCACGTGTGTCTGGGGCAATGGCAGCCCATCGAGTACGGC 300
 QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
 DB 301 AAGAAGAGCTGAATACCTGCCCTACATCACCAGCACGAATACTTCTCTGATTGGG 360
 QY 271 ProProLeuIleLeuProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
 DB 361 CCGCCGCTGCTCATCCCATGTATTTCCAGTACCAAGATCATCATGACCAATGTCGTCAT 420
 QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
 DB 421 AAGAACTGGTGGACCTGGCTGGGCGCTCAGCTACTACTATCCGGTCTTCTCATCCTAC 480
 QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
 DB 481 ATCCCTTTCTACGGCATCCTGGAGCCCTCTTCTCAACTTCATCAGGTTCTCTGGAG 540
 QY 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
 DB 541 AGCCACTGGTTGTGGGTGCACAGATGAATCACATCGTCATGGAGATGACAGGAG 600
 QY 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
 DB 601 GCCTACCGTACTGTTTCTAGTGGACACCTTAACCTTCAGATTTGAGCACCTCTTCCCCACC 660

QY 371 PheAsnAspTrpPheSerGlyHisLeuAsnPhenGlnIleGluHisLeuPheProThr 390
 Db 661 TTCAACGAGTGGTTCAGTGGACACCTTAACCTCCAGATTGAGCACCACTCTTCCCCACC 720
 QY 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410
 Db 721 ATGCCCGGCGACACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 780
 QY 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerIleu 430
 Db 781 GCGATTGAATACAGGAGAGCGGTACTAGGCGCCCTGCTGGACATCATCAGGTCCCTG 840
 QY 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
 Db 841 AAGAAGCTGGGAAGCTGTGGTGGACGCTACCTTCAAAA 882

RESULT 24

AAA09452
 ID AAA09452 standard; DNA; 1843 BP.

AC AAA09452;

XX 10-AUG-2000 (first entry)

XX Human contig DNA encoding desaturase homologue.

XX delta-6 desaturase; gamma-linolenic acid; biosynthesis;
 XX transgenic insect cell; polyunsaturated long chain fatty acid;
 KW antiinflammatory; antirheumatic; antiasthmatic; antipsoriatic;
 KW osteopathic; cytostatic; antidiabetic; dermatological; gynecological;
 KW anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;
 KW antiaggregant; vasotropic; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT mat_peptide 1..1842

FT FT /*tag= a
 FT FT /transl_except= (pos:883..885, aa:Xaa)
 FT FT /transl_except= (pos:961..963, aa:Xaa)
 FT FT /transl_except= (pos:1371..1374, aa:Xaa)
 FT FT /transl_except= (pos:1471..1473, aa:Xaa)
 FT FT /transl_except= (pos:1549..1551, aa:Xaa)
 FT FT /transl_except= (pos:1648..1650, aa:Xaa)
 FT FT /note= "Xaa not defined"

XX W0200020602-A2.

XX 13-APR-2000.

XX 29-SEP-1999; 99WO-US22686.

XX 05-OCT-1998; 98US-0103110.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Huang Y, Parker-barnes JM, Das T;

XX WPI; 2000-328935/28.

XX P-PSDB; AAY92617.

XX Novel transgenic insect cells comprising a nucleotide sequences which
 PT encode delta-6-desaturase or delta-12- desaturase, useful for producing
 PT poly-unsaturated long chain fatty acids, e.g. arachidonic acid

XX Example 13; Page 160-161; 170pp; English.

XX AAA09447-52 are human DNA sequences identified based on homology to
 CC Mortierella alpina delta-5 and delta-6 desaturase genes. The human
 CC DNA's were aligned based on areas of homology to form a contig.
 CC Consensus sequences were assembled. A contig, 2511785 overlaps with
 CC contig 3506132, and this new contig was called 2535 (AAA09453).

CC The fatty acid desaturases are able to catalyse the conversion of oleic
 CC acid to linoleic acid, linoleic acid to gamma-linolenic acid or of
 CC alpha-linolenic acid to stearidonic acid. Transgenic insect cells
 CC comprising a nucleotide sequence which encodes a polypeptide comprising
 CC residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6
 CC desaturase (AAY92599) or comprising delta-12 desaturase (AAY92600) are
 CC claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated
 CC from the recombinant insect cells are also claimed. Production of
 CC polyunsaturated long chain fatty acids (PUFAs) in insect cells has many
 CC advantages, as insect cells have greatly simplified lipid compositions,
 CC are not subject to external variable fluctuations, and can easily be
 CC maintained and manipulated. The oils are used in pharmaceutical
 CC compositions, infant formulas, dietary supplements or substitutes, and
 CC cosmetics (all claimed). The PUFA supplements have antiinflammatory,
 CC antirheumatic, antiasthmatic, antipsoriatic, osteopathic, cytostatic,
 CC antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,
 CC hypotensive, nephrotropic, vasodilator, antiaggregant and vasotropic
 CC activity.

XX SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Alignment Scores:

Pred No.: 3,46e-171 Length: 1843
 Score: 1646.00 Matches: 294
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 67.51% Indels: 0
 DB: 21 Gaps: 0

US-09-719-601-5 (1-444) x AAA09452 (1-1843)

QY 151 ValPheTyrPheGlyAsnGlyTrpLeuProThrLeuIleThrAlaPheValLeuAlaThr 170
 Db 1 GTCTTTTACTTGGCAATGGCTGATTCCTACCTCATACAGCCCTTGTCTGTGTACC 60
 QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
 Db 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGCTGTCTACAGAAA 120
 QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
 Db 121 CCCAAGTGGACACCACTTGTCCCAAAATCGTATTGGCCACCTTAAGGGTGGCTCTGCC 180
 QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
 Db 191 AACTGGTGGATCATCGCCACTTCCAGCACCCAGCCCAAGCCTTAACATCTTCCACAGGAT 240
 QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250
 Db 241 CCCGATGTGAACATGCTGCACGTGTTTGTCTGGGCGAATGGCAGCCCATCGAGTACGGC 300
 QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
 Db 301 AAGAAGAGCTGAAATACCTGCCCTTACATACCCAGCACCAATACTTCTTCTGATTGGG 360
 QY 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
 Db 361 CCGCGCTGCTCATCCCATGATTTTCCAGTACCAGATCATCATGACCATGATCGTCCAT 420
 QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
 Db 421 AAGAACTGGGTGGACCTGGCTGGCGCTGAGCTACTACATCCGCTTCTTCTCATCCCTAC 480
 QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
 Db 481 ATCCCTTTTACGGCATCCTGGAGCCCTCCCTTTTCTCACTTCACTCAGGTCTTCTGGAG 540
 QY 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
 Db 541 AGCCACTGGTTGTGTGGGTCCACAGATGAATTCATCTGTCATGGAGATTGACACGAG 600
 QY 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370

Db 601 GCCTACCGTGACTGTTTCAGTAGCCAGCTGACAGCCACCTGCAACGCTGGAGCGTCTTC 660
 Qy 371 PheAsnAspTrpPheSerGlyHisLeuAsnPhenGlnIleGluHisHisLeuPheProThr 390
 Db 661 TTCAACGAGCTGTTTCAGTGACACCTTAACCTTCAGATTGAGCACCACTTCTCCACC 720
 Qy 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410
 Db 721 ATGCCCGGCGACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 780
 Qy 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430
 Db 781 GGCATGATACACAGGAGCGCTACTAGGCGCTGCTGACATCATCAGGTCCCTG 840
 Qy 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
 Db 841 AAGAAGTCTGGGAAGCTGGCTGGACGCTACCTTCCAAA 882

RESULT 25

AA14593
 ID AA14593 standard; DNA; 1843 BP.

XX
 AC AA14593;

DT 08-AUG-2000 (first entry)

XX Nucleotide sequence of a contig of a human desaturase enzyme.

XX Delta5-desaturase; poly-unsaturated long chain fatty acid; PUFA;
 KW arachidonic acid; infant formula; dietary supplement; dietary substitute;
 KW cosmetic; stress; metabolic disorder; gastrointestinal difficulty;
 KW malabsorption; resenosis; angioplasty; inflammation; kidney stone;
 KW rheumatoid arthritis; asthma; psoriasis; osteoporosis; tract stone;
 KW cancer; cachexia; diabetes; eczema; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder;
 KW blood score; platelet aggregation; vasodilatation;
 KW gastro-intestinal bleeding; ss.

XX Homo sapiens.

XX WC2000020603-A1.

XX 13-APR-2000.

XX 29-SEP-1999; 99WO-US22692.

XX 05-OCT-1998; 98US-0103109.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Huang Y, Parker-Barnes JH, Das T;

XX WPI; 2000-364599/31..

XX P-PSDB; AAY84702.

XX Novel transgenic insect cell with modified delta-5-desaturase

XX production, useful for altering fatty acid biosynthesis -

XX Example 9; Page 147-148; 161pp; English.

XX AAA14588-94 represent contigs of a human desaturase. The specification
 CC describes a Mortierella alpina delta5-desaturase. The protein is
 CC involved in the biosynthesis of poly-unsaturated long chain fatty
 CC acids (PUFAs). The polynucleotide is to produce PUFAs, especially
 CC arachidonic acid. The oils produced by the invention are used in
 CC pharmaceutical compositions, infant formulas, dietary supplements,
 CC dietary substitutes, and cosmetics. The nutritional compositions can be
 CC used to treat normal individuals temporality exposed to stress, or
 CC individuals having specialized needs due to chronic or acute diseases
 CC (e.g. metabolic disorders such as gastrointestinal difficulties and/or
 CC malabsorption, and other disorders such as restenosis after angioplasty,
 CC symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis,

CC osteoporosis, kidney stones, tract stones, cancer, cachexia associated
 CC with cancer, diabetes, eczema, endometriosis, premenstrual syndrome,
 CC myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis,
 CC acute respiratory syndrome, hypertension, inflammatory skin disorders,
 CC as well as reduce blood score, inhibit platelet aggregation, cause
 CC vasodilatation, inhibit proliferation of vessel wall smooth muscle and
 CC fibrous tissue, prevent or reduce gastro- intestinal bleeding, and for
 CC geriatric treatments).

SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Alignment Scores:

Fred. No.: 3,46e-171 Length: 1843
 Score: 1646.00 Matches: 294
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 67.51% Indels: 0
 DB: 21 Gaps: 0

US-09-719-601-5 (1-444) x AAA14593 (1-1843)

Qy 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170
 Db 1 GTCTTTTACCTTGGCAATGCTGGATTCTCTACCTCATCAGCGCTTTGTCTTGTAC 60
 Qy 171 SerGlnAlaGlnIleGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
 Db 61 TCTCAGGCCCAAGCTGGCTGGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 120
 Qy 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
 Db 121 CCNAGTGGAACCACTTGTCCACAATTCGTTCATGGCCACTTAAGGGTGTCTGCC 180
 Qy 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
 Db 181 AACTGGTGGGAATCATGCCACTTCCAGCACACCAAGCCTAACATCTTCCAAAGGAT 240
 Qy 231 ProAspValAsnMetLeuHisValPheValLeuGlyLysTrpGlnProIleGluTyrGly 250
 Db 241 CCGGATGTGAACATGCTGGCAGCTGTTTGTCTGGCGAATGGCAGCCATCGATGAGGC 300
 Qy 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
 Db 301 AAGAAGAAGCTGAATACCTGCCTCAATCACCAGCACCAATCTTCTCTGATTGGG 360
 Qy 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleMetThrMetIleValHis 290
 Db 361 CCGCGCTGTCTCATCCCATGTTTCCAGTACCAATCATCATGACCATGATCGTCCAT 420
 Qy 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
 Db 421 AAGAAGCTGGTGGACCTGGCTGGCGCTCAGCTACTACATCCGTTCTTTCATCACCTAC 480
 Qy 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhenIleArgPheLeuGlu 330
 Db 481 ATCCCTTTCTACGGCATCTCTGGGAGCCCTCTTCTCACTCACTCATCAGTTCCTGGAG 540
 Qy 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
 Db 541 AGCCACTGGTTTGTGGTGCACAGATGAATCACAATCGTCATGAGATTGACCAAGGAG 600
 Qy 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
 Db 601 GCCTACCGTGACTGGTTTCAGTAGCCAGCTGACGCCACCTGCAACGCTGGAGAGTCTTC 660
 Qy 371 PheAsnAspTrpPheSerGlyHisLeuAsnPhenIleGluHisHisLeuPheProThr 390
 Db 661 TTCAACGAGCTGTTTCAGTGACACCTTAACCTTCAGATTGAGCACCACTTCTCCACC 720
 Qy 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410
 Db 721 ATGCCCGGCGACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 780

QY 411 GlyTieGluTyrGlnGluLysProLeuLeuAlaLeuLeuAspIleIleArgSerLeu 430
 Db 781 GGCATTGAATACAGGAGAGCCGCTACTGAGGGCCCTGCTGGACATCAATCAGGTCCTCG 840
 QY 431 LysLysSerGlyLysLeuTyrLeuAspAlaTyrIleHisLys 444
 Db 841 AAGAAGTCTGGGAAGCTGTGCTGGAGCCCTACCTTCACAAA 882

RESULT 26

ABS71825

ID ABS71825 standard; DNA; 1843 BP.

XX AC ABS71825;

XX DT 02-DEC-2002 (first entry)

XX DE Human delta5-desaturase Gene #7.

XX KW Human; delta5-desaturase; polyunsaturated fatty acid; DGLA;

XX KW dihomogamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;

XX KW eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;

XX KW gene; ds.

XX OS Homo sapiens.

XX PN US6432684-B1.

XX PD 13-AUG-2002.

XX PF 08-JAN-1999; 99US-0227613.

XX PR 11-APR-1997; 97US-0833610.

XX PR 10-APR-1998; 98WO-US07422.

XX PA (ABDO) ABBOTT LAB.

XX PI Mukerji P, Leonard AE, Huang Y, Das T;

XX PS WPI; 2002-689761/74.

XX PT Nucleic acids encoding human DELTA5-desaturase, useful for catalysing

XX PT the conversion of dihomogamma-linolenic acid to arachidonic acid and

XX PT in the conversion of 20:4n-3 to eicosapentaenoic acid -

XX PS Example 1; Figure 7; 88pp; English.

XX CC The invention relates to an isolated human delta5-desaturase nucleotide

XX CC sequence (I) which desaturates polyunsaturated fatty acids at

XX CC carbon 5. The nucleotide sequence (I) may be used in the recombinant

XX CC production of vectors and host cells for the production of delta5-

XX CC desaturase. Delta5-desaturase may be utilised in the conversion of

XX CC dihomogamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the

XX CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA or

XX CC polyunsaturated fatty acids produced from it may be added to

XX CC pharmaceutical compositions, nutritional compositions, animal feeds, as

XX CC well as other products such as cosmetics. ABS71819-ABS71854

XX CC represent human delta5-desaturase coding sequences and PCR primers of

XX CC the invention.

XX SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

XX Alignment Scores:

XX Pred. No.: 3,46e-171 Length: 1843

XX Score: 1646.00 Matches: 294

XX Percent Similarity: 100.00% Conservative: 0

XX Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 67.51% Indels: 0

XX DB: 24 Gaps: 0

XX US-09-719-601-5 (1-444) x ABS71825 (1-1843)

QY 151 ValPheTyrPheGlyAsnGlyTyrIleProThrIleuIleThrAlaPheValIleuAlaThr 170

Db 1 GTCTTTTACTTTGGCAATGGCTGGATTCTACCTCATCACGGCCCTTTGTCTCTGCTACC 60
 QY 171 SerGlnAlaGlnAlaGlyTyrLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
 Db 61 TCTCAGGCCCCAGCTGGATGGCTGCACATGATTATGGCCACCTCTCTGTCTACAGAAA 120
 QY 191 ProLysTyrAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerIle 210
 Db 121 CCCAAGTGGAAACCAACCTTGTCCACAAATTCGTCAATGGCCACTTAAAGGGTGCCTCTGCC 180
 QY 211 AsnTyrTyrAsnHisArgHisPheGlnHisAlaLysProAsnIlePheHisLysAsp 230
 Db 181 AACTGTGGATCATCGCCACTTCCAGCACCCAGCCAGCCCTAAATCTTCCACAGGAT 240
 QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTyrGlnProlleuTyrGly 250
 Db 241 CCCGATGTGAACATGCTGCACGTGTTTCTGGGCGAATGGCAGCCCATGAGTACGGC 300
 QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
 Db 301 AAGAAGAGCTGAATACCTGCTTACATACACAGCAGCATCATCATCATCATCATCATCAT 360
 QY 271 ProProlleuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
 Db 361 CCGCCCGCTGCTCATCCCATGATTTCAGTACAGATCATCATCATCATCATCATCATCAT 420
 QY 291 LysAsnTyrValAspLeuAlaTyrAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
 Db 421 AAGAACTGGTGGACCTGGCCCTGGGCGCTCAGCTACTACATCCGCTTCTTCATCACCTAC 480
 QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
 Db 481 ATCCCTTTTACGGCATCTCTGGAGCCCTCTCTTTCCTCAACTTCATCAGGTTCCTGGAG 540
 QY 331 SerHisTyrPheValTyrValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
 Db 541 AGCCACTGGTTTGTGTGGTGCACACAGATGAATCATCATCATCATCATCATCATCATCAT 600
 QY 351 AlaTyrArgAspTyrPheSerGlnLeuThrAlaThrCysAsnValGlnSerPhe 370
 Db 601 GCTTACGTCGTCAGTGTTCAGTACGTCAGTACGTCAGTACGTCAGTACGTCAGTACGTC 660
 QY 371 PheAsnAspTyrPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThr 390
 Db 661 TTCAACGACTGGTTTCACTGAGTACACCTTAATCTCCAGATTGACACCACTCTCTCCACC 720
 QY 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410
 Db 721 ATGCCCCGGCACAACTTACACAGATCGCCCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 780
 QY 411 GlyIleGluTyrGlnGluLysProLeuLeuAlaLeuLeuAspIleIleArgSerLeu 430
 Db 781 GGCATTGAATACCAAGGAGAGCCGCTTACTGAGGGCCCTGTGTGACATCATCAGGTCCCTG 840
 QY 431 LysLysSerGlyLysLeuTyrLeuAspAlaTyrLeuHisLys 444
 Db 841 AAGAAGTCTGGGAAGCTGTGCTGGAGCCCTACCTTCACAAA 882

RESULT 27

ABS76712

ID ABS76712 standard; cDNA; 1843 BP.

XX AC ABS76712;

XX XX

XX DT 12-DEC-2002 (first entry)

XX DE Human desaturase cDNA contig 2535.

XX XX

XX KW Human; ss; delta5 desaturase; polyunsaturated fatty acid;

XX KW PUFAs; nutritional; animal feed; cosmetic; skin aging; burn; angioplasty;

XX KW inflammation; rheumatoid arthritis; asthma; psoriasis; osteoporosis;

XX KW kidney stone; urinary tract stone; cancer; cachexia; diabetes; eczema;

XX KW AIDS; multiple sclerosis; blood pressure; platelet aggregation;

vasodilation; cholesterol; proliferation of fibrous tissue;
 endometriosis; myalgic encephalomyelitis; human breast milk;
 dietary supplement; Chromosome 11q12.

Homo sapiens.

US6428990-B1.

06-AUG-2002.

12-NOV-1999; 99US-0439261.

11-APR-1997; 97US-0833610.

10-APR-1998; 98WO-US07422.

08-JAN-1999; 99US-0227613.

(ABBO) ABBOTT LAB.

Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;

WPI; 2002-730518/79.

Producing a polyunsaturated fatty acid (PUFA), useful in dietary
 supplements and in treating diseases e.g., cancer, comprises expressing
 human delta 5-desaturase enzyme and exposing enzyme to substrate PUFA
 to convert to product PUFA -

Example 1; Fig 7; 104pp; English.

The invention relates to producing (M1) a polyunsaturated fatty acid
 (PUFA), comprising: (i) isolating a fully defined human delta5-desaturase
 gene sequence (I); (ii) constructing a vector comprising (I);
 (iii) introducing the vector into a host cell for expression of the
 human delta5-desaturase enzyme (II); and (iv) exposing (II) to a
 substrate PUFA (III) such that it is converted to a product PUFA (IV).
 The method is useful for producing a polyunsaturated fatty acid
 such as arachidonic acid (AA), eicosapentaenoic acid (EPA), adrenic
 acid, (n-3)-docosapentaenoic acid, (n-6)-docosapentaenoic acid and/or
 docosahexaenoic (DHA) acid. The PUFAs produced by the method, such
 as arachidonic acid (AA), eicosapentaenoic acid (EPA) and/or
 docosahexaenoic (DHA) acid, are useful for replicating the PUFA content
 of human breast milk or to alter the presence of PUFAs normally found
 in a non-human mammal's milk. PUFAs produced by (M1) may be added to a
 dietary substitute or supplement, particularly an infant formula, for
 patients undergoing intravenous feeding or for preventing or treating
 malnutrition or other conditions or disease states. The PUFAs are
 useful for producing nutritional compositions e.g., any food or
 preparation for human consumption including for enteral or parenteral
 consumption, which when taken into the body serve to nourish or build
 up tissues or supply energy and/or maintain, restore or support
 adequate nutritional status or metabolic function. The PUFAs are also
 useful in animal feed supplements to alter an animal tissue or milk
 fatty acid composition to one or more desirable for human or animal
 consumption, in animal feed substitutes, animal vitamins or in animal
 topical ointments. The PUFAs produced by this method are useful in
 producing pharmaceutical compositions for treating rough or aging skin,
 injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,
 asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,
 cachexia associated with cancer, diabetes, eczema, AIDS, multiple
 sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting
 platelet aggregation, inducing vasodilation, reducing cholesterol
 levels, inhibiting proliferation of fibrous tissue, treating
 endometriosis, and myalgic encephalomyelitis. The gene for delta5
 desaturase is located on chromosome 11q12. The present sequence
 is a partial cDNA for a human delta5 desaturase.

SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Alignment Scores:

Pred. No.: 3,466-171 Length: 1843
 Score: 1646.00 Matches: 294
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 67.51% Indels: 0
 DB: 24 Gaps: 0
 US-09-719-601-5 (1-444) x ABS76712 (1-1843)

QY 151 ValPheTyrPheGlyAsnGlyTrrPleProThrLeuIleThrAlaPheValLeuAlaThr 170
 DB 1 GTCTTTTACTTTGGCAATGGCTGGATTCTACCCCTCATCAAGGCTTTCTCTGTGTTACC 60
 QY 171 SerGlnAlaGlnAlaGlyTrrPleGlnHisAspTyrGlyHisLeuSerValTrrArgLys 190
 DB 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTCTACAGAAA 120
 QY 191 ProLysTrrPheAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
 DB 121 CCCAAGTGGAAACCACTCTCTCCACAAATTCGTTCATTCGTCCTTAAAGGCTGCTCTGCC 180
 QY 211 AsnTrrPheAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
 DB 181 AACTGGTGGATCATCGCCACTTCCAGCACCAAGCCAGCCTAACATCTTCCACAGGAT 240
 QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrrPleGlnProIleGluTrrGly 250
 DB 241 CCGGATGTGAACATGTCTGCACTGTGTTCTTGGGCAATGGCAGCCCATCGAGTACGGC 300
 QY 251 LysLysLysLeuLysTrrPheProTyrAsnHisGlnHisGluTrrPhePheLeuLeuGly 270
 DB 301 AAGAGAAGCTGAATACCTGCCCTACATCAATCACCAGCACGAATACTTCTTCTGATTGGG 360
 QY 271 ProProLeuLeuLeuProMetTrrPheGlnTrrGlnIleLeuMetThrMetIleValHis 290
 DB 361 CCGCCCTGCTCATCCCAATGATTTCCAGTACCAGATCATCATCACCATGATGTCCTAT 420
 QY 291 LysAsnTrrValAspLeuAlaTrrPheValSerTrrTrrIleArgPhePheLeuTrrTyr 310
 DB 421 AAGAACTGGTGGACCTGGCTGGGCGGTGAGTACTATCATCGGTTCTTCATCACCTAC 480
 QY 311 IleProPheTrrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
 DB 481 ATCCCTTTCTAGGCACTCTGGAGCCCTCTTCTTCTCACTTCACTCAGGTTCTCTGGAG 540
 QY 331 SerHisTrrPheValTrrPheValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
 DB 541 AGCCACTGGTTTGTGGGTGTCACACAGATGATCATCATGTCATGGAGATTGACCAGGAG 600
 QY 351 AlaTrrArgAspTrrPheSerSerGlnLeuThrAlaThrCysAsnValGluIleSerPhe 370
 DB 601 GCTATCCGTGACTGGTTCAGTACCCAGCTGACAGCCACCTGCAACGTGGAGAGTCTTTC 660
 QY 371 PheAsnAspTrrPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThr 390
 DB 661 TTCAACGACTGGTTCAGTGGACACCTTAATTCAGATTGAGCACCACCTCTTCCCCACC 720
 QY 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410
 DB 721 ATGCCCGGCAACAATTCACAAAGATGCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 780
 QY 411 GlyIleGluTrrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430
 DB 781 GGCATTGAATCAACGAGGAAGCGCTACTGAGGGGCCCTGCTGACATCATCATAGTCTCTG 840
 QY 431 LysLysSerGlyLysLeuTrrPheAspAlaTrrLeuHisLys 444
 DB 841 AAGAAGTCTGGGAAGGTGTGGCTGGAGCGCTACCTTACAAA 882

RESULT 28

AAF21845

ID AAF21845 standard; DNA; 1474 BP.

XX

AC AAF21845;

XX

DT 27-MAR-2001 (first entry)

XX

DE CDNA encoding human delta 6 desaturase D6DH-1, Incyte 2451043.

XX Human; ss; gene; D6DH-1; delta 6 desaturase-1; fatty acid desaturase; cardiovascular disease; angina pectoris; atheroma embolism; hypertension; atherosclerosis; arteriosclerosis; cardiac ischaemia; hyperlipidaemia; hypercholesterolaemia; hypertriglyceridaemia; gangrene; decubitus ulcer; mesenteric ischaemia; renal artery stenosis; stroke; nephrosclerosis; aging; Alzheimer's disease; angioimmunoblastic lymphadenopathy; anorexia; basal cell carcinoma; cardiac amyloidosis; cerebral amyloidosis; goiter; chronic lymphatic leukaemia; degenerative osteoarthritis; delirium; dementia; depression; dyskinesia; diabetic hyperosmolar nonketotic coma; glaucoma; hypercholesterolaemia; hypothermia; metabolic bone disease; osteoporosis; normal pressure hydrocephalus; diabetes; Reye's syndrome; Parkinson's disease; polymyalgia; rheumatism; prostatic carcinoma; renal amyloidosis; tuberculosis; urinary incontinence; galactosaemia; fatty acid metabolism disorder; Addison's disease; cystic fibrosis; fatty hepatocirrhosis; hyperadrenalemia; hypoadrenalemia; hyperlipaemia; hyperparathyroidism; hypoparathyroidism; lipid myopathy; obesity; lipodystrophy; phenylketonuria; cancer; Incyte 2451043.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 75..1412

FT /*tag= a

FT /*product= "D6DH-1"

XX US6492108-B1.

XX 10-DEC-2002.

XX 26-MAR-1998; 98US-0048888.

XX 26-MAR-1998; 98US-0048888.

XX (INCY-) INCYTE GENOMICS INC.

XX Hillman JL, Guegler KJ, Corley NC, Shan P;

XX WPI; 2003-327308/31.

XX P-PSDS; ABU08788.

XX New isolated polynucleotide encoding polypeptide having delta-6 desaturase activity for use in diagnosis, treatment and prevention of cardiovascular diseases, disorders of aging, disorders of fatty acid metabolism, and cancer -

XX Claim 3; Column 41-44; 39pp; English.

XX The invention relates to an isolated polynucleotide encoding a polypeptide comprising an amino acid sequence given in the specification.

XX The polypeptide has fatty acid desaturase activity or delta-6 desaturase activity. For use in the diagnosis, treatment and prevention of cardiovascular diseases (e.g. angina pectoris, atheroma embolism, atherosclerosis, arteriosclerosis, cardiac ischaemia, hypertension, hypercholesterolaemia, hyperlipidaemia, hypertriglyceridaemia, gangrene, mesenteric ischaemia, renal artery stenosis, stroke, nephrosclerosis), disorders of aging (e.g. Alzheimer's disease, angioimmunoblastic lymphadenopathy, anorexia, basal cell carcinoma, cardiac or cerebral amyloidosis, chronic lymphatic leukaemia, decubitus ulcers, degenerative osteoarthritis, delirium, dementia, depression, diabetes, dyskinesia, diabetic hyperosmolar nonketotic coma, glaucoma, hypercholesterolaemia, hypothermia, metabolic bone disease including osteoporosis, normal pressure hydrocephalus, Parkinson's disease, Reye's syndrome, polymyalgia, rheumatism, prostatic carcinoma, renal amyloidosis, tuberculous, urinary incontinence), disorders of fatty acid metabolism (e.g. Addison's disease, cystic fibrosis, fatty hepatocirrhosis, galactosaemia, goiter, hyperadrenalemia, hypoadrenalemia, obesity, hyperparathyroidism, hypoparathyroidism, hyperlipaemia, lipid myopathies, lipodystrophies, phenylketonuria) and cancer. The present sequence represents the cDNA encoding human delta 6 desaturase-1, D6DH-1, Incyte 2451043.

SQ Sequence 1717 BP; 330 A; 563 C; 482 G; 342 T; 0 other;

Alignment Scores:

Pred. No.: 8,528-162 Length: 1717

Score: 1560.50 Matches: 278

Percent Similarity: 76.23% Conservative: 62

Best Local Similarity: 62.33% Mismatches: 103

Query Match: 64.01% Indels: 3

DB: 25 Gaps: 2

US-09-719-601-5 (1-444) x ABX93651 (1-1717)

Qy 1 MetGlyLysGlyGlyAsnGlnGly-----GluGlyAlaAlaGluArgGluValSerVal 18

Db 75 ATGGGGGGGGTGGGGAGGCGGGACCGCGGGAGGAGCCCGCGGGGGGACCGCTG 134

Qy 19 ProThrPheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuVal 38

Db 135 CCACCTTTCTGCTGGAGGAGGATCCCGCGGCGACGACCGCGGGGACAGTGGCTGTC 194

Qy 39 IleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArg 58

Db 195 ATCGAGCGCGGTCTACGACATCAGCGCTGGGACAGCGGCACCCAGGGGGGACGCGC 254

Qy 59 ValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78

Db 255 CTCATCGGCCACCCAGCGGCTGAGGACGACGATGCCCTTCGTGCTTCATCAAGAT 314

Qy 79 LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGlyLeuAlaProGluGlu 98

Db 315 CTCAAATTTTGTGGCAAGTTCTTACAGCCCTGTTGATTGGAGAGCTGGCTCGGAAGAA 374

Qy 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118

Db 375 CCAGAGCAGGATGAGACCCCTGAATGGCAGCTGTCGAGACTTCGAGCCCTTGACACAG 434

Qy 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla 138

Db 435 GCAGCGAGGACATGAAGCTGTTGATGCGAGTCCACCTTCTTCTTCTTCTTCTGCGC 494

Qy 139 HisIleIleAlaLeuGluSerIleAlaThrPheThrValPheTyrPheGlyAsnGlyTrp 158

Db 495 CATCTCTGCGCATGGAGGTGCTGGCTGCTCTTATCTTCTCTCTCTCTCTCTCTCTCTG 554

Qy 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178

Db 555 GTGCCAGTCCCTGGCGGCTTCTATCTCTGCGCATCTCTCAGGCTCAGTCTGCTGCTG 614

Qy 179 GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis 198

Db 615 CAGCATACCTTGGGCCATGCTCCATCTTCAAGAGTCTCTGGTGGAAACACGCTGGCCAG 674

Qy 199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218

Db 675 AAGTTCGTGATGGGGCAGCTTAAGGGCTTCTCGCCCATCTGGTGGAACTTCGCCCACTT 734

Qy 219 GlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238

Db 735 CAGCACCAAGCCCAAGCCCAATCTTCCAAAGACCCAGACGTGAGCGGCGCGCTC 794

Qy 239 PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLys 258

Db 795 TTCCTCTCTGGGGAG---TCATCCGTCGATGATGGCAGAGAGAAACGACATACCTACCC 851

Qy 259 TyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyr 278

Db 852 TACAACCAAGCAGCACCTGTACTTCTTCTGATGGCGCGCGCTGCTCACCTGGTGAAC 911

Qy 279 PheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298

Db 912 TTGAAGTGGAAATCTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 971

Qy 299 AlaValSerTyrTyrIleArgPheIleThrTyrIleProPheTyrGlyIleLeuGly 318

```

Db 972 GCGCCAGCTCTATGCCGGTCTTCTATCTACCTCCCTCTACGGGTCCTGGG 1031
Qy 319 AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThr 338
Db 1032 GTGCTGCTCTCTCTTTGTTGCTGCTAGGCTCTGGAAGCCACTGCTGCTGTCGATCACA 1091
Qy 339 GlnMetAsnHisIleValMetGluIleAspGlnGluIleAlaTrpArgAspTrpPheSer 358
Db 1092 CAGATGACCACTCCCAAGAGATCGCCACGAGAGACCGGAGCTGGGTGAGTCTCT 1151
Qy 359 GlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHis 378
Db 1152 CAGCTGGCAGCCACTGCAACGTGAGCCCTCACTTTTCCACCACTGCTTCAGCGGCAC 1211
Qy 379 LeuAsnPheGlnIleGluHisIleLeuPheProThrMetProArgHisAsnLeuHisLys 398
Db 1212 CTCACCTTCCAGATCAGACCACTCTTCCCGAGATGCCGAGACACATCAGCCGG 1271
Qy 399 IleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTrpGlnGluLysPro 418
Db 1272 GTGGCCCGCTGCTCAAGTGGCTGTGTGCGCAAGCACGCGCTCAGCTACGAAGTGAAGGCC 1331
Qy 419 LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGlyLysLeuTrpLeu 438
Db 1332 TTCTCTCACCGCGCTGGTGACATCGTCAAGTCCCTGGAAGAGTCTGGTGACATCTGGCTG 1391
Qy 439 AspAlaTrpLeuHisLys 444
Db 1392 GAGCGCTACCTCCATCAG 1409

```

RESULT 31

AAA90954

ID AAA90954 standard; cDNA; 1757 BP.

XX

AC AAA90954;

XX

DT 15-JAN-2001 (first entry)

XX

DE Human fatty acid desaturase 3 coding sequence.

XX

KW Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;

XX

KW liver disease; coronary artery disease; cancer; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

XX

CDS 134..1471

XX

FT /*tag= a

XX

FT /product= FADS-3

XX

XX EP1035207-AL.

XX

XX 13-SEP-2000.

XX

XX 09-MAR-1999; 99EP-0104664.

XX

XX 09-MAR-1999; 99EP-0104664.

XX

XX (MULT-) MULTIGENE BIOTECH GMBH.

XX

XX Weber BHF, Marquardt A;

XX

XX WPI; 2000-559875/52.

XX

XX P-PSDB; AAY97540.

XX

XX Novel cDNA molecules encoding three human fatty acid desaturases,

XX

XX FADS1, FADS2 and FADS3, useful in the treatment of liver disease,

XX

XX coronary artery disease and cancer -

XX

XX Claim 2; Page 38-39; 72pp; English.

XX

XX This sequence encodes the human fatty acid desaturase, FADS-3, of the

CC invention. An antibody directed against the 3 FADS molecule of the
 CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or
 CC therapeutic purposes. The FADS coding sequences are useful in gene
 CC therapy. The polypeptide and antibodies are useful in screening for
 CC modulating drugs. The polypeptides are also useful for treating liver
 CC disease, coronary artery disease and cancer.
 CC Note: Two copies of the sequence listing are present within this
 CC patent, which contain different sequences. AAA90952 and AAA90955 are
 CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are
 CC stated as being SEQ ID's 7-22.

XX

SQ Sequence 1757 BP; 318 A; 580 C; 517 G; 342 T; 0 other;

Alignment Scores:

Pred. No.:	8-82e-162	Length:	1757
Score:	1560.50	Matches:	278
Percent Similarity:	76.23%	Conservative:	62
Best Local Similarity:	62.33%	Mismatches:	103
Query Match:	64.01%	Indels:	3
DB:	21	Gaps:	2

US-09-719-601-5 (1-444) x AAA90954 (1-1757)

Qy 1 MetGlyLysGlyGlyAsnGlnGly-----GluGlyAlaAlaGluArgGluValSerVal 18

Db 134 ATGGCGGGCGTCTGGGAGCGGGACCCGGGAGGAGACCCCGCAGCGCGGGGCGACCGCTG 193

Qy 19 ProThrPheSerTrpGlnGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuVal 38

Db 194 CCCACCTTCTGCTGGGAGCAGATCCCGCGCGCAGCACCGCCCGCGGCGACAAAGTGGCTGTC 253

Qy 39 IleAspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArg 58

Db 254 ATCGAGCGCGCGTCTACGACATCAGCCCTGGGCGACGCGCAGCCAGCCAGCGGGGCGAGCCGC 313

Qy 59 ValIleGlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78

Db 314 CTCATCGGCACACCGCGCTGAGGAGCGCCAGGATGCTTCGTCGCTTCCATCAAGAT 373

Qy 79 LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGlu 98

Db 374 CTCAAATTTTGGCGCAAGTTCTTACAGCCCTGTTGATTGGAGAGCTGCTCCGGGAAGAA 433

Qy 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118

Db 434 CCCAGCGAGATGACCCCTGATGCGAGCTGTCGAGACTTCGAGCCCTCGACCCAG 493

Qy 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla 138

Db 494 GCAGCGGAGACATGAAGCTGTTGATGCGAGTCCACCTTCTTCTTCTTCTTCTTCTTCTTCT 553

Qy 139 HisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTrpPheGlyAsnGlyTrp 158

Db 554 CACATCTGGCCATGAGGAGTGGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 613

Qy 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178

Db 614 GTGCCAGTCCCTGGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 673

Qy 179 GlnHisAspTrpGlyHisLeuSerValTrpArgLysProLysTrpAsnHisLeuValHis 198

Db 674 CAGCATGACCTGGGCCATGCTCCATCTTCAAGAGTCTCTGGTGGAAACACACGCGGCCAG 733

Qy 199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218

Db 734 AAGTTCGTGATGGGCGAGCTAAAGGCTTCTCCGCCCTTCTGGTGGAACTTCGCCCACTTC 793

Qy 219 GlnHisIleAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238

Db 794 CAGCACCGCCCAAGCCCACTTCTTCCAAAGACCCAGACGTGACGTGGCGGCCGCTC 853

Qy 239 PheValLeuGlyGluTrpGlnProIleGluTrpGlyLysLysLeuLysTrpLeuPro 258


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QY 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118
DB 1337 CCACGACGAGGATGACCCCTGAAATGCGAGCTGGTCGAGGACTTCGAGCCCTCGACACG 1278
QY 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla 138
DB 1277 GCAGCCGAGGACATGAAGCTGTTGATGCCAGTCCACCTTCCTTTCCTTACTGGGC 1218
QY 139 HisIleLeuAlaLeuGluSerIleAlaTrpPheThrValPheGlyAsnGlyTrp 158
DB 1217 CACATCTGGGCATGAGGCTGGCTGGCTCTTATCTACCTCTCGGCTCTGGCTGGCTGG 1158
QY 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178
DB 1157 GTGCCAGTGGCCCTGGCCCTTCATCTCTGCCATCTCTCAGGCTCAGTCTGGTGTCTG 1098
QY 179 GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis 198
DB 1097 CAGCATGACCTGGGCCATGCCCTCCATCTTCAAGAAGATCCTGGTGGAAACACGCTGGCCAG 1038
QY 199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218
DB 1037 AAGTTCGTGATGGGGAGCTTAAAGGCTTCTCCGCCACCTGGTGGAACTTCGCCACCTTC 978
QY 219 GlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238
DB 977 CAGCACCAAGCCAAAGCCCAACATCTTCACAAAGACCCAGACGTCGAGCGTGGCGCCGTC 918
QY 239 PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuPro 258
DB 917 TTCCTCTCTGGGGAG---TCATCGCTGAGTATGGCAAGAAAGAAACCCAGATACCTACCC 861
QY 259 TyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyr 278
DB 860 TACACCAAGCAGCACCTGCTACTTCTCTGATCGCGCGCGCTGCTCACCTGGTGAAC 801
QY 279 PheGlnTyrGlnIleLeuMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298
DB 800 TTTGAATGGAAATCTGGCGTACATGCTGTCATGTCGATGCGAGTGGCGGATTTGCTCTGG 741
QY 299 AlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGly 318
DB 740 GCGGCCGCTCTATGCGCGCTTCTTCTATCTCTACCTCCCTCTACGCGCTCCCTGGG 681
QY 319 AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThr 338
DB 680 GTGCTGCTCTTCTTGTCTGTCTGAGGCTCCTGGAAGCCCACTGCTGCTGTGATCACA 621
QY 339 GlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSer 358
DB 620 CAGATGAACCAATCCCAAGAGATCGCCACAGAGACACCGGACTGGTGGTCAGTCT 561
QY 359 GlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHis 378
DB 560 CAGCTGGCAGCACCTGCAAGCTGGAGCCCTCACTTTTACCAACTGCTTTCAGCGGCAC 501
QY 379 LeuAsnPheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLys 398
DB 500 CTCACCTTCCAGATCGACACCATCTTCCCGAGGATCGCGAGACACAACTACAGCCGG 441
QY 399 IleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysPro 418
DB 440 GTGGCCCGCTGGTCAAGTCGTGTGTCGAAGCAGCGCCCTCAGCTACGAAGTGAAGCC 381
QY 419 LeuLeuArgAlaLeuLeuAspIleLeuArgSerLeuLysSerGlyLysLeuTrpLeu 438
DB 380 TTCTTCACCGCGCTGTGGACATCGTCAAGTCCCTGGAAGAGTCTGGTGACATCTGGCTG 321
QY 439 AspAlaTyrLeuHisLys 444
DB 320 GACGCTTACCTCCATCAG 303
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RESULT 33

```
ABK35347/c
ID ABK35347 standard; cDNA; 1972 BP.
XX AC ABK35347;
XX DT 08-MAY-2002 (first entry)
XX DE Human cDNA encoding secreted protein #485.
XX KW Human; secreted protein; gene; ss; nutritional supplement; haemophilia;
XX KW viral infection; bacterial infection; fungal infection; diabetes; asthma;
XX KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour;
XX KW autoimmune thyroiditis; allergic reaction; neurodegenerative disease;
XX KW Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer;
XX KW coagulation disorder; inflammatory disorder; Crohn's disease; incision;
XX KW tissue regeneration; wound healing; burn; haematopoiesis;
XX KW myeloid cell deficiency; lymphoid cell deficiency.
XX OS Homo sapiens.
XX PN WO200177288-A2.
XX PD 18-OCT-2001.
XX PF 29-MAR-2001; 2001WO-US10224.
XX PR 06-APR-2000; 2000US-195582P.
XX PA (GEMY ) GENETICS INST INC.
XX PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
XX PI Gulukota K, Graham JR;
XX DR WPI; 2002-179321/23.
XX PT Five hundred and ninety two polynucleotides derived from a variety of
XX PT human tissue sources which encode secreted proteins, useful for
XX PT treating immune deficiencies and disorders such as autoimmune disorders
XX PS Claim 1; Page 321-322; 372pp; English.
XX CC The invention relates to 592 polynucleotides which have been derived from
XX CC a variety of human tissue sources and which encode novel secreted
XX CC proteins. The polynucleotides can be used as probes for the
XX CC identification and isolation of full length cDNA and genomic DNA. The
XX CC polynucleotides and proteins can also be used as nutritional supplements.
XX CC The proteins are useful in the treatment of various immune deficiencies
XX CC and disorders such as viral infections, bacterial infections, fungal
XX CC infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple
XX CC sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions
XX CC and conditions (e.g. asthma). They are also useful for treating
XX CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
XX CC disease), liver fibrosis, coagulation disorders (e.g. haemophilia),
XX CC inflammatory disorders (e.g. Crohn's disease) and tumours. They are also
XX CC useful for tissue regeneration, for wound healing and in the treatment of
XX CC burns, incisions and ulcers. The proteins are also useful for regulating
XX CC haematopoiesis and for treating myeloid or lymphoid cell deficiencies.
XX CC Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
XX SQ Sequence 1972 BP; 428 A; 523 C; 556 G; 465 T; 0 other;
Alignment Scores:
Pred. No.: 8,57e-157 Length: 1972
Score: 1516.00 Matches: 272
Percent Similarity: 76.08% Conservatives: 62
Best Local Similarity: 61.96% Mismatches: 99
Query Match: 62.18% Indels: 6
DB: 24 Gaps: 3
US-09-719-601-5 (1-444) x ABK35347 (1-1972)
QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluLeuGln 27
```

1864 GCGCGGACGACCGCGCTCAGGACCTACCGCGCTACTTCCCTGGACGAGTGCC 1805
 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValAsnIleThr 47
 1804 CAGCGCTCAGGCTGCGAGGCGGTGGCTAGTATGATGACCGTAAGTGTGTACAAATCAGC 1745
 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTrpAlaGlyCysAsp 67
 1744 GAGTTTCCCGCGCGGCTCAGGCGGCTCCCGGGTATCAGCCATCAGCCCGGCGGAT 1685
 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
 1684 GCCACGGATCCCTTTGTGGCTTCCACATCAACAGGGGCTTGTGAAGAAGTATATGAAC 1625
 88 ProLeuLeuIleGlyLeuLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
 1624 TCTCTCTGATGGAGAACTGCTCCAGAGACCGCCAGCTTTGAGCCCAACCAAGATAAA 1565
 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
 1564 GACCTGACAGATGAGTTCGGGAGCTCGCGCCACAGATGGAGGCTCATGAAG 1505
 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
 1504 GCCAACCATGCTTCTCTGCTGTATCTGCTGCTGACATCTTGTGCTGATGGTGAGCC 1445
 148 TrpPheThrValPheTyrrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
 1444 TGCTCACCTTTGGGTCTTTGGAGCTCTTTTTCCTCTCTCTCTCTCTCTCTCTCTCT 1385
 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrrGlyHisLeuSerVal 187
 1384 CTCAGTCAGTTCAGGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1325
 188 TyArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
 1324 TTGACACCTCAAGTGAACCATCTGCTACATCATTTTGTGATGGCCACCTGAGGG 1265
 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePhe 227
 1264 GCGCCCGCCAGTGTGGTGAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1205
 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
 1204 CGCAAGACCCAGACATCAACATG---CATCCCTCTCTCTCTCTCTCTCTCTCTCTCT 1148
 246 ProIleGluTyrrGlyLysLysLysLeuLysTyrrLeuProTyrrAsnHisGlnHisGluTyrr 265
 1147 TCTGTGAGCTTGGGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1088
 266 PhePheLeuIleGlyProProLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 285
 1087 TTTCTCTAAATGGGCGCCCGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1028
 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrrIleArg 305
 1027 TTTCTTATCCAGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 968
 306 PhePheLeuThrTyrrIleProPheTyrrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
 967 TTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 908
 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
 907 GTGAGTTCCTGGGAAAGCAACTGTTGTGGGTGACACAGATGACCAATATTCCTCATG 848
 346 GluIleAspGlnGluAlaTyrrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
 847 CACATTGATCATGACCGGACATGAGTGGGTTCACCCAGCTTCCAGGCGCACATGCAAT 788
 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385

787 GTCCACAAAGTCTGCCTTCAATGACTGGTTTCACTGAGGACCTCAACTTCCAGATTGAGCAC 728
 386 HisLeuPheProThrMetProArgHisAsnLeuHisIleAlaProLeuValLysSer 405
 727 CATCTTTTCCCAAGATGCTGACACAAATTACCAAAAGTGGCTCCCTGTGGTCACTCC 568
 406 LeuCysAlaLysHisGlyIleGluTyrrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
 667 TTGTGTGCCAAGCATGGCATAGTAGTACCAGTCCAGCCCTGCTGTGAGCCTTCGCGCAC 608
 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrrLeuHisLys 444
 607 ATCATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGTAGATGCCATCTTCTACCAA 551

RESULT 34
 AAA90955
 ID AAA90955 standard; cDNA; 4203 BP.
 XX
 AC AAA90955;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Human fatty acid desaturase 1 coding sequence.
 XX
 KW Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;
 KW liver disease; coronary artery disease; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1035207-A1.
 XX
 PD 13-SEP-2000.
 XX
 PF 09-MAR-1999; 99EP-0104664.
 XX
 PR 09-MAR-1999; 99EP-0104664.
 XX
 PA (MULT-) MULTIGENE BIOTECH GMBH.
 XX
 PI Weber BHF, Marquardt A;
 XX
 DR WPI; 2000-559875/52.
 XX
 PT Novel cDNA molecules encoding three human fatty acid desaturases,
 PT FADS1, FADS2 and FADS3, useful in the treatment of liver disease,
 PT coronary artery disease and cancer -
 XX
 PS Claim 2; Page 12-15; 72pp; English.
 CC
 CC This sequence encodes the human fatty acid desaturase, FADS1, of the
 CC invention. An antibody directed against the 3 FADS molecule of the
 CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or
 CC therapeutic purposes. The FADS coding sequences are useful in gene
 CC therapy. The polypeptide and antibodies are useful in screening for
 CC modulating drugs. The polypeptides are also useful for treating liver
 CC disease, coronary artery disease and cancer.
 CC Note: Two copies of the sequence listing are present within this
 CC patent, which contain different sequences. AAA90952 and AAA90955 are
 CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are
 CC stated as being SEQ ID's 7-22.
 XX
 SQ Sequence 4203 BP; 1138 A; 1025 C; 1003 G; 1037 T; 0 other;

Alignment Scores:
 Pred. No.: 2,67e-156 Length: 4203
 Score: 1516.00 Matches: 272
 Percent Similarity: 76.08% Conservative: 62
 Best Local Similarity: 61.96% Mismatches: 99
 Query Match: 62.18% Indels: 6
 DB: 21 Gaps: 3

US-09-719-601-5 (1-444) x AAA90955 (1-4203)

QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluIleGln 27
 Db 97 GCGCGGAGACCGCGGCTCAGGAGACTACCCCGCGCTACTTCACCTGGAGAGAGTGGCC 156
 QY 28 LysHisAsnLeuArgThrSerGlyLeuValIleAspArgLysValTyrAsnIleThr 47
 Db 157 CAGCGCTCAGGTCGAGGCGGTGGCTAGTGTAGTCGACCGTAAGGTGTACAACATCAGC 216
 QY 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyrAlaGlyGluasp 67
 Db 217 GAGTTACCCCGCGGATCCAGGGGCTCCCGGGTCATCAGCCATCGCCGGCGGAGT 276
 QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
 Db 277 GCCCGGATCCCTTTGTGGCTTCCACATCAACAGGGCTTGTGAAGATATATGAAC 336
 QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
 Db 337 TCTCTCCTGATTGGAGAACTGTCCAGAGACGCCAGCTTTGAGCCGCCCAAGATAAA 396
 QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
 Db 397 GAGCTGACAGATGAGTTCCGGAGCTCGGGCCACAGTCGAGCGATGGGCTCATGAG 456
 QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
 Db 457 GCCAACCAATGCTCTCTCTGCTGTACCTGTGCACATCTGCTGCTGCTGCTGCTG 516
 QY 148 TrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
 Db 517 TGGCTACCCCTTGGGTCTTTGGGAGCTCTTTTGGCTTCTCTCTCTCTCTCTCTCT 576
 QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187
 Db 577 CTCAGTGCAGTTCAGGCCAGGCTGGCTGGCTGCAGCATGACTTTGGGCACCTGTGGTC 636
 QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
 Db 637 TTCAGCACTCAAGTGGGAACCATCTGTACATCATTTTGTGATTGGCCCTTGAAGGG 696
 QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
 Db 697 GCCCGCGCAGTGTGTGAACACACATGCATCTCCAGCACCATGTCGCAAGCCCACTGCTC 756
 QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
 Db 757 CGCAAGAGCCAGACATCAACATG---CATCCCTTCTCTTTGCTTGGGGAAGATCCTC 813
 QY 246 ProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyr 265
 Db 814 TCTGTGAGCTTGGGAACAGAGAAATAATATATGCGGTACACACACAGCACAATAC 873
 QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMet 285
 Db 874 TTCTTCTTAATTTGGGCGCCAGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAT 933
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg 305
 Db 934 TTGTATTATCAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 993
 QY 306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
 Db 994 TTCTTCTCACTATATGTGCCACTATTGGGGCTGAAAGCTTCTCTGGGCTTTTCTTCATA 1053
 QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
 Db 1054 GTCAAGTTCTGGAAGCAACTGTTTGTGTGGTGACACATGAACATATTTCCCATG 1113
 QY 346 GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
 Db 1114 CACATTGATCATGACCGGAACATGGACTGGTGTTCACCCAGCTCCAGGCCACATGCAAT 1173
 QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385

Db 1174 GTCCAGAGTCTCCCTCAATGACTGTTGCTGAGGACACTCACTTCAGATTGAGCAC 1233
 QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
 Db 1234 CATCTTTTCCACGATGCTCGACACAATTACCAAAAGTGGCTCCCTGTGTGAGTCC 1293
 QY 406 LeuCyAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
 Db 1294 TTGTGTCCCAAGCATGCTAGTAGTACCAAGTCCAGCCCTGCTGTACGCTTCGCCGAC 1353
 QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
 Db 1354 ATCATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGTGCCTATCTTACCACAA 1410
 RESULT 35
 AAA90952
 ID AAA90952 standard; cDNA; 4205 BP.
 XX
 AC AAA90952;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Human fatty acid desaturase 1 coding sequence.
 XX
 XX Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;
 KW liver disease; coronary artery disease; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 79..1413
 FT /*tag= a
 FT /product= FADS-1
 XX
 EV EPI035207-A1.
 XX
 PD 13-SEP-2000.
 PF 09-MAR-1999; 99EP-0104664.
 XX
 PR 09-MAR-1999; 99EP-0104664.
 XX
 PA (MULT-) MULTIGENE BIOTECH GMBH.
 XX
 PI Weber BHF, Marquardt A;
 XX
 DR WPI; 2000-559875/52.
 DR P-PSDB; AAY97538.
 XX
 PT Novel cDNA molecules encoding three human fatty acid desaturases,
 FT FADS1, FADS2 and FADS3, useful in the treatment of liver disease,
 XX coronary artery disease and cancer -
 PS Claim 2; Page 34-36; 72pp; English.
 XX
 CC This sequence encodes the human fatty acid desaturase, FADS1, of the
 CC invention. An antibody directed against the 3 FADS molecule of the
 CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or
 CC therapeutic purposes. The FADS coding sequences are useful in gene
 CC therapy. The polypeptide and antibodies are useful in screening for
 CC modulating drugs. The polypeptides are also useful for treating liver
 CC disease, coronary artery disease and cancer.
 CC Note: Two copies of the sequence listing are present within this
 CC patent, which contain different sequences. AAA90952 and AAA90955 are
 CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are
 CC stated as being SEQ ID's 7-22.
 XX
 SQ Sequence 4205 BP; 1139 A; 1025 C; 1003 G; 1037 T; 1 other;
 Alignment Scores:
 Pred. No.: 2,68e-156 Length: 4205
 Score: 1516.00 Matches: 272

Percent Similarity:	76.08%	Conservative:	62
Best Local Similarity:	61.96%	Mismatches:	99
Query Match:	62.18%	Indels:	6
DB:	21	Gaps:	3
US-09-719-601-5 (1-444) x AAA90952 (1-4205)			
QY	11	AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln	27
DB	97	GCAGCGGAGACCGCGGCTACCGGACTACCGCGCTACTTCACCTGGGAGGAGTGCGC	156
QY	28	LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr	47
DB	157	CAGCGCTCAGGTGGCGAGGCGGTGGTGTAGTATGACCGCTAAGCTGTACACATCAGC	216
QY	48	LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp	67
DB	217	GAGTTTCAACCGCGGCTCCAGCGGGCTCCCGGGTCTATCAGCCACTACCGCGGCGAGG	276
QY	68	AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys	87
DB	277	GCACGGATCCCTTGTGGCTTCCACATCAACAGGGCTTGTGAAGATATATGAAC	336
QY	88	ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer	107
DB	337	TCTCTCTGATTGGAGAACTGTCTCCAGAGACCGCCAGCTTTGAGCCCAAGAAATAAA	396
QY	108	LysIleThrGluAspPheArgAlaLeuArgLysTrpAlaGluAspMetAsnLeuPheLys	127
DB	397	GAGTCAGACAGAGTTCGGGAGCTGCGGCCACAGTGGAGCGGATGGGCTCATGAG	456
QY	128	ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla	147
DB	457	GCCACCATGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	516
QY	148	TrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal	167
DB	517	TGCTCACCCTTGGGTCTTGGAGCTCTTTTGGCTCTCTCTCTCTCTCTCTCTCTCTCT	576
QY	168	LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal	187
DB	577	CTCAGTGCAGTTCAGGCCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	636
QY	188	TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly	207
DB	637	TTCAGCACCTCAAAAGTGAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	696
QY	208	AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe	227
DB	697	GCCCCCGCCAGTGGTGGACCAACATGCTTCCAGCACCATGCTGCAAGCCCACTGCTTC	756
QY	228	HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln	245
DB	757	CGCAAGACCCAGACATCAACATG---CATCCCTCTCTCTTTCCTTGGGAGATCCTC	813
QY	246	ProIleGluTrpGlyLysLysLysLeuLysLysTrpProTyrAsnHisGlnHisGluTyr	265
DB	814	TCGTGGAGCTTGGGAAACAGAGAAAATATATGCGGTACACCAACCCAGCACAAATAC	873
QY	266	PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleLeuMet	285
DB	874	TTCTTCTCTAAATGGGCCCCCAGCGCTTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCT	933
QY	286	ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTrpIleAspG	305
DB	934	TTTGTATTCAGCGAAGAGAGTGGGTGGATTTGGCTGGATGATTAACCTTCTACGTCCGC	993
QY	306	PhePheIleThrTrpIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe	325
DB	994	TTCTTCTCTCACTTATGTGCCACTATTGGGCTGGAAGCCCTCTCTGGGCTCTTCTCTATA	1053
QY	326	IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet	345

Db	1054	GTGAGGTTCTCGAAAGCAACTGGTTTGTGTGGGTGACACAGATGAACCATATTTCCCATG	1111
QY	346	GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn	365
Db	1114	CACATTGATCATGACCGGAACATGGACTGGTTTCCACCAGCTCCAGGCCACATGCAAT	1173
QY	366	ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis	385
Db	1174	GTCCACAAGTCTCCCTTCAATGACTGGTTCACTGAGTGGACACCTCAACTCCAGATTGAGCAC	1233
QY	386	HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer	405
Db	1234	CATCTTTTCCACAGATGCTCGACAAATACCAAAAGTGGCTCCCTGTGTGAGTCC	1293
QY	406	LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp	425
Db	1294	TTGTGTGCCAAGATGGCATAGTACCAAGTCCAGGCCCTCTGTCACGCTTGGCCGAC	1353
QY	426	IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys	444
Db	1354	ATCATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCCATCTTCACCAA	1410
RESULT 36			
ABX93652			
ID	ABX93652 standard; cDNA; 1928 BP.		
XX			
AC	ABX93652;		
XX			
DT	09-JUN-2003 (first entry)		
XX			
DE	cDNA encoding human delta 6 desaturase D6DH-2, Incyte 2056310.		
XX			
KW	Human; ss; gene; D6DH-2; delta 6 desaturase-2; fatty acid desaturase; cardiovascular disease; angina pectoris; atheroma embolism; hypertension; atherosclerosis; arteriosclerosis; cardiac ischaemia; hyperlipidaemia; hypercholesterolaemia; hypertriglyceridaemia; gangrene; decubitus ulcer; mesenteric ischaemia; renal artery stenosis; stroke; nephrosclerosis; aging; Alzheimer's disease; angioimmunoblastic lymphadenopathy; anorexia; basal cell carcinoma; cardiac amyloidosis; cerebral amyloidosis; goiter; chronic lymphatic leukaemia; degenerative osteoarthritis; delirium; dementia; depression; dyskinesia; diabetic hyperosmolar nonketotic coma; glaucoma; hypercholesterolaemia; hypothermia; metabolic bone disease; osteoporosis; normal pressure hydrocephalus; diabetes; Reye's syndrome; Parkinson's disease; polymyalgia; rheumatism; prostatic carcinoma; renal amyloidosis; tuberculous; urinary incontinence; galactosaemia; fatty acid metabolism disorder; Addison's disease; cystic fibrosis; fatty hepatocirrhosis; hyperadrenalism; hypoadrenalism; hyperlipaemia; hyperparathyroidism; hypoparathyroidism; lipid myopathy; obesity; lipodystrophy; phenylketonuria; cancer; Incyte 2056310.		
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	84..1418		
CDS	/*tag= a		
FT	/product= "D6DH-2"		
XX			
PN	US6492108-B1.		
XX			
PD	10-DEC-2002.		
XX			
PF	26-MAR-1998; 98US-0048888.		
XX			
PR	26-MAR-1998; 98US-0048888.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
XX			
PI	Hillman JL, Guesler KJ, Corley NC, Shah P;		
XX			
DR	WPI; 2003-327308/31.		
DR	P-PSDB; ABU08789.		
XX			
PT	New isolated polynucleotide encoding polypeptide having delta-6		

desaturase activity for use in diagnosis, treatment and prevention of cardiovascular diseases, disorders of aging, disorders of fatty acid metabolism, and cancer -

Claim 1; Column 45-48; 39pp; English.

The invention relates to an isolated polynucleotide encoding a polypeptide comprising an amino acid sequence given in the specification. The polypeptide has fatty acid desaturase activity or delta-6 desaturase activity. For use in the diagnosis, treatment and prevention of cardiovascular diseases (e.g. angina pectoris, atheroma embolism, atherosclerosis, arteriosclerosis, cardiac ischaemia, hypertension, hypercholesterolaemia, hyperlipidaemia, hypertriglyceridaemia, gangrene, mesenteric ischaemia, renal artery stenosis, stroke, nephrosclerosis), disorders of aging (e.g. Alzheimer's disease, angioimmunoblastic lymphadenopathy, anorexia, basal cell carcinoma, cardiac or cerebral amyloidosis, chronic lymphatic leukaemia, decubitus ulcers, degenerative osteoarthritis, delirium, dementia, depression, diabetes, dyskinesia, diabetic hyperosmolar nonketotic coma, glaucoma, hypercholesterolaemia, hypothermia, metabolic bone disease including osteoporosis, normal pressure hydrocephalus, Parkinson's disease, Reye's syndrome, polymyalgia, rheumatism, prostatic carcinoma, renal amyloidosis, tuberculosis, urinary incontinence), disorders of fatty acid metabolism (e.g. Addison's disease, cystic fibrosis, fatty hepatocirrhosis, galactosaemia, goiter, hyperadrenalemia, hypoadrenalemia, obesity, hyperparathyroidism, hypoparathyroidism, hyperlipaemia, lipid myopathies, lipodystrophies, phenylketonuria) and cancer. The present sequence represents the cDNA encoding human delta 6 desaturase-2, D6DH-2, Incyte 2056310.

Sequence 1928 BP; 433 A; 551 C; 520 G; 424 T; 0 other;

Alignment Scores:

Pred. No.:	1.07e-156	Length:	1928
Score:	1515.00	Matches:	272
Percent Similarity:	76.08%	Conservative:	62
Best Local Similarity:	61.96%	Mismatches:	99
Query Match:	62.14%	Indels:	6
DB:	25	Gaps:	3

US-09-719-601-5 (1-444) x ABX93652 (1-1928)

Qy	11	AlaAlaGluArgGluValSerValProthr-----PheSerTrpGluGluIleGln	27
Db	102	GCAGCGAGAGCGCGGCTCAGGACCTACCCGCGCTACTTCACCTGGGAGGAGTGCC	161
Qy	28	LysHisAlaLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr	47
Db	162	CAGCGCTCAGGCTGCGAGGCGGTGGCTAGTGTGACCGTAAAGGTGTACAATCAGC	221
Qy	48	LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp	67
Db	222	GAGTTCACCGCGCGCATCCAGGGGGCTCCGGGTGTCATCAGCCACTACCGCGGCGAGAT	281
Qy	68	AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys	87
Db	282	GCCACGGATCGCTTTGTGGCTTCCATCATCAACAGGCGCTTGTGAAGAGATATATGAC	341
Qy	88	ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer	107
Db	342	TCTCTCCCTGATGGAGAACTGTCTCCAGAGAGCGCCAGCTTTGAGCCCAAGAAATAAA	401
Qy	108	LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys	127
Db	402	GAGCTGACAGATAGTTCGGGAGGTGGCGGCCACAGTGAGCGGATGGGCTCATGAAG	461
Qy	128	ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla	147
Db	462	GCCAAACCATGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	521
Qy	148	TrpPheThrValPheThrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal	167
Db	522	TGGCTCACCTTTGGGTCTTTGGGACGTCCTTTTGGCCCTTCTCTGTCGCTGCTGCTG	581

Qy	168	LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal	187
Db	582	CTCAGTGCAAGTTCAGGCCCGAGCTGGCTGGCTGACGATGACTTTGGGACACTGTCGGTC	641
Qy	188	TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly	207
Db	642	TTCAGCACCTCAAGAGTGAACCATCTGTACATCATTTTGTGATGGCCACCTGAAGGGG	701
Qy	208	AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe	227
Db	702	GCCCCCGCGTGTGGTGAACCATGTCATCTCCAGCACCATGCGGACCCCACTGCTTC	761
Qy	228	HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyTrpGln	245
Db	762	CGCAAGAGCCAGACATCAACATG---CATCCCTTCTCTCTTCTGGGAGATCCTC	818
Qy	246	ProIleGlyTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys	265
Db	819	TCGTGGAGCTTGGGAAACAGAGAAATAATATATATATATATATATATATATATATAT	878
Qy	266	PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMet	285
Db	879	TTCTTCTTAAATTTGGGCCCCAGCCTTGTGCTCTCTACTTCCAGTGGTATATTTCTAT	938
Qy	286	ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTrpIleArg	305
Db	939	TTTGTATATCCAGCAAGAGAGTGGGTGGTGGCTGGATGATGATGATGATGATGATG	998
Qy	306	PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe	325
Db	999	TTCTTCTTCACTTATGTGCCACTATTTGGGCTGAAGCCTTCTTGGGCTTTTCTTCATA	1058
Qy	326	IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet	345
Db	1059	GTGAGTTCCTGGAAAGCAACTGGTTTGTGTGGGTGACACAGATGAACCATATTCCTCATG	1118
Qy	346	GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn	365
Db	1119	CACATTGATCATGACCGGACATGAGTGGTGGTTCACCCAGCTCCAGGCCACATGCAAT	1178
Qy	366	ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis	385
Db	1179	GTCCACAGTCTGCTTCAATGACTGGTTCAGTGAGACCTCAACTTCAGATTGAGCAC	1238
Qy	386	HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer	405
Db	1239	CATCTTTTCCACGATGCTCGACACATATACCAAGTGGTCCCTCTGCTGCTGCTGCTG	1298
Qy	406	LeuCysAlaLysHisGlyIleGlyTrpGlnGluLysProLeuLeuArgAlaLeuLeuAsp	425
Db	1299	TTGTGTGCAAGCATGGCATAGATACCATGTCAGTCCAAAGCCCTGCTGTCAGCCTTCGCGAC	1358
Qy	426	IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys	444
Db	1359	ATCATCCACTACTAAAGAGTTCAGGCGAGCTCTGGTAGATGCCTATCTTCCACCA	1415

RESULT 37

AAK94234
ID AAK94234 standard; cDNA; 2236 BP.

AC AAK94234;

DT 06-NOV-2001 (first entry)

DE Human full-length cDNA, SEQ ID NO: 2826.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.

XX Homo sapiens.

PN BP1130094-A2.

OS Homo sapiens.
 XX EP1074617-A2.
 XX 07-FEB-2001.
 XX 28-JUL-2000; 2000EP-0116126.
 XX 29-JUL-1999; 99JP-0248036.
 XX 27-AUG-1999; 99JP-0300253.
 XX 11-JAN-2000; 2000JP-0118776.
 XX 09-JUN-2000; 2000JP-0183767.
 XX 02-JUN-2000; 2000JP-0241899.
 XX (HELI-) HELIX RES INST.
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 XX full-length cDNAs defined in the specification, and for the detection
 XX and/or diagnosis of the abnormality of the proteins encoded by the
 XX full-length cDNAs -
 XX Claim 8; SEQ ID 14196; 2537pp + CD ROM; English.
 XX The present invention describes primer sets for synthesizing 5602
 XX full-length cDNAs defined in the specification. Where a primer set
 XX comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 XX to the complementary strand of a polynucleotide which comprises one of
 XX the 5602 nucleotide sequences defined in the specification, where the
 XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 XX of an oligonucleotide comprising a sequence complementary to the
 XX complementary strand of a polynucleotide which comprises a 5'-end
 XX sequence and an oligonucleotide comprising a sequence complementary to a
 XX polynucleotide which comprises a 3'-end sequence, where the
 XX oligonucleotide comprises at least 15 nucleotides and the combination of
 XX the 5'-end sequence/3'-end sequence is selected from those defined in
 XX the specification. The primer sets can be used in antisense therapy and
 XX in gene therapy. The primers are useful for synthesizing polynucleotides,
 XX particularly full-length cDNAs. The primers are also useful for the
 XX detection and/or diagnosis of the abnormality of the proteins encoded by
 XX the full-length cDNAs. The primers allow obtaining of the full-length
 XX cDNAs easily without any specialised methods. AAH03186 to AAH13628 and
 XX AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
 XX AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
 XX represent oligonucleotides, all of which are used in the exemplification
 XX of the present invention.
 XX SQ Sequence 1856 BP; 423 A; 517 C; 496 G; 420 T; 0 other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 2,166-156 Length: 1856
 XX Score: 1512.00 Matches: 276
 XX Percent Similarity: 76.07% Conservative: 61
 XX Best Local Similarity: 62.30% Mismatches: 96
 XX Query Match: 62.02% Indels: 10
 XX DB: 22 Gaps: 5
 XX
 XX US-09-719-601-5 (1-444) x AAH15766 (1-1856)
 XX
 XX QY 5 GlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGlu 24
 XX DB 34 GGGACCGGGCTCAGGAGCCTACCCCGGC-----TACTTCACCTGGGAC 78
 XX
 XX QY 25 GluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyr 44
 XX DB 79 GAGGTGGCCCGCCGCTCAGGGTGCAGGCGGTGGTGTAGTCGACCGCTAAGGTGTAC 138
 XX
 XX QY 45 AsnIleThrLysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyrAla 64
 XX DB 1139 AATCATCAGCGAGTTCCACCGCGGCATCCAGGGGGCTCCGGGTTCATCAGCCATCAGCC 198
 XX QY 65 GlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLys 84
 XX DB 199 GGGCAGGATGCCAGGATCCCTTTGTGGCCCTTCCACATCAACAAGGGCTTTGTGAAGAAG 258
 XX QY 85 PheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGly 104
 XX DB 259 TATATGAACCTCTCTCTGATTGGAGAACTGTCTCCAGAGCAGCCAGCTTTGAGCCACCC 318
 XX QY 105 LysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsn 124
 XX DB 319 AAGAATAAAGAGCTGACAGATGAGTTCCGGGAGCTGCGGGCCACAGTGGAGCGGATGGG 378
 XX QY 125 LeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGlu 144
 XX DB 379 CTCATGAAGGCCAACCACTGTCTTCTGTGTACCTGTGTCACATTTTGTGTGTGAT 438
 XX QY 145 SerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThr 164
 XX DB 439 GGTGAGCCTGGCTCACCTTTGGGTCTTTGGAGCTCTTTTGGCTCTCTCTCTCTCTCTCT 498
 XX QY 165 AlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHis 184
 XX DB 499 GCGGTCTCTCAGTGCAGTTCAGGCCAGGCTGGCTGGCTGCAGCATGACTTTTGGGAC 558
 XX QY 185 LeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHis 204
 XX DB 559 CTGTGGTCTTCAGCAGCCTCAAGTGAACCATCTGTACATCATTTTGTGATTGGCCAC 618
 XX QY 205 LeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysPro 224
 XX DB 619 CTGAAGGGGGCCCCCGCAGTGTGGTGAACCAACATGCTTCCAGCACCATGCGCAAGGCC 678
 XX QY 225 AsnIlePheHisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGly 242
 XX DB 679 AACTGCTTCGCGAAGACCCACACATCAACATG---CATCCCTTCTCTTTGCTGGG 735
 XX QY 243 GluTrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGln 262
 XX DB 736 AAGATCTCTCTGTGGAGCTTGGGAAACAGAGAAATAATATATATATATATATATATAT 795
 XX QY 263 HisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGln 282
 XX DB 796 CACAAATATCTTCTCTATATGGGCCCCCAGCCTTGTGCTCTCTCTCTCTCTCTCTCT 855
 XX QY 283 IleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyr 302
 XX DB 856 ATTTTCTATTTGTATCCAGCGAAAGAGTGGGTGGACTTGGCTGGATGATTACCTTC 915
 XX QY 303 TyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPhe 322
 XX DB 916 TAGTCCTGCTTCTCTCTATGTGCCACTATTGGGG---CTGAAGCCCTCTCTGGGC 972
 XX QY 323 LeuAsnPheIle---ArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsn 341
 XX DB 973 CTTTCTCTCATAGTCAGGTCTCTGGAAGCAACTGGTTGTGTGGGTGCACAGATGAAC 1032
 XX QY 342 HisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThr 361
 XX DB 1033 CATATTCCCATGCATGATCATCCGGAACATGGACTGGGTTCACCCAGCTCCAG 1092
 XX QY 362 AlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPhe 381
 XX DB 1093 GCCACATGCAATGTCCACAGTCTGCTTCAATGACTGGTTCAGTGGACACCTCACTTC 1152
 XX QY 382 GlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaPro 401
 XX DB 1153 CAGATTGACACCATCTTTTCCCGAGTGCCTGCACCAATATACCAAAATGGCTCCC 1212
 XX QY 402 LeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArg 421
 XX DB 1213 CTGGTGCAGTCTTGTGTGGCAGCATGGCATAGATAGTACCATGCCAAGCCCTGCTGCA 1272

QY 422 AlaLeuLeuAspIleAArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyr 441
 Db 1273 GCCTCGCGCAGCATCATCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCCTAT 1332
 QY 442 LeuHisLys 444
 Db 1333 CTTACCAA 1341

RESULT 39
 ID AAA49932 standard; cdna; 1335 BP.
 XX AAA49932;
 AC
 XX 10-OCT-2000 (first entry)
 XX
 DE Human delta-5-desaturase cDNA.

XX Delta-5-desaturase; human; polyunsaturated fatty acid;
 KW arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;
 KW docosahexaenoic acid; nutrition; feedstuff; ss.
 XX Homo sapiens.
 XX WO200040705-A2.

PN 13-JUL-2000.
 XX 29-DEC-1999; 99WO-US31163.
 PF 08-JAN-1999; 99US-0227613.
 XX (ABBO) ABBOTT LAB.

XX Mukerji P, Leonard AEV, Huang Y, Parker-Barnes JM;
 DR WPI; 2000-465975/40.
 DR P-PSDB; AAY95445.
 XX New polypeptide useful for preparation of nutritional supplements based
 PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids
 PT at carbon 5 -

XX Claim 1; Fig 12; 127pp; English.
 XX The present sequence is that of cDNA encoding human
 CC delta-5-desaturase (see AAY95445), an enzyme that catalyzes the
 CC conversion of dihomogamma-linolenic acid to arachidonic acid (AA)
 CC and of 20:4n-3 to eicosapentaenoic acid (EPA). The cDNA was
 CC isolated on the basis of homology to Mortierella alpina desaturase
 CC gene sequences, involving the isolation of contigs from a database
 CC and PCR amplifications. The isolated cDNA can be used in the
 CC recombinant production of the delta-5-desaturase. The enzyme can
 CC be expressed in eukaryotic or prokaryotic host cells, especially
 CC Escherichia coli, cyanobacteria, Bacillus subtilis, yeast cells,
 CC fungal cells, mammalian cells, plant cells or insect cells
 CC (especially Spodoptera frugiperda) using a vector comprising the
 CC human delta-5-desaturase nucleotide sequence. Transgenic plants
 CC capable of producing polyunsaturated fatty acid (PUFA) in their
 CC seeds, and transgenic mammals are also claimed. AA and EPA can be
 CC used as substrates for the production of other PUFAs, especially
 CC docosapentaenoic acid or docosahexaenoic acid, using additional
 CC desaturase enzymes. The PUFA products are used in nutritional,
 CC veterinary and pharmaceutical compositions which can be administered
 CC to animals or humans as a dietary substitute/supplement.

XX Sequence 1335 BP; 282 A; 400 C; 334 G; 319 T; 0 other;
 Alignment Scores:
 Pred. No.: 3,64e-156 Length: 1335
 Score: 1508.00 Matches: 271
 Percent Similarity: 75.85% Conservative: 62

Best Local Similarity: 61.73% Mismatches: 100
 Query Match: 61.85% Indels: 6
 DB: 21 Gaps: 3
 US-09-719-601-5 (1-444) x AAA49932 (1-1335)
 QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27
 Db 19 GCGCGCGAGACCGCGGCTCAGGGACCTACCCCGCGCTACTTCCACCTGGACGAGGTGGCC 78
 QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgGlyValTrpSerIleThr 47
 Db 79 CAGCGCTCAGGGTCGAGGAGCGGTGGCTAGTAGTCACCGTAAGGTGTACAAATCAGC 138
 QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTrpArgGluAsp 67
 Db 139 GAGTTTACCGCGCGCATCCAGGGGCTCCCGGTCATCAGCCACTACCGCGGCGAGGAT 198
 QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
 Db 199 GCCACGATCCCTTTGTGGCTTCCACATCAACAGGGCTTGTGAAGAGTATATGAAC 258
 QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
 Db 259 TCTCTCTGATTCGAGACTGTCTCCAGAGCAGCCAGCTTTGAGCCACCAGAAATAAA 318
 QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
 Db 319 GAGCTGACAGATGATTCGGGAGCTCGCGGCCACAGTGGAGCGGATGGGCTCATGAAG 378
 QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
 Db 379 GCCAACCATGTCTTCTTCTGCTGTACCTGCTGCACATCTTGTGCTGGATGTGCGAGCC 438
 QY 148 TrpPheThrValPheTrpPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
 Db 439 TGGCTCACCTTTGGGTCTTTGGGACGCTCTTTTGGCTTCTCTCTCTCTCTCTCTCTCT 498
 QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerVal 187
 Db 499 CTCAGTCAGTTTCCAGGCCAGGCTGGCTGCTGCAGCATGCTTTGGGCACTTGTGGTCC 558
 QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
 Db 559 TTCAGCACCTCAAAGTGGAAACCATCTGCTACATCATTTTGTGATTGGCCACCTGAAGGG 618
 QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisIleAlaLysProAsnIlePhe 227
 Db 619 GCCCGCGCAGTTGGTGGAAACCATGCTTCCAGCACCATGCCAGACCCCACTGCTTC 678
 QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
 Db 679 CGCAAGACCCAGACATCAACATG---CATCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 735
 QY 246 ProlleGluTrpGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 265
 Db 736 TCTGTGGAGCTTGGGAACAGAAATAATATATGCGGTACCAACACCCAGCAATAATAC 795
 QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTrpPheGlnTrpIleMet 285
 Db 796 TTCCTCTTAATTTGGGCCCCCAGCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 855
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTrpTrpIleArg 305
 Db 856 TTGTGTATCCAGCGAAAGAGTGGGTGGACTTGGCTGGATGATTACTTCTAGTCCGC 915
 QY 306 PhePheIleThrTrpIleProPheTrpGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
 Db 916 TTCCTCTCACTTATGTGCCACTTGGGCTGAAGGCTTCTCTCTCTCTCTCTCTCTCTCT 975
 QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
 Db 976 GTCAGGTTCTTGGAAAGCAACTGGTTTGTGGGTGGACACAGATGAACATATTTCCCA 1035

QY 346 GluileaspGlnGluAlaTyArgAspTrpPheSerSergInleuThrAlaThrCysAsn 365
 Db 1036 CACATTGATCATGACCGGAACATGACCTGGTTTCCACCCAGCTCTCCGGCACATGCAAT 1095
 QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
 Db 1096 GTCCACAAAGTCTGCTTCAATGACTGGTTTCAGTGGACACCTCAACTTCCAGATTGAGCAC 1155
 QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisIleAlaProLeuValLysSer 405
 Db 1156 CATCTTTTCCACGATGCCCTCGACACAAATTACCACAAAGTGGCTCCCTGGTGCACTCC 1215
 QY 406 LeuCysAlaLysHisGlyIleGluThrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
 Db 1216 TTGTGTGCCAAGCTGGCATAGTACAGTCCAAAGCCCTGCTGTCAGCCTTCGCCGAC 1275
 QY 426 IleileArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyLeuHisLys 444
 Db 1276 ATCATCCACTCACTAAAGGAGTCAGGGCAGCTCTGGCTAGATGCTATCTTCACAA 1332
 RESULT 40
 ID AAF25236 standard; DNA; 1335 BP.
 XX AAF25236;
 AC AAF25236;
 DT 30-APR-2001 (first entry)
 XX Nucleotide sequence of a human delta5 desaturase.
 DE delta5 desaturase; desaturase gene; elongase gene; fatty acid;
 KW eicosanoid; nutrition; infant formula; dietary supplement;
 KW dietary substitute; animal feed; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH 1.1335
 CDS /*tag= a
 FT /product= "delta5 desaturase"
 FT
 FN WO200104636-A1.
 PD 18-JAN-2001.
 XX 11-JUL-2000; 2000WO-US19011.
 XX 12-JUL-1999; 99US-0351525.
 XX (UYOH-) UNIV OHIO.
 XX Kopchick JJ, Kelder B;
 XX WPI; 2001-182622/18.
 DR P-PSDB; AAB31686.
 XX
 PT New compositions comprising cells that express desaturases and
 PT elongases, for synthesizing essential fatty acids or long-chain
 PT polyunsaturated fatty acids, used in nutritional, cosmetic or animal
 PT feed formulations -
 XX Disclosure; Fig 18; 93pp; English.
 XX The present sequence encodes a delta5 desaturase. The desaturase
 CC polynucleotide sequence was used to transfect mammalian cells, to
 CC produce animal cells expressing a desaturase gene and/or an elongase
 CC gene. Compositions comprising cells of the invention are useful for
 CC synthesizing essential fatty acids, their derivatives or downstream
 CC products, as well as altered levels of long-chain polyunsaturated
 CC fatty acids and eicosanoids. The compositions are useful in nutritional
 CC formulae, e.g. infant formula, dietary supplements or dietary
 CC substitutes for both humans and animals. The compositions are also

CC useful in cosmetic or animal feed formulations. Furthermore, the
 CC compositions may also be used as fat free media or as research reagents.
 XX Sequence 1335 BP; 282 A; 400 C; 334 G; 319 T; 0 other;

Alignment Scores:
 Pred. No.: 3.64e-156 Length: 1335
 Score: 1508.00 Matches: 271
 Percent Similarity: 75.8% Conservative: 62
 Best Local Similarity: 61.7% Mismatches: 100
 Query Match: 61.8% Indels: 6
 DB: 22 Gaps: 3

US-09-719-601-5 (1-444) x AAF25236 (1-1335)

QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluLeuGln 27
 Db 19 GCGCGGAGACCGCGGCTCAGGACCTACCCCGCGCTACTTCCCTGGAGCAGGTGCC 78
 QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyAsnIleThr 47
 Db 79 CAGCGCTCAGGCTGCGAGGAGCGGTGGCTAGTATCGACCGTAAGGTGTACAACATCAGC 138
 QY 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyAlaGlyGluAsp 67
 Db 139 GAGTTCACCGCGGCTCAGGCGGCTCCCGGCTATCAGCCACTACCGCGGCGGAT 198
 QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
 Db 199 GCCAGGATCCCTTTGTGGCTTCCACATCAACAAGGCGCTTGTGAAGAATATATGAAC 258
 QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
 Db 259 TCTCTCTGATTGGAGAACTGTCTCAGACAGCCAGCTTGGAGCCACCAAGAAATAA 318
 QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
 Db 319 GAGCTGACAGATGAGTTCGCGGAGCTGCGGGCCACAGTGGAGCGCATGGGGCTCATGAAG 378
 QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
 Db 379 GCCAACCATGTCTTCTCTGTGTACCTGTGTCACATCTTGTCTGGTGGTGGTGCAGCC 438
 QY 148 TrpPheThrValPheTyPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
 Db 439 TGGCTCACCTTGGTCTTGGGAGCTCTTTTGGCCCTCTCTCTCTGTGCGGTGCTG 498
 QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyArgHisLeuSerVal 187
 Db 499 CTCAGTGCAGTTTCAGGCCCGAGGCTGGCTGTCAGCATGACTTTGGGCACCTGTCGGTC 558
 QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
 Db 559 TTCAGCACCTCAAGTGGAGAACCATCTGTACATCATTTTGTGTTGGCCACCTGAGGGG 618
 QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysAlaLysProAsnIlePhe 227
 Db 619 GCCCGCGCAGTTGGTGGAAACCATGCACTTCCAGCACCATGCCAAGCCCACTGCTTC 678
 QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
 Db 679 CGCAAGACCCAGACATCAACATG---CATCCCTCTCTTTGGCTTGGGGAGATCCTC 735
 QY 246 ProIleGluTyArgLysLysLysLysLysTyLeuProTyAsnHisGlnHisGluTyArg 265
 Db 736 TCTGTGGAGCTTGGGAAACAGAAAGAAAAATATATGCGGTACACACACAGCACAATATAC 795
 QY 266 PhePheLeuIleGlyProProLeuLeuLeuProMetTyArgPheGlnTyArgIleMet 285
 Db 796 TTCTTCTTAATTGGGCCCGCCAGCCCTGTGCTCTCTACTTCCAGTGGTATATTTCAT 855
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyArgIleArg 305

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Db      856 TTTGTTATCCACGGAAGAGTGGGTGGACTTGGCTGGATGATTACCTTCTAGTCGCG 915
QY      306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db      916 TTTCTTCCACCTTATGTGCCACTATTGGGCTGAAAGCCTTCTGGGCTTTTCTTCATA 975
QY      326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
Db      976 GTGAGGTTCTCTGAAAGCAACTGGTTGTGGGTGACACAGATGAACCATATTCCCAIG 1035
QY      346 GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
Db      1036 CACATTGATCATGACCGGAACATGGACTGGTTTCCACCCAGCTCTGCCCACATGCAAT 1095
QY      366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
Db      1096 GTCCACAGTCTGCGCTTCAATGACTGGTTTCAGTGGACACCTCAACTCCAGATTGAGCAC 1155
QY      386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
Db      1156 CATCTTTTCCACAGATGCTCGACACAAATTACCAAAAGTGGCTCCCTGGTGAGTCC 1215
QY      406 LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
Db      1216 TTGTGTGCCAAGCGTGGCATAGAGTACCAGTCCAGCCCTGCTGTGAGCCTTCGCCGAC 1275
QY      426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db      1276 ATCATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCCCTATCTTCACCAA 1332
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Search completed: December 10, 2003, 18:36:35
Job time : 346 secs

XX Bandman O, Hillman JL, Tang YT, Lal P, Corley NC, Guesler KJ;
 PI Gorgone GA, Baughn MR;
 XX WPI; 2000-117171/10.
 DR P-PSDB; AAY59182.
 XX
 PT New polypeptide, its antagonist useful for treatment and prevention of
 PT neurological, inflammatory, reproductive, endocrine, cell proliferative
 PT and smooth muscle disorders -
 XX
 XX Claim 7; Page 85; 88pp; English.
 XX
 CC The invention provides human oxidoreductase proteins (HORP)
 CC (AY59178-183) and nucleic acid sequences (AY48243-248) encoding HORP-1
 CC to HORP-6. The HORP proteins can be expressed by standard recombinant
 CC methodology. Pharmaceutical compositions comprising the HORP proteins are
 CC useful for preventing or treating disorders associated with decreased
 CC expression or activity of HORP while HORP antagonists are useful for
 CC preventing or treating disorders associated with increased expression of
 CC HORP. Such disorders include neurological, autoimmune, reproductive,
 CC cell proliferative, vesicle trafficking, endocrine disorders and cancer
 CC in mammal, especially in humans. HORP is useful for producing antibodies
 CC and for drug screening using libraries of compounds. HORP polynucleotides
 CC and their antibodies are useful for diagnosis of disorders associated
 CC with HORP expression. The present sequence represents a cDNA encoding
 CC the HORP-5 protein.
 XX
 SQ Sequence 3184 BP; 648 A; 956 G; 929 G; 651 T; 0 other;
 Query Match 100.0%; Score 3184; DB 21; Length 3184;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGCGAGCGAGGCGAGGCGTGGGCGAGGCGCGCGTGGGAGGAGTAGGAGAGAC 60
 DB 1 CTCGCGAGCGAGGCGAGGCGTGGGCGAGGCGCGCGTGGGAGGAGTAGGAGAGAC 60

QY 61 AAAAGCCGAAAGCGAAGGCGCGCGTGGGCGAGGCGCGCGTGGGAGGAGCGCGTCTGTG 120
 DB 61 AAAAGCCGAAAGCGAAGGCGCGCGTGGGCGAGGCGCGCGTGGGAGGAGCGCGTCTGTG 120

QY 121 CAGCGAGGAGCGCGCGCGGAGGCGCGAGTGCAGCGGCGCTGCAGTCCGCGAGCGAGCA 180
 DB 121 CAGCGAGGAGCGCGCGGAGGCGCGAGTGCAGCGGCGCTGCAGTCCGCGAGCGAGCA 180

QY 181 TGGGAAAGGAGGAGGAAACAGGCGAGGCGCGCGAGGCGCGAGTGCAGTCCGCGAGCG 240
 DB 181 TGGGAAAGGAGGAGGAAACAGGCGAGGCGCGCGAGGCGCGAGTGCAGTCCGCGAGCG 240

QY 241 TCAGCTGGGAGGAGATTTCAGAGCATTAACCTGCGCAGCAGTGGGCTGGTCAATTGACC 300
 DB 241 TCAGCTGGGAGGAGATTTCAGAGCATTAACCTGCGCAGCAGTGGGCTGGTCAATTGACC 300

QY 301 GCAAGGTTTACACATACCAAAATGGTCCATCCAGCACCCCGGGGGCGAGCGGTCATCG 360
 DB 301 GCAAGGTTTACACATACCAAAATGGTCCATCCAGCACCCCGGGGGCGAGCGGTCATCG 360

QY 361 GGCACCTACCTGGAGAGATGCAACGGATGCGCTCCGCGCGCTTCCACCTGACCTGGAAT 420
 DB 361 GGCACCTACCTGGAGAGATGCAACGGATGCGCTCCGCGCGCTTCCACCTGACCTGGAAT 420

QY 421 TCGTGGGCAAGTTCTTTGAAACCCCTGCTGATTGGTGAATCGGCCCGGAGGAGCCAGGCC 480
 DB 421 TCGTGGGCAAGTTCTTTGAAACCCCTGCTGATTGGTGAATCGGCCCGGAGGAGCCAGGCC 480

QY 481 AGGACACGCGAAGAACTCAAGATCACTAGAGACTTCGGGCGCTGAGGAGCGGCTG 540
 DB 481 AGGACACGCGAAGAACTCAAGATCACTAGAGACTTCGGGCGCTGAGGAGCGGCTG 540

QY 541 AGGACATGAACCTGTTCAAGACCAACACCGTGTCTTCTCCTCTCTCTCTCTCTCTCA 600
 DB 541 AGGACATGAACCTGTTCAAGACCAACACCGTGTCTTCTCCTCTCTCTCTCTCTCTCA 600

601 TCGCCCTGGAGAGCATTTGCTTCTACTGCTTCTACTTGGCAATGGCTGGATTCTTA 660
 601 TCGCCCTGGAGAGCATTTGCTTCTACTGCTTCTACTTGGCAATGGCTGGATTCTTA 660

661 CCCTCATCAGCGCCTTTGCTTCTACTGCTTCTACTGCTTCTACTTGGCAATGGCTGGATTCTTA 720
 661 CCCTCATCAGCGCCTTTGCTTCTACTGCTTCTACTGCTTCTACTTGGCAATGGCTGGATTCTTA 720

721 ATTATGGCCACCTGCTGCTTCTACTGCTTCTACTGCTTCTACTTGGCAATGGCTGGATTCTTA 780
 721 ATTATGGCCACCTGCTGCTTCTACTGCTTCTACTGCTTCTACTTGGCAATGGCTGGATTCTTA 780

781 TCATTGGCCACTTAAAGGGTGCCTTCTGCTTCTACTGCTTCTACTTGGCAATGGCTGGATTCTTA 840
 781 TCATTGGCCACTTAAAGGGTGCCTTCTGCTTCTACTGCTTCTACTTGGCAATGGCTGGATTCTTA 840

841 AGCCCAAGCCTTAACATCTTCCACAGGATCCGATGTAACATCTGCACTGCTTGGTTC 900
 841 AGCCCAAGCCTTAACATCTTCCACAGGATCCGATGTAACATCTGCACTGCTTGGTTC 900

901 TGGGCGAATGGCAGCCCATCGAGTACGGCAAGAAAGAGCTGAATACTGCTTACCAATC 960
 901 TGGGCGAATGGCAGCCCATCGAGTACGGCAAGAAAGAGCTGAATACTGCTTACCAATC 960

961 ACCAGCAGAAATCTTCTTCTGATGGCGCGCGCTGCTCATCCCAATGATTTCCAGT 1020
 961 ACCAGCAGAAATCTTCTTCTGATGGCGCGCGCTGCTCATCCCAATGATTTCCAGT 1020

1021 ACCAGATCATGATGACCATGATCGTCCATAAGAACTGGGTGGAGCTGCTGCTGGGCGCTCA 1080
 1021 ACCAGATCATGATGACCATGATCGTCCATAAGAACTGGGTGGAGCTGCTGCTGGGCGCTCA 1080

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1141 TTTTCTCACTTCACTAGGTTCTTGGAGAGCACTGGTCTTGTGGGTTCACACAGATGA 1200
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1201 ATCAGATCTGATGAGATTGACAGGAGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 1201 ATCAGATCTGATGAGATTGACAGGAGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260

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 1261 CAGCCACCTGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320

1321 TCCAGATTGAGCACCACCTTCTTCCCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 1321 TCCAGATTGAGCACCACCTTCTTCCCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380

1381 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 1381 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440

1441 GGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 1441 GGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500

1501 ACCTTACAAATGAAGCCACAGCCCGGGGACACCTGCGGGAGGGGTGCGAGTGGGGTG 1560
 1501 ACCTTACAAATGAAGCCACAGCCCGGGGACACCTGCGGGAGGGGTGCGAGTGGGGTG 1560

1561 ATGGCCAGAGGAATGATGGGCTTTTCTTCTGAGGGGTGTCCGAGAGGCTGGTGTATGCAC 1620
 1561 ATGGCCAGAGGAATGATGGGCTTTTCTTCTGAGGGGTGTCCGAGAGGCTGGTGTATGCAC 1620

1621 TGCTACGGAAGCCCATGTTGGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1680
 1621 TGCTACGGAAGCCCATGTTGGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1680

[illegible]

1046 CCATAGAACTGGTGGACCTGGCTGGGCGCTCAGCTACTACATCGGTTCTTCATCAC 1105
Db
693 CCATAGAACTGGTGGACCTGGCTGGGCGCTCAGCTACTACATCGGTTCTTCATCAC 752
Qy
1106 CTACATCCCTTTCTACGGCATCTGGAGACCTTCCTTTTCTCAATTCATCAGGTTCT 1165
Db
753 CTACATCCCTTTCTACGGCATCTGGAGACCTTCCTTTTCTCAATTCATCAGGTTCT 812
Qy
1166 GGAGAGCACTGGTTGTGTGGGTCAACAGATGAATCAGTCATCGTATGGAGATTGAACA 1225
Db
813 GGAGAGCACTGGTTGTGTGGGTCAACAGATGAATCAGTCATCGTATGGAGATTGAACA 872
Qy
1226 GGAGGCTACCTGACTGGTTCACTAGTACCCAGCTGACAGCACCTGCAACCTGGAGCAGTC 1285
Db
873 GGAGGCTACCTGACTGGTTCACTAGTACCCAGCTGACAGCACCTGCAACCTGGAGCAGTC 932
Qy
1286 CTCTCTCAACGACTGGTTAGTGGACACCTTAATCTCCAGATTGACACCACTCTTCCC 1345
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933 CTCTCTCAACGACTGGTTAGTGGACACCTTAATCTCCAGATTGACACCACTCTTCCC 992
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1346 CACCATGCCCGGCACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAA 1405
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993 CACCATGCCCGGCACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAA 1052
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Db
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1646 TTCTCCCTTTCTCTCTCTCTTTTCTCTTCAATCTCCCATAGACCTCGCCCTCATG 1705
Db
1293 TTCTCCCTTTCTCTCTCTCTTTTCTCTTCAATCTCCCATAGACCTCGCCCTCATG 1352
Qy
1706 GGACTGCTCCCTCAGCTCAGCCATCAGCCATGGCCCTCCAGTGGCTCCTAGCCC 1765
Db
1353 GGACTGCTCCCTCAGCTCAGCCATCAGCCATGGCCCTCCAGTGGCTCCTAGCCC 1412
Qy
1766 CTTCTTCCAGAGAGAGGTGGCCACCGGGGTGGCTGTCTCTTACCTCCACTCTCT 1825
Db
1413 CTTCTTCCAGAGAGAGGTGGCCACCGGGGTGGCTGTCTCTTACCTCCACTCTCT 1472
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Db
1473 GCCCTAAGATGGAGAGACAGCGGTCCATGGGTCTGGCTGTGAGTCTCCCTTGC 1532
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1886 AGCTGTGTCATAGGCAATCAACCCCGCTTTGGTTCTTTCAGATGCTCTGGGTTCTAGG 1945
Db
1533 AGCTGTGTCATAGGCAATCAACCCCGCTTTGGTTCTTTCAGATGCTCTGGGTTCTAGG 1592
Qy
1946 GGCAGTCTAGTGGGAGGGCCCTGACCTCCCGCTGGCTTCACTCTCCCTGACG 2005
Db
1593 GGCAGTCTAGTGGGAGGGCCCTGACCTCCCGCTGGCTTCACTCTCCCTGACG 1652
Qy
2006 GCTGCCATTGTGCCACCTTTTCATAGAGAGCCCTGCTTTGTTCAAAAGCTCGGCTCTCCC 2065
Db
1653 GCTGCCATTGTGCCACCTTTTCATAGAGAGCCCTGCTTTGTTCAAAAGCTCGGCTCTCCC 1712
Qy
2066 TCCTCAGCTGGTTAAGTACCGAGGCTCTCTTAAGATGTCAGGGCCCGCAGCCCGC 2125
Db
1713 TCCTCAGCTGGTTAAGTACCGAGGCTCTCTTAAGATGTCAGGGCCCGCAGCCCGC 1772
Qy
2126 GGGCACAGCCCAACCTTGGCCCTGGAGAGTCTCTCCACCCCATCACTAGATGC 2185

RESULT 6

1773 GGGCACAGCCAGCCCAACCTTGGGCCCTGGAAGAGTCTCCACCCTCATCTAGATGC 1832
Qy
2186 TCTGACCTGGCTTTTCAAGGCCCCATTCCACCGCTCCCACTTTGAGCCTGTGACCT 2245
Db
1833 TCTGACCTGGCTTTTCAAGGCCCCATTCCACCGCTCCCACTTTGAGCCTGTGACCT 1892
Qy
2246 TGGACCAAAAGGGGAGTCCCTCTCTCTTGTGACTCAGCAGAGGCAAGTGGCCACGTCA 2305
Db
1893 TGGACCAAAAGGGGAGTCCCTCTCTCTTGTGACTCAGCAGAGGCAAGTGGCCACGTCA 1952
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2306 GGGAGGGGCGGCTGGCTGGAGCTCAGCCACCTTCCAGCTTTTCTCAGGGTGTCT 2365
Db
1953 GGGAGGGGCGGCTGGCTGGAGCTCAGCCACCTTCCAGCTTTTCTCAGGGTGTCT 2012
Qy
2366 GAGTCCAAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTATCAGCTGGCA 2425
Db
2013 GAGTCCAAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTATCAGCTGGCA 2072
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2426 GTGCCAGCAATCTCTGGCCATTTGGCCCGCAGGGGACGTGGCCCTGCGAGGTGACGA 2485
Db
2073 GTGCCAGCAATCTCTGGCCATTTGGCCCGCAGGGGACGTGGCCCTGCGAGGTGACGA 2131
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2486 GGGCACTGGAGCTGGAGGTCTCGTCCAGCCCTCCCATCTCGGGGCTCTGTGTGGAC 2545
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2132 GGGCACTGGAGCTGGAGGTCTCGTCCAGCCCTCCCATCTCGGGGCTCTGTGTGGAC 2191
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2546 GGGCTGGCTCAGGCACTCTCTCTGTGAACCTGCCCTTACTGTGTTTAACTGTGCTC 2605
Db
2192 GGGCTGGCTCAGGCACTCTCTCTGTGAACCTGCCCTTACTGTGTTTAACTGTGCTC 2251
Qy
2606 CAGGATGATTTCTGATAGGAGGGGCGGAGGGCTGGCCCTTGTGACAACTTGCCTTCA 2665
Db
2252 CAGGATGATTTCTGATAGGAGGGGCGGAGGGCTGGCCCTTGTGACAACTTGCCTTCA 2311
Qy
2666 CCACATGCCCTTGGCTCGGTGGCCCTGACTGTCTAGGAGGGCCAGGAGGAGCGGGA 2725
Db
2312 CCACATGCCCTTGGCTCGGTGGCCCTGACTGTCTAGGAGGGCCAGGAGGAGCGGGA 2371
Qy
2726 GGGAGTCTCAGAGAGGCTCCCTGAGGGGCTGGGAGGGGTACCTCATAGAGGACAG 2785
Db
2372 GGGAGTCTCAGAGAGGCTCCCTGAGGGCTGGGAGGGGTACCTCATAGAGGACAG 2431
Qy
2786 GGTGAGTCTGAGAGAGAGGAGTGGGGCTGAGGTGTGGTGTGAGTGGGAGCGGGC 2845
Db
2432 GGTGAGTCTGAGAGAGAGGAGTGGGGCTGAGGTGTGGTGTGAGTGGGAGCGGGC 2491
Qy
2846 AAGTCAGAGGGGAGGAGGAGTCCCTGGAGGATCTGAGCTCTGTTCAGTCTAAC 2905
Db
2492 AAGTCAGAGGGGAGGAGGAGTCCCTGGAGGATCTGAGCTCTGTTCAGTCTAAC 2551
Qy
2906 CACTAATCAGTCTTAGATTTCAGGGAGGGCAGGACCAACAACTCAGAAATGGGGCTT 2965
Db
2552 CACTAATCAGTCTTAGATTTCAGGGAGGGCAGGACCAACAACTCAGAAATGGGGCTT 2611
Qy
2966 TCGGGAGGGGCTAGTCCCTCCAGCTTAAGCAGCCAGGAGGACCTGCATTAAGCA 3025
Db
2612 TCGGGAGGGGCTAGTCCCTCCAGCTTAAGCAGCCAGGAGGACCTGCATTAAGCA 2671
Qy
3026 TCTGGTGGCCATGGCAATGGCATGCCCTCCAGCTACTGTATGCCCGCAGCA 3085
Db
2672 TCTGGTGGCCATGGCAATGGCATGCCCTCCAGCTACTGTATGCCCGCAGCA 2731
Qy
3086 GGCAGATGAACCCATAGGAGCTCATCGTAAATGTTTATCATGTACTTCCCAACCCCTA 3145
Db
2732 GGCAGATGAACCCATAGGAGCTCATCGTAAATGTTTATCATGTACTTCCCAACCCCTA 2791
Qy
3146 CATTCTTGAATAAATAAGGAATTTTA 3174
Db
2792 CATTCTTGAATAAATAAGGAATTTTA 2820

1 ATTCAGTGGTTCACCTGCTTTTACCTTTGGCAATGGCTGGATTCCTACCTCATCAGGCCC 60
675 TTGTCCTTGTCTACTCTTCAGGCCCAAGCTGTGATGGCTGCAACATGATATGGCCACCTG 734
61 TTGTCCTTGTCTACTCTTCAGGCCCAAGCTGTGATGGCTGCAACATGATATGGCCACCTG 120
735 TCTGTCTACAGAAAACCCCAAGTGGAAACCACTTGTCCCAAAATTCGTTCATTGGCCACTTA 794
121 TCTGTCTACAGAAAACCCCAAGTGGAAACCACTTGTCCCAAAATTCATTCATTGGCCACTTA 180
795 AAGGTCCTCTGTCACCAATGCTGGAAATCATTCGCCACTTCACGACCAACGCAAGCCTAAC 854
181 AAGGTCCTCTGTCACCAATGCTGGAAATCATTCGCCACTTCACGACCAACGCAAGCCTAAC 240
855 ATCTTCCACAAGGATCCCGATGTAACATGCTGACGCTGTGTTGTTCTGGGGGAATGGCAG 914
241 ATCTTCCACAAGGATCCCGATGTAACATGCTGACGCTGTGTTGTTCTGGGGGAATGGCAG 300
915 CCCATCGAGTACGGCAAGGAAGCTGAAATACCTGCCCCCAATCAATCAACGACGCAATAC 974
301 CCCATCGAGTACGGCAAGGAAGCTGAAATACCTGCCCCCAATCAATCAACGACGCAATAC 360
975 TTCTTCTGATTTGGGCGCGCTGCTCATCCCGATGATTTCCAGTACCGATCATCATG 1034
361 TTCTTCTGATTTGGGCGCGCTGCTCATCCCGATGATTTCCAGTACCGATCATCATG 420
1035 ACCATGATCGTCATGAAGAACTGGGTGGACCTGGCGCTGGCGCTGAGCTACTACATCCGG 1094
421 ACCATGATCGTCATGAAGAACTGGGTGGACCTGGCGCTGGCGCTGAGCTACTACATCCGG 480
1095 TTCTTCTGATTTGGGCGCGCTGCTCATCCCGATGATTTCCAGTACCGATCATCATG 1154
481 TTCTTCTGATTTGGGCGCGCTGCTCATCCCGATGATTTCCAGTACCGATCATCATG 540
1155 ATCAGGTTCTGAGAGGACCTGTTGTTGTTGGTGCACACAGATGAATCACATCGTCATG 1214
541 ATCAGGTTCTGAGAGGACCTGTTGTTGTTGGTGCACACAGATGAATCACATCGTCATG 600
1215 GAGATTGACAGAGGACCTACCGTGAACCTGTTGAGTACGAGTACGAGCCACCTGCAAC 1274
601 GAGATTGACAGAGGACCTACCGTGAACCTGTTGAGTACGAGTACGAGCCACCTGCAAC 660
1275 GTGGAGCAGTCTTCTTCAACGACTGGTTGAGTGGACCTTAACCTCCAGATTCGAGCAC 1334
661 GTGGAGCAGTCTTCTTCAACGACTGGTTGAGTGGACCTTAACTTCAGATTCGAGCAC 720
1335 CACCTCTTCCCAACCATGCCCCGGCACAACTTACAAAGATCGCCCCGCTGGTGAAGTCT 1394
721 CACCTCTTCCCAACCATGCCCCGGCACAACTTACAAAGATCGCCCCGCTGGTGAAGTCT 780
1395 CTATGTCCCAAGCATGGCATTAATACAGGAGAGCCCTACTGAGGCGCTGCTGGAC 1454
781 CTATGTCCCAAGCATGGCATTAATACAGGAGAGCCCTACTGAGGCGCTGCTGGAC 840
1455 ATCATCAGTTCCTTGAAGAGTCTGGGAAGCTGTGGCTGGAAGCTTACCAATGA 1514
841 ATCATCAGTTCCTTGAAGAGTCTGGGAAGCTGTGGCTGGAAGCTTACCAATGA 900
1515 AGCCACAGCCCCCGGACACCGTGGGAAGGGGTGAGGTGGGGTGAATGGCCAGAGGAAT 1574
901 AGCCACAGCCCCCGGACACCGTGGGAAGGGGTGAGGTGGGGTGAATGGCCAGAGGAAT 960
1575 GATGGGCTTTGTTCTGAGGGGTGTCGAGAGGCTGGTGTATCACTGTCTCAGGACCCC 1634
961 GATGGGCTTTGTTCTGAGGGGTGTCGAGAGGCTGGTGTATCACTGTCTCAGGACCCC 1020
1635 ATGTTGGAATCTTCTCCCTTTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1694
1021 ATGTTGGAATCTTCTCCCTTTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
1695 CTGCGCTCATGGGACCTGCGCTCTCAGCGCTGAGCCATCAGCCATGCGCTCCCGAGTG 1754

1081 CTGCGCTCATGGGACCTGCGCTCTCAGCGCTCAGCCATCAGCCATGCGCTCCCGAGTG 1140
1755 CTTCTTAGCCCCCTCTTCCAAAGAGCAGAGAGTGGCCACCGGGGTGCTCTGTCTCTAC 1814
1141 CTTCTTAGCCCCCTCTTCCAAAGAGCAGAGAGTGGCCACCGGGGTGCTCTGTCTCTAC 1200
1815 CTTCACTCTCTGCCCCCTAAAGATGGAGGAGACACAGCGTCCATGGGTCTGGCTGTGAG 1874
1201 CTTCACTCTCTGCCCCCTAAAGATGGAGGAGACACAGCGTCCATGGGTCTGGCTGTGAG 1260
1875 TCTCCCTTTCAGCCTGGTCTACTAGGCATCACCCCGCTTGGTCTTTCAGATGCTCTTG 1934
1261 TCTCCCTTTCAGCCTGGTCTACTAGGCATCACCCCGCTTGGTCTTTCAGATGCTCTTG 1320
1935 GGGTTCATAGGGCAGGTCTTAGTGGGAGGGCCCTGACCCCTCCCGGCTGGCTTCAC 1994
1321 GGGTTCATAGGGCAGGTCTTAGTGGGAGGGCCCTGACCCCTCCCGGCTGGCTTCAC 1380
1995 TCTCCCTGACGGTGCATTTGGTCCACCTTTTCATAGAGGCTGCTTTGTTCACAAAGC 2054
1381 TCTCCCTGACGGTGCATTTGGTCCACCTTTTCATAGAGGCTGCTTTGTTCACAAAGC 1440
2055 TCGGCTCTCTCTCTGAGCTCGGTTAAGTACCCGAGGCTCTCTTAAAGATGTCAGGGC 2114
1441 TCGGCTCTCTCTCTGAGCTCGGTTAAGTACCCGAGGCTCTCTTAAAGATGTCAGGGC 1500
2115 CCCAGGCCCGGGCAGAGCCAGCCAAACCTTTGGGCTCTGGAAGTCTCTCCACCCCAT 2174
1501 CCCAGGCCCGGGCAGAGCCAGCCAAACCTTTGGGCTCTGGAAGTCTCTCCACCCCAT 1560
2175 CACTAGAGTCTCTGACCCCTGGGCTTTACGGGCCCATTTCCACCGCTCTCCCAACTGA 2234
1561 CACTAGAGTCTCTGACCCCTGGGCTTTACGGGCCCATTTCCACCGCTCTCCCAACTGA 1620
2235 GCCTGTGACCTTGGGACCCAAAGGGGAGTCCCTGCTCTCTTGTGACTCAGCAGAGGAGT 2294
1621 GCCTGTGACCTTGGGACCCAAAGGGGAGTCCCTGCTCTCTTGTGACTCAGCAGAGGAGT 1680
2295 GGCCACCTTCAGGAGGGGCGGCTGGCTGGAGGCTCAGCCACCCCTCCAGCTTTTCTCT 2354
1681 GGCCACCTTCAGGAGGGGCGGCTGGCTGGAGGCTCAGCCACCCCTCCAGCTTTTCTCT 1740
2355 CAGGCTGTCTGAGGTCCTGAGCAATCTGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTTA 2414
1741 CAGGCTGTCTGAGGTCCTGAGCAATCTGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTTA 1800
2415 TCAGTGGGACGTGCCAGCCAAATCCCTGGGCAATTTGGCCCCCAGGGGACGTGGGCCCTGC 2474
1801 TCAGTGGGACGTGCCAGCCAAATCCCTGGGCAATTTGGCCCCCAGGGGACGTGGGCCCTGC 1859
2475 AGGCTGCAGGAGGCACTGGAGCTGGAGGCTCTGCTCCAGCCCTCCCCATCTCGGGGCT 2534
1860 AGGCTGCAGGAGGCACTGGAGCTGGAGGCTCTGCTCCAGCCCTCCCCATCTCGGGGCT 1919
2535 GCTGTGTGAGCGGCTGCTCAGGCACTCTCTGTCTGAACTGCTGCTTACTGTGTTA 2594
1920 GCTGTGTGAGCGGCTGCTCAGGCACTCTCTGTGTGAACTGCTGCTTACTGTGTTA 1979
2595 ACCTGTTGCTCCAGGATGCAATTCATAGAGGGGGGGCAGGGCTGGGCTCTGTGACAA 2654
1980 ACCTGTTGCTCCAGGATGCAATTCATAGAGGGGGGGCAGGGCTGGGCTCTGTGACAA 2039
2655 TCTGCTTTTACCAATGGCTTGCCTCGGTGGCCCTGACTGTGAGGAGGGCCAGGGAG 2714
2040 TCTGCTTTTACCAATGGCTTGCCTCGGTGGCCCTGACTGTGAGGAGGGCCAGGGAG 2099
2715 GCAGGCGGAGGAGTCTCAGGAGGAGTGCCTCAGGGGCTGGGAGGGGTACTCTC 2774
2100 GCAGGCGGAGGAGTCTCAGGAGGAGTGCCTCAGGGGCTGGGAGGGGTACTCTC 2159
2775 ATGAGGACCAAGGCTGAGAGGAGGAGGAGGCTGGGGCTGGAGGCTGTGAGGCTGTG 2834
2160 ATGAGGACCAAGGCTGAGAGGAGGAGGAGGAGGCTGGGGCTGGAGGCTGTGAGGCTGTG 2219

Db

Db 1860 GTCTGGGAGGATCTCTGAGCTGCTGTTGCACTCTAAACCCACTAATCACTTCTTAGATTCA 1919
Qy 2928 GGGGAAGGCGAGGACCAACAACTCAGAAATGGGGGCTTTTGGGGAGGGGCGCTAGTCCCC 2987
Db 1920 GGGGAAGGCGAGGACCAACAACTCAGAAATGGGGGCTTTTGGGGAGGGGCGCTAGTCCCC 1979
Qy 2988 CCAGCTCTAAGCAGCAGGAGGACCTGCACTCTAAGCATCTGGGTTCGCAATGGCAATGGC 3047
Db 1980 CCAGCTCTAAGCAGCAGGAGGACCTGCACTCTAAGCATCTGGGTTCGCAATGGCAATGGC 2039
Qy 3048 ATGCCCCCGAGCTACTGTATGCCCCCGACCCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 3107
Db 2040 ATGCCCCCGAGCTACTGTATGCCCCCGACCCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 2099
Qy 3108 CTGATCGTAAATGTTTATCATCTTACTTCTCCACCCCTACATTTTTCGAAATAAATAAGG 3167
Db 2100 CTGATCGTAAATGTTTATCATCTTACTTCTCCACCCCTACATTTTTCGAAATAAATAAGG 2159
Qy 3168 AATTTT 3173
Db 2160 AATTTT 2165

RESULT 10
AAH15815
ID AAH15815 standard; cDNA; 2146 BP.
XX
XX
XX AC AAH15815;
XX
XX DT 26-JUN-2001 (first entry)
XX
XX DE Human cDNA sequence SEQ ID NO:14291.
XX
XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX OS Homo sapiens.
XX
XX FN EP1074617-A2.
XX
XX PD 07-FEB-2001.
XX
XX PF 28-JUL-2000; 2000EP-0116126.
XX
XX PR 29-JUL-1999; 99JP-0248036.
XX
XX PR 27-AUG-1999; 99JP-0300253.
XX
XX PR 11-JAN-2000; 2000JP-0118776.
XX
XX PR 02-MAY-2000; 2000JP-0183767.
XX
XX PR 09-JUN-2000; 2000JP-0241899.
XX
XX PA (HELI-) HELIX RES INST.
XX
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.
XX
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
XX
XX PT full-length cDNAs defined in the specification, and for the detection
XX
XX PT and/or diagnosis of the abnormality of the proteins encoded by the
XX
XX PT full-length cDNAs -
XX
XX PS Claim 8; SEQ ID 14291; 2537pp + CD ROM; English.
XX
XX CC The present invention describes primer sets for synthesizing 5602
XX
XX CC full-length cDNAs defined in the specification. Where a primer set
XX
XX CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
XX
XX CC to the complementary strand of a polynucleotide which comprises one of
XX
XX CC the 5602 nucleotide sequences defined in the specification, where the
XX
XX CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX
XX CC of an oligonucleotide comprising a sequence complementary to the
XX
XX CC complementary strand of a polynucleotide which comprises a 5'-end
XX
XX CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.
SQ Sequence 2146 BP; 403 A; 651 C; 626 G; 466 T; 0 other;
Query Match 66.9%; Score 2130.2; DB 22; Length 2146;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2143; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1027 TCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGCCCGCTCAGCTACT 1086
Db 1 TCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCGCTCAGCTACT 60
Qy 1087 ACATCGGTTCTTCATCACTACCTCTTCTACGGCATCTCTGGAGCCCTCTCTTTTCC 1146
Db 61 ACATCGGTTCTTCATCACTACCTCTTCTACGGCATCTCTGGAGCCCTCTCTTTTCC 120
Qy 1147 TCAACTTTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTTCACACAGATGAATCACA 1206
Db 121 TCACTTTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTTCACACAGATGAATCACA 180
Qy 1207 TCGTCATGAGATTGACACAGGAGGCTTACCGTACTGGTTTCTAGTACGACGCTGACAGCA 1266
Db 181 TCGTCATGAGATTGACACAGGAGGCTTACCGTACTGGTTTCTAGTACGACGCTGACAGCA 240
Qy 1267 CTGCAACGCTGAGCAGTCTTCTTCAACGACTGGTTCTAGTGGACACCTTAACTTCCAGA 1326
Db 241 CTGCAACGCTGAGCAGTCTTCTTCAACGACTGGTTCTAGTGGACACCTTAACTTCCAGA 300
Qy 1327 TTGAGCACCACCTTCTCCACCATGCCCCGCGCAACAATTACAAAGATCGCCCCGCTGG 1386
Db 301 TTGAGCACCACCTTCTCCACCATGCCCCGCGCAACAATTACAAAGATCGCCCCGCTGG 360
Qy 1387 TGAAGTCTCTATGTGCCAAGCATGCAATTAATACAGAGAGGCGCTTACTGAGGGGCC 1446
Db 361 TGAAGTCTCTATGTGCCAAGCATGCAATTAATACAGAGAGGCGCTTACTGAGGGGCC 420
Qy 1447 TGCTGGACATCATCAGTCCCTGAAGAAAGTCTGGGAAGCTGTGGTGGACGCTTACCTTC 1506
Db 421 TGCTGGACATCATCAGTCCCTGAAGAAAGTCTGGGAAGCTGTGGTGGACGCTTACCTTC 480
Qy 1507 ACAATGAAGCCACAGCCCCCGGGACACCGTGGGAGAGGCTGAGGTGGGTGATGGCC 1566
Db 481 ACAATGAAGCCACAGCCCCCGGGACACCTGTGGGAAGGCTGAGGTGGGTGATGGCC 540
Qy 1567 AGAGGAATCATGGGCTTTTGTCTGAGGGGTCTCCGAGAGGCTGGTGTATGACCTGCTCA 1626
Db 541 AGAGGAATCATGGGCTTTTGTCTGAGGGGTCTCCGAGAGGCTGGTGTATGACCTGCTCA 600
Qy 1627 CGGACCCCATGTTGATCTTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1686
Db 601 CGGACCCCATGTTGATCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Qy 1687 ATAGCACCTCGCCCTCATGGGACCTTCCCTCCCTCAGCCGCTCAGCCATCAGCCATGGGCC 1746
Db 661 ATAGCACCTCGCCCTCATGGGACCTTCCCTCCCTCAGCCGCTCAGCCATCAGCCATGGGCC 720
Qy 1747 TCCAGTGTCTCTAGCCCTTCTTCCAAAGAGAGAGAGGTGGCCACACCGGGGTGGCTTC 1806
Db 721 TCCAGTGTCTCTAGCCCTTCTTCCAAAGAGAGAGAGGTGGCCACACCGGGGTGGCTTC 780
Qy 1807 TGTCTTACCTCCACTCTCTGCCCCCTTAAAGATGGAGGAGACCAGCGGTCTCATGGGTCTGG 1866

CC lower cholesterol levels, inhibit proliferation of vessel wall smooth
CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
CC and other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat
CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
XX
SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Query Match 60.9%; Score 1937.6; DB 19; Length 2257;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;

QY 233 GCCACCTTCAGCTGGAGAGATTCAGAAAGATAACCTGCGCAGCAGATGGGGTGT 292
DB 15 GCGTACTTCACCTGGAGAGGTGGCCAGCGCTCAGGGTGGAGAGCGGTGCTAGT 74

QY 293 CATTCACCGCAAGTTTACAACTACCAATGGTCCATCCAGCACCCGGGGGCGCAGCG 352
DB 75 GATCGACCGTAAGTGTACAACTACAGCGAGTTTCAACCGCGGCATCCAGGGGGTCCCG 134

QY 353 GGTTCATCGGCACTAGCTCGGAGAGATGCAACGGATGCTTCGGCGCTTCCACCTGA 412
DB 135 GGTTCATCGACCACTACCGCGGCGAGATGCCAGGATCCCTTTGGCGCTTCCACATCA 194

QY 413 CTTGGAAATTCGTGGGCAAGTTCTTGAACCCCTGCTGATGTGTAATGGCCCGGAGGA 472
DB 195 CAAGGGCTTTGTAAGAAGTATATGAATCTCTCTGATGGAGAACTGTCTCCAGAGCA 254

QY 473 GCCAGCGGAGCACCGGCAAGTCTTCAAGACCAACCTGCTGATGTGTAATGGCCCGGAGGA 532
DB 255 GCCAGCTTTGAGCCCAACCAAGATTAAGAGCTGACAGATGATTCGGGAGCTGGGGC 314

QY 533 GACGGCTGAGGACATGAACCTGTTCAGAACCAACCTGCTTCTCTCTCTCTCTCTGCG 592
DB 315 CACAGTGGAGCGATGGGCTCATGAAGGCCAACCATGTCTTCTCTCTGTGACCTGCT 374

QY 593 CCACATCATCGCCCTGGAGAGCAATGATGGTTCAGTGTCTTCTACTTTGGCAATGGCTG 652
DB 375 GCACATCTTGTGTGATGGTGTGAGCTGGCTGACCCCTTGGGTCTTTGGGACGTCCTT 434

QY 653 GATTCCTACCTCTATC---ACGGCTTTGCTTGTGTACCTCTCAGGCGCCCAAGCTGGATG 709
DB 435 TTTGGCCCTTCTCTCTGTGGGTGTGCTCAGTGAGTTCAGAGGCCCAAGCTGGATG 494

QY 710 GCTGCAACATGATTAATGGCCACTGTCTGTCTCAGAAACCCCAAGTGGAACCACTTGT 769
DB 495 GCTGCAACATGATTAATGGCCACTGTCTGTCTCAGAAACCCCAAGTGGAACCACTTGT 554

QY 770 CCACAAATTCGTCAATGGCCACTTAAAGGTGTCTCTGCCAATGGTGAATCATCGCCA 829
DB 555 CCACAAATTCGTCAATGGCCACTTAAAGGTGTCTCTGCCAATGGTGAATCATCGCCA 614

QY 830 CTTCCAGCACACGCCAAGCTTAACATCTTCCAAAGGATCCCGATGTGAACATGTGCA 889
DB 615 CTTCCAGCACACGCCAAGCTTAACATCTTCCAAAGGATCCCGATGTGAACATGTGCA 674

QY 890 GGTGTTTGTTCGGGCAATGGCCATCGAGTACGGCAAGAGCTGGAATACCT 949
DB 675 CGTGTGTTGTTCGGGCAATGGGAGCCCATCGAGTACGGCAAGAGCTGGAATACCT 734

QY 950 GCCCTACAATCACAGCACGAATACTTCTTCTGATTTGGGCGCGCGTGTCTATCCCCAT 1009
DB 735 GCCCTACAATCACAGCACGAATACTTCTTCTGATTTGGGCGCGCGTGTCTATCCCCAT 794

QY 1010 GTATTTCCAGTACAGATCATATGACCATGATGTGTCCTTAAGAACTGGTGACCTGGC 1069
DB 795 GTATTTCCAGTACAGATCATATGACCATGATGTGTCCTTAAGAACTGGTGACCTGGC 854

QY 1070 CTGGGCGGTGAGCTACTACATCCGGTTCTTTCATCACCTACATCCCTTTCTACGGCATCCT 1129
DB 855 CTGGGCGGTGAGCTACTACATCCGGTTCTTTCATCACCTACATCCCTTTCTACGGCATCCT 914

QY 1130 GGGAGCCCTCCTTTTCTCAACTTCATCAGTTCCTGGAGAGCCACTGGTTGTGGGT 1189
DB 915 GGGAGCCCTCCTTTTCTCAACTTCATCAGTTCCTGGAGAGCCACTGGTTGTGGGT 974

QY 1190 CACACAGATGAATCACATCGTCATGGAGATTGACAGAGGCTTACCGTACCTGTTTAC 1249
DB 975 CACACAGATGAATCACATCGTCATGGAGATTGACAGAGGCTTACCGTACCTGTTTAC 1034

QY 1250 TAGCAGCTGACGCCACCTGCAACGTGGAGAGTCTTCTTCAACACTGGTTCACTGG 1309
DB 1035 TAGCAGCTGACGCCACCTGCAACGTGGAGAGTCTTCTTCAACACTGGTTCACTGG 1094

QY 1310 ACACCTTAACCTTCAGATTGAGCACCACTCTTCTCCCACTGCGCGGACAACTTACA 1369
DB 1095 ACACCTTAACCTTCAGATTGAGCACCACTCTTCTCCCACTGCGCGGACAACTTACA 1154

QY 1370 CAAGATGCCCGCGTGTGAAGTCTCTATGTGCCAAGCATGGCATTAAGTACAGAGAA 1429
DB 1155 CAAGATGCCCGCGTGTGAAGTCTCTATGTGCCAAGCATGGCATTAAGTACAGAGAA 1214

QY 1430 CCGCTACTGAGGGCCCTGTGTGACATCATCAGTCCCTGAAAGTCTGGGAAGCTGTG 1489
DB 1215 CCGCTACTGAGGGCCCTGTGTGACATCATCAGTCCCTGAAAGTCTGGGAAGCTGTG 1274

QY 1490 GCTGAGCGCTTACCTTCAAAATGAAGCAGAGCCCGGGGACACCGTGGGAAGGGGTG 1549
DB 1275 GCTGAGCGCTTACCTTCAAAATGAAGCAGAGCCCGGGGACACCGTGGGAAGGGGTG 1334

QY 1550 CAGTGGGGTTCATGGCCAGAGGAATGATGGCTTTTGTCTGAGGGGTGTCCGAGAGGCT 1609
DB 1335 CAGTGGGGTTCATGGCCAGAGGAATGATGGCTTTTGTCTGAGGGGTGTCCGAGAGGCT 1394

QY 1610 GGTGTATGCACTGTCTACGAGCCCATGTTGGATCTTTCTCTCTCTCTCTCTCTCTTTT 1669
DB 1395 GGTGTATGCACTGTCTACGAGCCCATGTTGGATCTTTCTCTCTCTCTCTCTCTCTTTT 1454

QY 1670 CTCCTCATCTCCCCCATAGCACCTGCTCATGGAGCTGCTCCCTCCCTCAGCCGTCA 1729
DB 1455 CTCCTCATCTCCCCCATAGCACCTGCTCATGGAGCTGCTCCCTCCCTCAGCCGTCA 1514

QY 1730 GCCATCAGCCATGCGCCCTCCAGTGCCTCTAGCCCTTTCTTCCAAAGAGCAGAGAGTG 1789
DB 1515 GCCATCAGCCATGCGCCCTCCAGTGCCTCTAGCCCTTTCTTCCAAAGAGCAGAGAGTG 1574

QY 1790 GCCACGGGGGTGCTGTCTCTACCTCCACTCTGCTCCCTTAAAGTGGAGAGGACCA 1849
DB 1575 GCCACGGGGGTGCTGTCTCTACCTCCACTCTGCTCCCTTAAAGTGGAGAGGACCA 1634

QY 1850 GCGGTTCATGGGTCTGGCTGTGAGTCTCCCTTTCAGCCTGTGTCACCTAGGCATCACCCC 1909
DB 1635 GCGGTTCATGGGTCTGGCTGTGAGTCTCCCTTTCAGCCTGTGTCACCTAGGCATCACCCC 1694

QY 1910 GCTTTGTTCTTTCAGATGCTTTGGGTTTCATAGGGGAGGTCCTAGTGGGAGGGCC 1969
DB 1695 GCTTTGTTCTTTCAGATGCTTTGGGTTTCATAGGGGAGGTCCTAGTGGGAGGGCC 1754

QY 1970 CTTGACCTCTCCGCGCTGCTTCTCTCTGAGCGTGCATTTGTCCACCTTTTCAT 2029
DB 1755 CTTGACCTCTCCGCGCTGCTTCTCTCTGAGCGTGCATTTGTCCACCTTTTCAT 1814

QY 2030 AGAGAGGCTCTTTGTTTACAAAGTGGGTCTCCCTCTGTCAGCTGGTTAAGTACCCG 2089
DB 1815 AGAGAGGCTCTTTGTTTACAAAGTGGGTCTCCCTCTGTCAGCTGGTTAAGTACCCG 1874

QY 2090 AGGCTCTCTTAAAGATGCCAGGGCCCGAGCCCGGGGACACAGCCCAACCTTGG 2149
DB 1875 AGGCTCTCTTAAAGATGCCAGGGCCCGAGCCCGGGGACACAGCCCAACCTTGG 1934

QY 2150 GCTCTGGAAGAGTCTTCCACCCCATCACTAGAGTGTCTGTACCTGGGCTTTCAGGGCC 2209
DB 1935 GCTCTGGAAGAGTCTTCCACCCCATCACTAGAGTGTCTGTACCTGGGCTTTCAGGGCC 1994

QY 2210 CCATTCACGCGCTCCCAACTTGGAGCTGTGACCTTGGACCAACAAAGGGGAGTCCCTCG 2269
 Db |||||
 QY 1995 CCATTCACGCGCTCCCAACTTGGAGCTGTGACCTTGGACCAACAAAGGGGAGTCCCTCG 2054
 Db |||||
 QY 2270 TCTTTGTGACTCAGCAGAGCGAGTGGCCACGTTTCAGGAGGCGCGGTGGCTGGAGG 2329
 Db |||||
 QY 2055 TCTTTGTGACTCAGCAGAGCGAGTGGCCACGTTTCAGGAGGCGCGGTGGCTGGAGG 2114
 Db |||||
 QY 2330 CTCAGCCACCCCTCCAGCTTTCTCTCAGGCTGTGCTGAGTCCAAAGATTCTGGAGCAATC 2389
 Db |||||
 QY 2115 CTCAGCCACCCCTCCAGCTTTCTCTCAGGCTGTGCTGAGTCCAAAGATTCTGGAGCAATC 2174
 Db |||||
 QY 2390 TGACCTTCTCCAAAGCTCTGTATCAGCTGGGCGAGTGCACCAATCCTGGCCATTT 2449
 Db |||||
 QY 2175 TGACCTTCTCCAAAGCTCTGTATCAGCTGGGCGAGTGCACCAATCCTGGCCATTT 2234
 Db |||||
 QY 2450 GGGCCGAGGGGAGCTGGGCGCTG 2473
 Db |||||
 QY 2235 GGGCCCA-GGGGAGCTGGGCGCTG 2257
 Db |||||

RESULT 12

AA00910
 ID AA00910 standard; DNA; 2257 BP.

XX AC AA00910;

XX DT 26-MAR-1999 (first entry)

XX DE Human desaturase gene contig 253538a.

XX KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed; human; ss.

XX OS Homo sapiens.

XX FT Key Location/Qualifiers
 FT CDS 1..2256

FT /*tag= a

FT /note= "contains internal stop codons"

XX WO9846764-A1.

XX 22-OCT-1998.

XX 10-APR-1998; 98WO-US07421.

XX 24-OCT-1997; 97US-0956985.

XX 11-APR-1997; 97US-0833610.

XX 11-APR-1997; 97US-0834033.

XX 11-APR-1997; 97US-0834655.

XX (ABBO) ABBOTT LAB.

XX (CALJ) CALGENE LLC.

XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;

XX Thurmond J;

XX WPI; 1999-080739/07.

XX P-PSDB; AA095514.

XX Nucleic acid construct able to express fatty acid desaturase in

XX plants - useful in human or animal nutrition, as cosmetics and

XX therapeutically, e.g. for restenosis, cancer and diabetes

XX Claim 48; Page 161-162; 210pp; English.

XX The invention relates to a nucleic acid construct that contains at least

XX one of the nucleotide sequences (AA00989 to AA00891) encoding

CC Mortierella alpina delta 6, delta 12 and delta 5 desaturases (AA095504 to
 CC AA095506) respectively, coupled to an expression control sequence
 CC functional in plants. Recombinant plant cells containing at least one DNA
 CC encoding a M. alpina fatty acid desaturase (FAD), can be used for the
 CC production of polyunsaturated fatty acid (PUFA). These recombinant cells
 CC or plants containing them are used to produce oils such as linoleic
 CC acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic
 CC acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils
 CC are used: (i) to treat malnutrition; (ii) in infant feeding formulas; or
 CC dietary supplements or substitutes, for use in humans or animals; (iii)
 CC for treating disorders associated with inadequate consumption or
 CC production of PUFA (or their metabolites such as prostaglandins), e.g.
 CC restenosis after angioplasty, inflammation; AIDS, rheumatoid arthritis,
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics,
 CC and (v) as animal feeds. Fragments of the DNA are used as probes to
 CC isolate related coding sequences. Recombinant plants can produce high
 CC yields of PUFA, since new pathways can be created and unwanted ones
 CC suppressed. Plants can be engineered to express oils of particular PUFA
 CC composition, e.g. one similar to that in human milk, and product recovery
 CC is simpler than with e.g. fish. Sequences AA00904-910 represent DNA
 CC sequences of various contigs of human desaturase genes which are similar
 CC to the M. alpina desaturase sequences.

XX SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Query Match 60.9%; Score 1937.6; DB 20; Length 2257;
 Best Local Similarity 92.1%; Pred. No. 0;
 Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;

QY 233 GCCACCTTTCAGCTGGGAGGATTCAGAGCAATAACCTGCGCACCGACATGGGTGGT 292
 Db |||||
 QY 15 GCGTACTTTCACCTGGGACGAGTGGCCCGCAGCGTTCAGGGTCCGAGGAGCGGTAGT 74
 Db |||||
 QY 293 CATTGACCGCAGGTTTACACATCACCAGTGTCCATCCAGCACCGCGGGCGCACGC 352
 Db |||||
 QY 75 GATCAGCCGTAAGGTGTACACATCAGCGAGTTCACCGCGCGGATCCAGGGGGCTCCG 134
 Db |||||
 QY 353 GGTTCATCGGGCCTACTAGCTGGAGAGATGCAACGAGTCCCTTCGCGCGCTTCCACCTGA 412
 Db |||||
 QY 135 GGTTCATCGGGCCTACTAGCTGGAGAGATGCAACGAGTCCCTTCGCGCGCTTCCACCTGA 194
 Db |||||
 QY 413 CTGTGAATTCGTGGGCAAGTCTTGAACCCCTGCTGATTTGGTGAACCTGGCCCGAGGA 472
 Db |||||
 QY 195 CAAGGGCTTGTGAAGAGATATGAACTCTCTCTGATTTGAGAACTGTCTCCAGAGCA 254
 Db |||||
 QY 473 GCCACGAGGACCAAGCAAGTCAAGAGTCACTGAGGACTTCCGGGCGCTGAGGAA 532
 Db |||||
 QY 255 GCCACGCTTGGAGCCACCAAGATTAAGAGCTGACAGATGATTCGGGAGCTCGGCG 314
 Db |||||
 QY 533 GACGGCTGAGGACATGAACCTGTTCAAGACCAACGAGTCTTCTCTCTCTCTCTCTCTG 592
 Db |||||
 QY 315 CACAGTGGAGCGGATGGGGCTCATGAAGGCCAACCATGTCTTCTCTCTCTCTCTCTCT 374
 Db |||||
 QY 593 CCACATCATCGGCTGGAGCAGCATGTCATGTTCTCACTGCTTCTACTTGTGCAATGGCTG 652
 Db |||||
 QY 375 GCACATCTGCTGCTGATGGTGGCAGCTGGCTGAGCTGACCTTTGGGCTTTGGGACGCTT 434
 Db |||||
 QY 653 GATTTCCTACCTCATC---ACGGCCTTGTCTTGTCTGCTCTCAGGCGCCAGCTGGATG 709
 Db |||||
 QY 435 TTTGGCCTTCTCTCTCTGTCGCGTGTCTGCTCAGTTCAGTTCAGAGGCGCCAAAGCTGG 494
 Db |||||
 QY 710 GCTGCAACATGATTATGGCCACCTGCTGTCTACGAAAAACCAAGTGGAAACCACTTGT 769
 Db |||||
 QY 495 GCTGCAACATGATTATGGCCACCTGCTGTCTACGAAAAACCAAGTGGAAACCACTTGT 554
 Db |||||
 QY 770 CCACAAATTCGTCATTGGCCACTTAAAGGGTGGCTCTGCCAATCTGGTGAATCATGCCA 829
 Db |||||
 QY 555 CCACAAATTCGTCATTGGCCACTTAAAGGGTGGCTCTGCCAATCTGGTGAATCATGCCA 614
 Db |||||
 QY 830 CTTCCAGCACCGCCAGGCTTAACATCTTCCACAGGATCCCGATGCAATCATGCTGCA 889
 Db |||||
 QY 615 CTTCCAGCACCGCCAGGCTTAACATCTTCCACAGGATCCCGATGCAATCATGCTGCA 674
 Db |||||

949 890 CGTGTGTTGTTCTGGCGAATGCGACCCATCGAGTACGGCAAGAAAGCTGAATACCT 949
Db 675 CGTGTGTTGTTCTGGCGAATGCGACCCATCGAGTACGGCAAGAAAGCTGAATACCT 734
Qy 950 GCCCTACAAATCACAGACGAAATACCTTCTCTGATTTGGCGCGCGCTGCTCATCCCAT 1009
Db 735 GCCCTACAAATCACAGACGAAATACCTTCTCTGATTTGGCGCGCGCTGCTCATCCCAT 794
Qy 1010 GTATTTCCAGTACAGATCATCATGATCGTCCATTAAGAACTGGGTGACCTGGC 1069
Db 795 GTATTTCCAGTACAGATCATCATGATCGTCCATTAAGAACTGGGTGACCTGGC 854
Qy 1070 CTGGCGCGTACGATACATCCGCTTCTCATACCTATACCTTCTACGCGATCCT 1129
Db 855 CTGGCGCGTACGATACATCCGCTTCTCATACCTATACCTTCTACGCGATCCT 914
Qy 1130 GGGAGCCCTCTTTCTCACTTACATCAGCTTCTCTGAGAGCCACCTGTTGTTGGGT 1189
Db 915 GGGAGCCCTCTTTCTCACTTACATCAGCTTCTCTGAGAGCCACCTGTTGTTGGGT 974
Qy 1190 CACACAGATGAATCACATCGTATGAGATTTGACAGAGGCTTACCGTACCTGTTTACG 1249
Db 975 CACACAGATGAATCACATCGTATGAGATTTGACAGAGGCTTACCGTACCTGTTTACG 1034
Qy 1250 TAGCCAGTACAGCCACCTGACAGTGGAGCTGCTTCTTCAAGCACTGTTTCACTGG 1309
Db 1035 TAGCCAGTACAGCCACCTGACAGTGGAGCTGCTTCTTCAAGCACTGTTTCACTGG 1094
Qy 1310 ACACCTTAACTTCCAGATTTGAGACCACTCTTCCACCATGCCCCGGGACCACTTACA 1369
Db 1095 ACACCTTAACTTCCAGATTTGAGACCACTCTTCCACCATGCCCCGGGACCACTTACA 1154
Qy 1370 CAAGATGCCCGCTGTTGAGTCTTATGTCGAAGCTGCTGGAAGTCTGGAAGCTGTG 1489
Db 1215 GCCGCTACTGAGGCGCTCTGGAATCATCATGAGTCTGGAAGTCTGGAAGCTGTG 1274
Qy 1490 GCTGAGCCCTTACCTTCAAAATGAGCCACAGCCCGCGGAGACCCCTGGGAGAGGGTG 1549
Db 1275 GCTGAGCCCTTACCTTCAAAATGAGCCACAGCCCGCGGAGACCCCTGGGAGAGGGTG 1334
Qy 1550 CAGGTGGGCTGATGGCCAGAGGATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCT 1609
Db 1335 CAGGTGGGCTGATGGCCAGAGGATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCT 1394
Qy 1610 GGTGTATGCACTGCTACGAGCCCATGTTGGATCTTTTCTCCCTTCTCTCTCTCTTTT 1569
Db 1395 GGTGTATGCACTGCTACGAGCCCATGTTGGATCTTTTCTCCCTTCTCTCTCTCTTTT 1454
Qy 1670 CTCTTACATCTCCCCATAGCACCCCTGCTCATGAGCTGCTGCTTCTCTCTCTCTCTCTCA 1729
Db 1455 CTCTTACATCTCCCCATAGCACCCCTGCTCATGAGCTGCTGCTTCTCTCTCTCTCTCTCA 1514
Qy 1730 GCCATAGCCATGGCCCTCCAGTGCCTTCTAGCCCTTCTTCCAGGAGCAGAGAGGTG 1789
Db 1515 GCCATAGCCATGGCCCTCCAGTGCCTTCTAGCCCTTCTTCCAGGAGCAGAGAGGTG 1574
Qy 1750 GCCACCGGGGTGGCTGCTCTACCTACCTCTCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCT 1849
Db 1575 GCCACCGGGGTGGCTGCTCTACCTACCTCTCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCT 1634
Qy 1850 GCGGTCCATGGGTCTGGCTGCTGAGTCTTCCCTTCTGCAAGCTGCTGCTGCTGCTGCTGCTGCT 1909
Db 1635 GCGGTCCATGGGTCTGGCTGCTGAGTCTTCCCTTCTGCAAGCTGCTGCTGCTGCTGCTGCTGCT 1694
Qy 1910 GCTTTGTTCTTTCAGATGCTCTTGGGTTTATAGGGGAGGCTCTAGTGGGAGGGCC 1969
Db 1695 GCTTTGTTCTTTCAGATGCTCTTGGGTTTATAGGGGAGGCTCTAGTGGGAGGGCC 1754
Qy 1970 CTGACCCCTCCGGGCTGGCTTCACTCTCCCTGACGGCTGCTGCTGCTGCTGCTGCTGCTGCTTTCAT 2029

1755 CTTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCAATGTTGTCACCTTTTCAT 1814
Qy 2030 AGAGAGGCTGCTTTGTTTACAAAGCTCGGCTCTCCCTCTCGAGCTCGGTTAAGTACCGG 2089
Db 1815 AGAGAGGCTGCTTTGTTTACAAAGCTCGGCTCTCCCTCTCGAGCTCGGTTAAGTACCGG 1874
Qy 2090 AGGCTCTCTTAAAGATGTCAGGGGCCCCAGGCCCCCGGGGACAGCCAGCCAAACCTTTGG 2149
Db 1875 AGGCTCTCTTAAAGATGTCAGGGGCCCCAGGCCCCCGGGGACAGCCAGCCAAACCTTTGG 1934
Qy 2150 GGCCTGGAAGAGTCTCTCAACCCCATCTAGAGTCTCTGACCTTGGGCTTTTTCAGGGCC 2209
Db 1935 GGCCTGGAAGAGTCTCTCAACCCCATCTAGAGTCTCTGACCTTGGGCTTTTTCAGGGCC 1994
Qy 2210 CCATTCCACCGCTCTCCCAACTGTGACCTTGGACCTTGGACCTTGGACCTTGGACCTTGGACCT 2269
Db 1995 CCATTCCACCGCTCTCCCAACTGTGACCTTGGACCTTGGACCTTGGACCTTGGACCTTGGACCT 2054
Qy 2270 TCTTGTGACTCAGACAGAGGCTGTCAGCTTTCAGAGGGGCGGCTGCTGCTGAGG 2329
Db 2055 TCTTGTGACTCAGACAGAGGCTGTCAGCTTTCAGAGGGGCGGCTGCTGCTGAGG 2114
Qy 2330 CTCAGCCACCTCCAGCTTTTCTCAGGCTGCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCT 2389
Db 2115 CTCAGCCACCTCCAGCTTTTCTCAGGCTGCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCT 2174
Qy 2390 TCACCTTCTCCAAAGGCTCTGTTATCAGTGGGCTGTCAGGAGGCGGCTGCTGCTGAGG 2449
Db 2175 TCACCTTCTCCAAAGGCTCTGTTATCAGTGGGCTGTCAGGAGGCGGCTGCTGCTGAGG 2234
Qy 2450 GGGCCCAAGGGGACGCTGGGCGCTG 2473
Db 2235 GGGCCCAAGGGGACGCTGGGCGCTG 2257

RESULT 13
AAV82642
ID AAV82642 standard; DNA; 2257 BP.
XX AAV82642;
AC AAV82642;
XX DT 11-FEB-1999 (first entry)
XX Contig 253538a encoding a desaturase enzyme.
DE Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.
XX Homo sapiens.
XX MO9846765-A1.
XX 22-OCT-1998.
XX 10-APR-1998; 98MO-US07422.
XX 11-APR-1997; 97US-0833610.
XX (ABBO) ABBOTT LAB.
XX (CALJ) CALGENE LLC.
XX Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
XX Thurmond J;
XX WPI; 1999-009334/01.
XX P-PSDB; AAW85135.
XX New nucleic acid encoding delta5 and other desaturase enzymes -

PT useful in production of oils of increased arachidonic acid content,
PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
XX
PS Claim 86; Pages 111-112; 153pp; English.

XX The present sequence encodes a human desaturase enzyme. The enzyme
CC sequence is used in the methods of the invention. The specification
CC describes methods for desaturating a fatty acid and for producing a
CC desaturated fatty acid by expressing increased levels of a desaturase.
CC The enzyme can be used for desaturating fatty acids. The enzyme can be
CC used to produce polyunsaturated fatty acids, which can be used for
CC treating malnutrition, in pharmaceutical compositions, in cosmetics or
CC in animal feed. The polyunsaturated fatty acids can be used for treating
CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,
CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.
CC They can also be used to inhibit platelet aggregation, cause
CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
CC wall smooth muscle and fibrous tissue, reduce or prevent
CC gastro-intestinal bleeding and other side effects caused by non-steroidal
CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual
CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after
CC viral infections, treat AIDS, multiple sclerosis, acute respiratory
CC syndrome, hypertension and inflammatory skin disorders.

XX Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Query Match 60.9%; Score 1937.6; DB 20; Length 2257;

Best Local Similarity 92.1%; Pred. No. 0;

Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;

QY	233	GCCACCTTCAGCTGGGAGAGATTTCAGAAAGATACCTCGCACACGACAGTGGGCTGT	292
DB	15	GCCTACTTTCACCTGGGACGAGGTGGCCAGCGCTCAGGTCGGAGGCGTGGCTAGT	74
QY	293	CATTGACCGCAAGTTTACAAATACCAATGGTCCATCCAGCACCCGGGGGGCAGCG	352
DB	75	GATCGACCGTAAGGTGTACAAATACAGCGAGTTTCAACCGCGCATCCAGGGGGTCCCG	134
QY	353	GGTCATCGGCACCTAGCTGGAGAGATGCAACGAGTCTTCCGGCGCTTCCACCTGA	412
DB	135	GGTCATCAGCCATACCCCGGCGAGGATGCCAGGATCCCTTTGGGCTTCCATCA	194
QY	413	CTTGGAAATCTGGGCAAGTTTGTAAACCCCTGTGATTGGTGAATCGGCCCGGAGGA	472
DB	195	CAAGGGCTTGTGAAGATATATGAATCTCTCTGATTGAGAACTGTCTCCAGACA	254
QY	473	GCCAGCCAGGACCAAGGCAAGTCAAGATCACTGAGGATCTCCGGGCGCTGAGGA	532
DB	255	GCCAGCTTTGAGCCCAAGAAATAAAGAGCTGACAGATAGTTCGGGAGTGGGCG	314
QY	533	GAGCGCTGAGGACATGAACCTGTTCAAGACCAACCGTGTCTCTCTCTCTCTCTG	592
DB	315	CACAGTGGAGCGGATGGGCTCATGAAGGCCAACCATGTCTTCTCTCTCTCTCTG	374
QY	593	CCACATATCGCCCTGGAGAGCATTCAGTGGTTCAGTCTCTCTCTCTCTCTCTCTG	652
DB	375	GCACATCTTGTCTGTGATGGTGGAGCTGGCTCACCCCTTTGGGTCTTTGGGAC	434
QY	653	GATTCTTACCTCATC---ACGGCTTTGTCCTTGTGATCTCTCAGGCGCCCAAGCTG	709
DB	435	TTTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG	494
QY	710	GCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAACCAAGTGGAAACACCT	769
DB	495	GCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAACCAAGTGGAAACACCT	554
QY	770	CCACAAATTCGTCTATTGGCCACTTAAAGGGTGGCTCTGCCAATCGTGGAAATCAT	829
DB	555	CCACAAATTCGTCTATTGGCCACTTAAAGGGTGGCTCTGCCAATCGTGGAAATCAT	614
QY	830	CTTCCAGCACCAAGCTTAAATCTTCCCAAGGATCCCGATGTGAACATGTGCA	889
DB	615	CTTCCAGCACCAAGCTTAAATCTTCCCAAGGATCCCGATGTGAACATGTGCA	674

QY 1770 CCGTACCTCCGGCTGGCTTCACTCTCCCTGACGCTGCCATGTTGCCACCTTTTCAT 2029
 Db 1755 CCGTACCTCCGGCTGGCTTCACTCTCCCTGACGCTGCCATGTTGCCACCTTTTCAT 1814
 QY 2030 AGAGAGGCTCTTTGTTTACAAAGCTCGGGTCTCCCTCTGACGCTCGGTTAAGTACCCG 2089
 Db 1815 AGAGAGGCTCTTTGTTTACAAAGCTCGGGTCTCCCTCTGACGCTCGGTTAAGTACCCG 1874
 QY 2090 AGGCTCTCTTAAGATGTCAGGGGCCAGCGCCGGGACACGCGCCAAACCTTGG 2149
 Db 1875 AGGCTCTCTTAAGATGTCAGGGGCCAGCGCCGGGACACGCGCCAAACCTTGG 1934
 QY 2150 GCCCTGGAAGTCTCTCCACCCCATCACTAGAGTCTCTGACCTTGGGCTTTACGGGCC 2209
 Db 1935 GCCCTGGAAGTCTCTCCACCCCATCACTAGAGTCTCTGACCTTGGGCTTTACGGGCC 1994
 QY 2210 CCAATTCACCGCTCCCAACTTGAGCTGTGACCTTGGGACCAAGGGGAGTCCCTCG 2269
 Db 1995 CCAATTCACCGCTCCCAACTTGAGCTGTGACCTTGGGACCAAGGGGAGTCCCTCG 2054
 QY 2270 TCTCTTGTGACTCAGCAGAGGCACTGGCCACGTTTCAGGGAGGGGCCGCTGGCTGGAGG 2329
 Db 2055 TCTCTTGTGACTCAGCAGAGGCACTGGCCACGTTTCAGGGAGGGGCCGCTGGCTGGAGG 2114
 QY 2330 CTCACCCACCTCCAGCTTTTCTCAGGGTGTCTGAGTCTCAAGATCTCGAGCAATC 2389
 Db 2115 CTCACCCACCTCCAGCTTTTCTCAGGGTGTCTGAGTCTCAAGATCTCGAGCAATC 2174
 QY 2390 TGACCTCTCTCAAAAGGCTCTGTTATCAGCTGGGCACTGCGCAATCCCTGGCCATT 2449
 Db 2175 TGACCTCTCTCAAAAGGCTCTGTTATCAGCTGGGCACTGCGCAATCCCTGGCCATT 2234
 QY 2450 GGCCCCAGGGGACCTGGGCCCTG 2473
 Db 2235 GGCCCCA-GGGACGCGGCCCTG 2257

RESULT 14
 AAA49939
 ID AAA49939 standard; cDNA; 2257 BP.
 XX
 AC AAA49939;
 XX
 DT 10-OCT-2000 (first entry)
 XX
 DE Human delta-5-desaturase-related contig 253538a.
 XX
 KW Delta-5-desaturase; human; polyunsaturated fatty acid;
 KW arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;
 KW docosahexaenoic acid; nutrition; feedstuff; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1299
 FT /*tag= a
 XX
 PN WO200040705-A2.
 XX
 PD 13-JUL-2000.
 XX
 PF 29-DEC-1999; 99WO-US31163.
 XX
 PR 08-JAN-1999; 99US-0227613.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Mukerji P, Leonard ABY, Huang Y, Parker-Barnes JM;
 XX
 DR WPI; 2000-465975/40.
 DR P-PSDB; AAY95446.
 XX
 PT New polypeptide useful for preparation of nutritional supplements based

PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids
 at carbon 5 -

XX Example 1; Fig 8; 127pp; English.

XX The present sequence is that of contig 253538a, a contig produced
 CC from overlapping contigs 2535 (see AAA49938) and 3854933 (see
 CC AAA49936), which were isolated from the Incyte LifeSeq database on
 CC the basis of homology to Mortierella alpina delta-5-desaturase and
 CC delta-6-desaturase cDNA sequences. The contig includes a partial
 CC open reading frame that aligns with M. alpina delta-5- and
 CC delta-6-desaturase sequences. The contig was utilised in the
 CC isolation of cDNA (see AAA49932) encoding human delta-5-desaturase
 CC (see AAY95445). Delta-5-desaturase catalyzes the conversion of
 CC dihomogamma-linolenic acid to arachidonic acid and of 20:4n-3 to
 CC eicosapentaenoic acid. Recombinant enzyme, expressed in prokaryotic
 CC or eukaryotic hosts using the isolated human delta-5-desaturase
 CC cDNA, can be used in the production of polyunsaturated fatty acids
 CC that may be added to nutritional, veterinary and pharmaceutical
 CC compositions.

XX Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Query Match 60.9%; Score 1937.6; DB 21; Length 2257;

Best Local Similarity 92.1%; Pred. No. 0; Mismatches 174; Indels 4; Gaps 2;

Matches 2086; Conservative 0;

QY 233 GCCACCTTCAGCTGGAGGAGATTTCAGAAAGCATAACTTCGCGCACCGACAGTGGGTGTGT 292
 Db 15 GCGCTACTTCACTGGAGGAGGTGCCCGACGCTCAGGGTCCGAGGAGCGGTGGCTAGT 74
 QY 293 CATTGACCGAGGTTTACAAATCAATCAAAATGGTCCATCCAGCACCCGGGGGGCCAGCG 352
 Db 75 GATCGACCTTAAGGTGTACAAATCAGCGAGTTCACCGCCGGCATCCAGGGGGGTCCCG 134
 QY 353 GGTATCGGGCACTACGCTGGAGAGATGCAACGAGATGCTTCGCGCGCTTCACCCCTGA 412
 Db 135 GGTATCAGCCACTACGCGGGCAGGATGCCAGGATCCCTTTGTGGCTTCCACATCAA 194
 QY 413 CTGGAAATTCGTGGGCAAGTTCCTTGAACCCCTGCTGATGTGTGAAGTGGCCCGGAGGA 472
 Db 195 CAAGGGCTTGTGAAGAAGTATATGAACCTCTCTCTGATTTGAGAAGTGTCTCCAGAGCA 254
 QY 473 GCCCAGCAGGACCGGACGCAAGAACTCAAGATCACTAGAGGACTTCGCGGCCCTCAGGAA 532
 Db 255 GCCACCTTTGACCCACCAAGAAATAGAGTGACAGATGATTCGCGGAGCTCGGGC 314
 QY 533 GACGGTGGAGCATGAACCTGTTCAAGACCAACACGATGTTCCTCTCTCTCTCTCTCTG 592
 Db 315 CACAGTGGAGCGGATGGGGCTCATGAAGGCCAACCATGTCTCTCTCTCTCTCTCTCTCT 374
 QY 593 CCACATCATCGCCCTCGAGAGCATTCATGGTTCATGTCTTCTTCTTCTTCTTCTTCTG 652
 Db 375 GCACATCTTGTCTGTGATGGTGCAGCTTGGCTCACCTTTGGGCTTTTGGAGCTCCTT 434
 QY 653 GATTCTCACTCACTC ---ACGGCCCTTTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 709
 Db 435 TTGGCCCTTCTCTCTCTGTGCGGTGCTGCTCAGTGCAGTTCAGCAGGCCCAAGCTGGATG 494
 QY 710 GCTGCAACATGATATGGCCACCTGTCTCTTACAGAAAACCAAGTGGAAACCACTTCT 769
 Db 495 GCTGCAACATGATATGGCCACCTTAAAGGGTGCCTCTGCAAACTGTGTGAATCATGCCA 554
 QY 770 CCACAAATTCGTATTTGGCCACTTAAAGGGTGCCTCTGCAAACTGTGTGAATCATGCCA 614
 Db 555 CCACAAATTCGTATTTGGCCACTTAAAGGGTGCCTCTGCAAACTGTGTGAATCATGCCA 614
 QY 830 CTTCCAGCAGCAGCCCAAGCTTAACATCTTCACAGAGTCCGATGTGAATCATGCTGCA 889
 Db 615 CTTCCAGCAGCAGCCCAAGCTTAACATCTTCACAGAGTCCGATGTGAATCATGCTGCA 674
 QY 890 CGTGTGTGTCTGGGCGAATGGCAGGCCATCCAGTACGGCAAGAGAGTGAATCAATCT 949

Db 375 GCACATCTTGCTGCTGGATGCTGACGCTGGCTCACCCCTTTGGGTCTTTGGGAGCTCCCT 434
Qy 653 GATTCCTACCTCATC--ACGGCTTTGCTTGTCTACCTCTCAGGCCCAAGCTGGATG 709
Db 435 TTTGCCCTTCTCTCTGTGGGTGCTGCTCAGTGAGTTTCAGAGGCCCAAGCTGGATG 494
Qy 710 GCTCAACATGATTTATGGCCACCTGTCTGTCTACAGAAAACCAAGTGGAAACCACTTGT 769
Db 495 GCTCAACATGATTTATGGCCACCTGTCTGTCTACAGAAAACCAAGTGGAAACCACTTGT 554
Qy 770 CCACAAATTCGTATTCGGCCACTTAAAGGTGCTCTGCCAATCTGGTGGAAATCATGCCA 829
Db 555 CCACAAATTCGTATTCGGCCACTTAAAGGTGCTCTGCCAATCTGGTGGAAATCATGCCA 614
Qy 830 CTTCCAGCACCAAGCCATCAATCTTCCCAAGGATCCCGATGTGAACATGTGTGCA 889
Db 615 CTTCCAGCACCAAGCCATCAATCTTCCCAAGGATCCCGATGTGAACATGTGTGCA 674
Qy 890 CGTGTGTTGTTCTGGCGAATGGACCCATCGAGTACGGCAAGAGCTGAATACCT 949
Db 675 CGTGTGTTGTTCTGGCGAATGGACCCATCGAGTACGGCAAGAGCTGAATACCT 734
Qy 950 GCCCTACAATCACAGACAGAACTACTTCTCTCATTTGGGCGCGCTGTCTATCCCAT 1009
Db 735 GCCCTACAATCACAGACAGAACTACTTCTCTCATTTGGGCGCGCTGTCTATCCCAT 794
Qy 1010 GTATTTTCAGTACAGATCATCATGATCGTCCATAGAACTGGGTGGACCTGGC 1069
Db 795 GTATTTTCAGTACAGATCATCATGATCGTCCATAGAACTGGGTGGACCTGGC 854
Qy 1070 CTGGGCGCTCAGTACTACATCCGGTCTTCTCATCAGCTACATCCCTTTCTACGGCATCT 1129
Db 855 CTGGGCGCTCAGTACTACATCCGGTCTTCTCATCAGCTACATCCCTTTCTACGGCATCT 914
Qy 1130 GGGAGCCCTCTTTCTCTCAATTCATCAGTTCTCTGGAGAGCACTGGTTGTGGGT 1189
Db 915 GGGAGCCCTCTTTCTCTCAATTCATCAGTTCTCTGGAGAGCACTGGTTGTGGGT 974
Qy 1190 CACACAGATGAATCACATGTCATGGAGATTGACAGAGGCCCTACCGTCACTGGTTTAC 1249
Db 975 CACACAGATGAATCACATGTCATGGAGATTGACAGAGGCCCTACCGTCACTGGTTTAC 1034
Qy 1250 TAGCAGCTGACAGCCACCTGCAACGCTGGAGCAGTCTCTTTCAACGACTGGTTTCACTGG 1309
Db 1035 TAGCAGCTGACAGCCACCTGCAACGCTGGAGCAGTCTCTTTCAACGACTGGTTTCACTGG 1094
Qy 1310 ACACCTTAACTTCAGATTGACAGCAGCTCTTCCCAACCATGCCCCGGGCACTTACA 1369
Db 1095 ACACCTTAACTTCAGATTGACAGCAGCTCTTCCCAACCATGCCCCGGGCACTTACA 1154
Qy 1370 CAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACAGGAGAA 1429
Db 1155 CAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACAGGAGAA 1214
Qy 1430 GCCGCTACTAGAGCCCTGTCTGGACATCATCAGTCTCCTGAAAGTCTGGGAAGCTGTG 1489
Db 1215 GCCGCTACTAGAGCCCTGTCTGGACATCATCAGTCTCCTGAAAGTCTGGGAAGCTGTG 1274
Qy 1490 GCTGAGCCCTTACCTTCAAAATGAAGCCACAGCCCCCGGACACCGTGGGAAGGGGTG 1549
Db 1275 GCTGAGCCCTTACCTTCAAAATGAAGCCACAGCCCCCGGACACCGTGGGAAGGGGTG 1334
Qy 1550 CAGTGGGGTGAATGGCCAGAGAAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCT 1609
Db 1335 CAGTGGGGTGAATGGCCAGAGAAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCT 1394
Qy 1610 GGTGTATGCACTGTACAGGACCCCATGTTGGATCTTTCCTCTTCTCTCTCTCTCTTTT 1669
Db 1395 GGTGTATGCACTGTACAGGACCCCATGTTGGATCTTTCCTCTCTCTCTCTCTCTTTT 1454
Qy 1670 CTCCTTACATCTCCCCCATAGCACCTTCCCTCTCATGGAGCTTGCCTCCCTCAGCCCTCA 1729
Db 1455 CTCCTTACATCTCCCCCATAGCACCTTCCCTCTCATGGAGCTTGCCTCCCTCAGCCCTCA 1514

Qy 1730 GCCATCAGCCATGGCCCTCCAGTGCCTCTTAGCCCTTCTTCCAGGAGCAGAGAGTG 1789
Db 1515 GCCATCAGCCATGGCCCTCCAGTGCCTCTTAGCCCTTCTTCCAGGAGCAGAGAGTG 1574
Qy 1790 GCCACGGGGGTGCTGTCTTCTACCTCCATCTCTGTGCCCTTAAAGATGGGAGAGACA 1849
Db 1575 GCCACGGGGGTGCTGTCTTCTACCTCCATCTCTGTGCCCTTAAAGATGGGAGAGACA 1634
Qy 1850 GGGGTCCATGGTCTGGCTGTGAGTCTCCCTTGCAGCTGGTCACTAGGATCACCCT 1909
Db 1635 GGGGTCCATGGTCTGGCTGTGAGTCTCCCTTGCAGCTGGTCACTAGGATCACCCT 1694
Qy 1910 CGCTTTGGTCTTCAAGATGCTCTTTGGGTTCATAGGGGACAGTCTCTAGTCGGGAGGSC 1969
Db 1695 CGCTTTGGTCTTCAAGATGCTCTTTGGGTTCATAGGGGACAGTCTCTAGTCGGGAGGSC 1754
Qy 1970 CTTGACCTCCCGGCTTGGCTTCACTCTCTGAGCTGCCATTTGGTCCACCTTTTCTAT 2029
Db 1755 CTTGACCTCCCGGCTTGGCTTCACTCTCTGAGCTGCCATTTGGTCCACCTTTTCTAT 1814
Qy 2030 AGAGAGGCTGCTGCTTTGTACAAAGCTCGGGTCTCTCTCTCTGAGCTCGGTTTAAAGTACC 2089
Db 1815 AGAGAGGCTGCTGCTTTGTACAAAGCTCGGGTCTCTCTCTCTGAGCTCGGTTTAAAGTACC 1874
Qy 2090 AGGCTCTCTTAAGATGCTCAGGGCCCAAGGCCCGGGGACAGCCAGCCCAAACTTGG 2149
Db 1875 AGGCTCTCTTAAGATGCTCAGGGCCCAAGGGCCCGGGGACAGCCAGCCCAAACTTGG 1934
Qy 2150 GGCCTGGAAGAGTCTCTCCACCCCATCACTAGAGTCTCTGACCTTGGGCTTTTCAAGGSC 2209
Db 1935 GGCCTGGAAGAGTCTCTCCACCCCATCACTAGAGTCTCTGACCTTGGGCTTTTCAAGGSC 1994
Qy 2210 CCATTCACCGCTCTCCCAATTTAGAGCTGTGACCTTGGGACCAAGGGGAGTCCCTCG 2269
Db 1995 CCATTCACCGCTCTCCCAATTTAGAGCTGTGACCTTGGGACCAAGGGGAGTCCCTCG 2054
Qy 2270 TCTCTGTGACTCAGCAGAGCAGTGGCAGCTTTCAGGAGGGGGCGCTGGCTGGAGG 2329
Db 2055 TCTCTGTGACTCAGCAGAGCAGTGGCAGCTTTCAGGAGGGGGCGCTGGCTGGAGG 2114
Qy 2330 CTCAGCCCACTCTCAGCTTTTCTCAGGGTGTCTGAGGTCTTCAAGATTTCTGGAGCAATC 2389
Db 2115 CTCAGCCCACTCTCAGCTTTTCTCAGGGTGTCTTCTCAGGGTCTTCAAGATTTCTGGAGCAATC 2174
Qy 2390 TCAGCCCTTCTCCAAAGGCTCTTATCAGCTGGGAGTGGCAGCAATCCCTGGCCATTT 2449
Db 2175 TGACCTTCTCCAAAGGCTCTTATCAGCTGGGAGTGGCAGCAATCCCTGGCCATTT 2234
Qy 2450 GGCCCCCAGGGGACGTGGGCCCTG 2473
Db 2235 GGCCCCA-GGGGACGTGGGCCCTG 2257

RESULT 17

AB571826

ID AB571826 standard; DNA; 2257 BP.

XX

AC AB571826;

XX

DT 02-DEC-2002 (first entry)

XX

Human delta5-desaturase gene #8.

DE

XX

Human; delta5-desaturase; polyunsaturated fatty acid; DGLA;

KW dihydro-gamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;

KW eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;

KW gene; ds.

XX

OS Homo sapiens.

XX

PN US6432684-B1.

XX

PD 13-AUG-2002.
XX 08-JAN-1999; 99US-0227613.
XX 11-APR-1997; 97US-0833610.
PR 10-APR-1998; 98WO-US07422.
XX (ABBO) ABBOTT LAB.
XX Mukerji P, Leonard AE, Huang Y, Das T;
PI WPI; 2002-689761/74.
XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing
PT the conversion of dihomogamma-linolenic acid to arachidonic acid and
PT in the conversion of 20:4n-3 to eicosapentaenoic acid -
XX Example 1; Figure 8; 88pp; English.
XX The invention relates to an isolated human delta5-desaturase nucleotide
CC sequence (I) which desaturates polyunsaturated fatty acids at
CC carbon 5. The nucleotide sequence (I) may be used in the recombinant
CC production of vectors and host cells for the production of delta5-
CC desaturase. Delta5-desaturase may be utilised in the conversion of
CC dihomogamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the
CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA Or
CC polyunsaturated fatty acids produced from it may be added to
CC pharmaceutical compositions, nutritional compositions, animal feeds, as
CC well as other products such as cosmetics. ABS71819-ABS71854
CC represent human delta5-desaturase coding sequences and PCR primers of
CC the invention.
XX Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;
SQ
Query Match 60.9%; Score 1937.6; DB 24; Length 2257;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;
QY 233 GCCACCTTCAGCTGGGAGAGATTTCAGAGCATACCTGCGCACCGACAGTGGGTGT 292
DB 15 GCGTACTTCCTCTGGGACGAGTGGCGCCAGCGCTCAGGGTGGGAGCGGTGGTAGT 74
QY 293 CATGACCGCAAGTTTACAAATACCAATGGTCCATCCAGCACCCGGGGGGCAGCG 352
DB 75 GATCGACCGTAAGTGTACAAATACAGCGAGTTTCAACCGCGGCAATCCAGGGGGTCCCG 134
QY 353 GGTCACTCGGCACATACCTGGAGAGATGCAACGAGTGGCTTCGGCGCTTCACCTGA 412
DB 135 GGTCACTCAGGCACATACCGCGGCGAGGATGCCAGGATCCCTTTGTGGCTTCCACATCA 194
QY 413 CCTGGAAATTCGTGGCAAGTTCTTTGAAACCCCTGCTGATGTGAATCGGCCCGGAGGA 472
DB 195 CAAGGGCTTGTGAAGAGTATATGAATCTCTCTGATTTGGAGAACTGTCTCCAGAGCA 254
QY 473 GCCCAGCAGGACACCGCAAGACTCAAGATCACTGAGACTTCGGGCGCTGAGAA 532
DB 255 GCCCAGCTTTGAGCCCAACCAAGATAAAGAGCTGACAGATGAGTTCCGGAGCTGGGGC 314
QY 533 GACGGCTGAGGACATGAACCTGTTCAAGACCAACCACTGCTTCTCTCTCTCTCTGGC 592
DB 315 CACAGTGGAGCGGATGGGCTCATGAGGCCAACCACTGTCTTCTCTGTGTACCTGCT 374
QY 593 CCACATCATCGCTTGAGAGCATTTGATGTTTCACTGTTTCTTCTTGGCAATGGCTG 652
DB 375 GCACATCTTGTCTGTGATGTTGAGCTGGCTGACCTTTCCTTGGGTCTTTGGGACGTCTT 434
QY 653 GATTCCTACCTCATC---ACGGCTTGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 709
DB 435 TTTGCCCTTCTCTCTGTGGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 494
QY 710 GCTGCAACATGATATGCAACCTGTCTGTCTACAGAAACCCCAAGTGGAAACCACTTGT 769
DB 495 GCTGCAACATGATATGCAACCTGTCTGTCTACAGAAACCCCAAGTGGAAACCACTTGT 554

QY 770 CCACAAATTCGTCATTGGCCACTTAAAGGGTGCCTTGCCTCAACTGCTGGAATCATCGCA 829
DB 555 CCACAAATTCGTCATTGGCCACTTAAAGGGTGCCTTGCCTCAACTGCTGGAATCATCGCA 614
QY 830 CTTCCAGCAGCAGCCCAAGCCTAAACATCTTCCACAGGATCCCGATGTGAACATCTGCA 889
DB 615 CTTCCAGCAGCAGCCCAAGCCTAAACATCTTCCACAGGATCCCGATGTGAACATCTGCA 674
QY 890 CGTGTCTTGTCTGGGCGAATGCGAGCCCATCGAGTACGGCAAGAGAACTGAAATACCT 949
DB 675 CGTGTCTTGTCTGGGCGAATGCGAGCCCATCGAGTACGGCAAGAGAACTGAAATACCT 734
QY 950 GCCTTCAATCAGCAGCAGCAATATCTTCTCTGATTTGGGCGCGCTGCTCATCCCAT 1009
DB 735 GCCTTCAATCAGCAGCAGCAATATCTTCTCTGATTTGGGCGCGCTGCTCATCCCAT 794
QY 1010 GTATTTCCAGTACAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGC 1069
DB 795 GTATTTCCAGTACAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGC 854
QY 1070 CTGGGCGCTCAGCTATACATCCGGTCTTTCATCAGCTACATCCCTTTCTACGGCATCT 1129
DB 855 CTGGGCGCTCAGCTATACATCCGGTCTTTCATCAGCTACATCCCTTTCTACGGCATCT 914
QY 1130 GGGAGCCCTCTTCTCTCAACTTTCATCAGTTCTGGAGAGCACTGTTGTGTGGGT 1189
DB 915 GGGAGCCCTCTTCTCTCAACTTTCATCAGTTCTGGAGAGCACTGTTGTGTGGGT 974
QY 1190 CACACAGATGAATCAGATGTCATGAGATGTGACAGAGGCTTACCGTACCTGTTGAG 1249
DB 975 CACACAGATGAATCAGATGTCATGAGATGTGACAGAGGCTTACCGTACCTGTTGAG 1034
QY 1250 TAGCCAGCTCAGCAGCAGCTGCAACGTGGAGAGTCTTCTTCAACGACTGGTTCAGTGG 1309
DB 1035 TAGCCAGCTCAGCAGCAGCTGCAACGTGGAGAGTCTTCTTCAACGACTGGTTCAGTGG 1094
QY 1310 ACACCTTAACTTCAGATTGAGCAGCAACACCTTTCCTCCACCATGCCCGGCACTTACA 1369
DB 1095 ACACCTTAACTTCAGATTGAGCAGCAACACCTTTCCTCCACCATGCCCGGCACTTACA 1154
QY 1370 CAAATCGCCCGCTGTGTAAGTCTCTATGTGCAAGCAGTGGCATTTGAATACCGAGAGAA 1429
DB 1155 CAAATCGCCCGCTGTGTAAGTCTCTATGTGCAAGCAGTGGCATTTGAATACCGAGAGAA 1214
QY 1430 GCCCTTACTGAGGCGCTGTGGAATCATCAGTCTTCCCAAGAGTCTGGGAAGCTGTG 1489
DB 1215 GCCCTTACTGAGGCGCTGTGGAATCATCAGTCTTCCCAAGAGTCTGGGAAGCTGTG 1274
QY 1490 GCTGGAGCCTTACTTCAAAATGAGCCACAGCCCCCGGACACCGTGGGAGGGGTG 1549
DB 1275 GCTGGAGCCTTACTTCAAAATGAGCCACAGCCCCCGGACACCGTGGGAGGGGTG 1334
QY 1550 CAGTGGGGTGTATGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCT 1609
DB 1335 CAGTGGGGTGTATGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCT 1394
QY 1610 GGTGTATGCACTGTACGAGCCCATGTTGGATCTTTCTCCCTTCTCTCTCTCTCTCTTTT 1669
DB 1395 GGTGTATGCACTGTACGAGCCCATGTTGGATCTTTCTCCCTTCTCTCTCTCTCTCTTTT 1454
QY 1670 CTCCTTCACTCTCCCATAGCACCTGCTCATGAGGACTGCTCCCTCTCCCTCAGCCGTCA 1729
DB 1455 CTCCTTCACTCTCCCATAGCACCTGCTCATGAGGACTGCTCCCTCTCCCTCAGCCGTCA 1514
QY 1730 GCCATCAGCCATGCGCCCTCCAGTGGCTCTTAGGCCCTTCTTCCAGGAGCAGAGAGTG 1789
DB 1515 GCCATCAGCCATGCGCCCTCCAGTGGCTCTTAGGCCCTTCTTCCAGGAGCAGAGAGTG 1574
QY 1790 GCCACCGGGGTGCTGTCTTACCTCCTCACTCTCTGCTCCCTAAAGATGGAGGAGACCA 1849
DB 1575 GCCACCGGGGTGCTGTCTTACCTCCTCACTCTCTGCTCCCTAAAGATGGAGGAGACCA 1634

195 CAAGGGCCCTGTGAAGAGTATATGAATCTCTCTCTGATTGGAGACTGTCTCAGAGCA 254
 473 GCCACGACGAGACACAGGCAAGACTCAAGATCACTAGAGACTTCCGGGCCCTGAGGAA 532
 255 GCCAGCTTTGAGCCCAACCAAGATTAAGAGAGCTGACAGATGATTTCCGGAGCTGCGGCG 314
 533 GACGGCTGAGGACATGAACCTCTCAAGACCAACACAGTGTCTCTCTCTCTCTCTCTCTGGC 592
 315 CACAGTGAGCGGATGGGGCTCATGAGGCCAACCATGTCTCTCTCTCTCTCTCTCTCTCTCT 374
 593 CCACATCATCGCCCTGGAGAGCAATGSCATGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 652
 375 GCACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 434
 653 GATTCCTACCCCTCATC-...ACGGCCTTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 709
 435 TTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 494
 710 GCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAACCAAGTGGAAACCACTTGT 769
 495 GCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAACCAAGTGGAAACCACTTGT 554
 770 CCACAAATTCGTCATTTGGCCACTTAAAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 829
 555 CCACAAATTCGTCATTTGGCCACTTAAAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 614
 830 CTTCCAGCACCGCCCAAGCTTAACATCTTCCAGAGGATCCCGATGTGAACATCTGCA 889
 615 CTTCCAGCACCGCCCAAGCTTAACATCTTCCAGAGGATCCCGATGTGAACATCTGCA 674
 890 CGTGTGTTGTTCTGGGCGAATGGCAGCCCATCGAGTACGSCAGAGAGAGCTGAATACCT 949
 675 CGTGTGTTGTTCTGGGCGAATGGCAGCCCATCGAGTACGSCAGAGAGAGCTGAATACCT 734
 950 GCCTCAATCAACAGCAGATATCTTCTCTCTGATTGGGCGCGCTCTCTCTCTCTCTCTCTCT 1009
 735 GCCTCAATCAACAGCAGATATCTTCTCTCTGATTGGGCGCGCTCTCTCTCTCTCTCTCTCT 794
 1010 GTATTTCCAGTACAGATCATATGACCATGATCGTCCATAGAGTCTGGTGGACCTGGC 1069
 795 GTATTTCCAGTACAGATCATATGACCATGATCGTCCATAGAGTCTGGTGGACCTGGC 854
 1070 CTGGGCGCTCAGCTACTATCCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1129
 855 CTGGGCGCTCAGCTACTATCCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 914
 1130 GGGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1189
 915 GGGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 974
 1190 CACACAGATGAATCAGATCGTCTATGGAGATTGACAGAGGCTTACCGTACTGTTTCTAG 1249
 975 CACACAGATGAATCAGATCGTCTATGGAGATTGACAGAGGCTTACCGTACTGTTTCTAG 1034
 1250 TAGCCAGCTGACAGCCACCTGCAACCTGGAGAGTCTCTTCAACGACTGTTTCTAGTGG 1309
 1035 TAGCCAGCTGACAGCCACCTGCAACCTGGAGAGTCTCTTCAACGACTGTTTCTAGTGG 1094
 1310 ACACCTTAATTCAGATTGAGACCACTCTTCCCAACCATGCCCCGCGCACCACTTACA 1369
 1095 ACACCTTAATTCAGATTGAGACCACTCTTCCCAACCATGCCCCGCGCACCACTTACA 1154
 1370 CAAGATCGCCCCCTCTGTGAACTCTATGTGCAAGCATGGCAATTAATACAGAGAA 1429
 1155 CAAGATCGCCCCCTCTGTGAACTCTATGTGCAAGCATGGCAATTAATACAGAGAA 1214
 1430 GCGCTACTAGGGCCCTCTGTGACATCATCAGTCTCTGAGAGTCTGGGAGCTGTG 1489
 1215 GCGCTACTAGGGCCCTCTGTGACATCATCAGTCTCTGAGAGTCTGGGAGCTGTG 1274
 1490 GCTGGAGCGCTACTCTCACAAATGAAGCCACAGCCCGCGGACACCGTGGGGAAGGGGTG 1549

1275 GCTGGACGCTACTCTTCAAAATGAAGCCACAGCCCCCGGGACACCGTGGGGAAGGGGTG 1334
 1550 CAGTGGGGTGTATGGCCAGAGGAATGATGGGCTTTTGTCTCAGGGGTGTCCGAGAGGCT 1609
 1335 CAGTGGGGTGTATGGCCAGAGGAATGATGGGCTTTTGTCTCAGGGGTGTCCGAGAGGCT 1394
 1610 GGTGTATGACATGCTCAGCGAACCCCATGTTGATCTTCTCCTTCTCCTCTCTCTCTCTTTT 1669
 1395 GGTGTATGACATGCTCAGCGAACCCCATGTTGATCTTCTCCTTCTCCTCTCTCTCTTTT 1454
 1670 CTCTTCAACATCTCCCCCATAGCACCTGCTCTCATGGGACCTGCTCCTCTCAGCGCTCA 1729
 1455 CTCTTCAACATCTCCCCCATAGCACCTGCTCTCATGGGACCTGCTCCTCTCAGCGCTCA 1514
 1730 GCATCAGCCATGGCCCTCCAGTGTCTCCTAGCCCTTCTTCCAGAGAGAGAGAGGTG 1789
 1515 GCATCAGCCATGGCCCTCCAGTGTCTCCTAGCCCTTCTTCCAGAGAGAGAGAGGTG 1574
 1790 GCCACGGGGTGGCTCTGTCTACCTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1849
 1575 GCCACGGGGTGGCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1634
 1850 GCCTTCCATGGGTCTGGCTGTGAGTCTCCTCTCTCAGCGCTGCTCTCTCTCTCTCTCTCTCT 1909
 1635 GCCTTCCATGGGTCTGGCTGTGAGTCTCCTCTCTCAGCGCTGCTCTCTCTCTCTCTCTCTCT 1694
 1910 CGCTTTGGTCTTTCAGATGCTCTTGGGTTCATAGGGCAGGTCTCTAGTCTGGGAGGGCC 1969
 1695 CGCTTTGGTCTTTCAGATGCTCTTGGGTTCATAGGGCAGGTCTCTAGTCTGGGAGGGCC 1754
 1970 CTTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2029
 1755 CTTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1814
 2030 AGAGAGCGCTCTCTTGTTCAGAGTCTGGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2089
 1815 AGAGAGCGCTCTCTTGTTCAGAGTCTGGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1874
 2090 AGGCTCTCTTAAAGATGCTCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCC 2149
 1875 AGGCTCTCTTAAAGATGCTCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCC 1934
 2150 GCGCTGAAAGAGTCTCTCAGCCCATCATCTAGAGTGTCTGACCTCTGGGCTTTTTCAGGGCC 2209
 1935 GCGCTGAAAGAGTCTCTCAGCCCATCATCTAGAGTGTCTGACCTCTGGGCTTTTTCAGGGCC 1994
 2210 CCACTTCCAGCGCTCTCCCACTTGGAGCTGTGACCTTGGGACCAAGGGGGAGTCTCTCTCG 2269
 1995 CCACTTCCAGCGCTCTCCCACTTGGAGCTGTGACCTTGGGACCAAGGGGGAGTCTCTCTCG 2054
 2270 TCTCTTGTGACTCAGCAGAGGCGAGTGGCCACGTTTCAAGGGAGGGGGCGGCTGGAGG 2329
 2055 TCTCTTGTGACTCAGCAGAGGCGAGTGGCCACGTTTCAAGGGAGGGGGCGGCTGGAGG 2114
 2330 CTGAGCCACCTCTCAGCTTTTCTCAGGGGTCTCTGAGGTCCAGATTTCTGAGGCAATC 2389
 2115 CTCAGCCACCTCTCAGCTTTTCTCAGGGGTCTCTGAGGTCCAGATTTCTGAGGCAATC 2174
 2390 TGACCTCTCTCAGAGGCTCTGTTATCAGTGGGCGAGTGGCCAAATCTCTGCGCAATTT 2449
 2175 TGACCTCTCTCAGAGGCTCTGTTATCAGTGGGCGAGTGGCCAAATCTCTGCGCAATTT 2234
 2450 GGGCCCAAGGGGAGTGGGGCCCTG 2473
 2235 GGGCCCAAGGGGAGTGGGGCCCTG 2257

RESULT 19
 AAV63642
 ID AAV63642 standard; cDNA; 1843 BP.
 XX
 AC AAV63642;
 XX

DT	15-FEB-1999 (first entry)	QY	810	AACGTGGGAATCATGCCCACTTCCAGCACACGCGCAAGCCTAACATCTTCCACAGGAT	869
XX		DB	181	AACGTGGGAATCATGCCCACTTCCAGCACACGCGCAAGCCTAACATCTTCCACAGGAT	240
DE	Contig 2535 encoding a human desaturase enzyme.	QY	870	CCCGATGTGAACATGCTGCACGCTGTTTGTCTGGGCGAAATGGCAGCCCATCGAGTACGGC	929
XX	Fatty acid; desaturase; polyunsaturated fatty acid; malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes; eczema; platelet aggregation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome; human; myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.	DB	241	CCCGATGTGAACATGCTGCACGCTGTTTGTCTGGGCGAAATGGCAGCCCATCGAGTACGGC	300
XX		QY	930	AAGAAGAGCTGAAATACCTGCCCTACAATCACAGCAGCAAGAACTTCTTCTGATTTGGG	989
OS	Hom sapiens.	DB	301	AAGAAGAGCTGAAATACCTGCCCTACAATCACAGCAGCAAGAACTTCTTCTGATTTGGG	360
XX		QY	990	CGCGCTGCTCATCCCATGATTTCCAGTACCAGATCATCATGACCATGCTCCAT	1049
XX	WO9846763-A1.	DB	361	CGCGCTGCTCATCCCATGATTTCCAGTACCAGATCATCATGACCATGCTCCAT	420
XX	22-OCT-1998.	QY	1050	AAGAAGCTGGGTGGACCTGGCTGGCGCTCAGCTACTATACATCCGGTCTTTCATCACCTAC	1109
XX	10-APR-1998; 98WO-US07126.	DB	421	AAGAAGCTGGGTGGACCTGGCGCTGGCGCTCAGCTACTATACATCCGGTCTTTCATCACCTAC	480
XX	11-APR-1997; 97US-0834655.	QY	1110	ATCCCTTTCTAGGCGATCTGGGAGCCCTCTTCTTCTCACTTCACTCAGGTCTCTGGAG	1169
XX	(ABBO) ABBOTT LAB.	DB	481	ATCCCTTTCTAGGCGATCTGGGAGCCCTCTTCTTCTCACTTCACTCAGGTCTCTGGAG	540
XX	(CALJ) CALGENE LLC.	QY	1170	AGCCACTGGTGTGTGGGTCCACACAGATGAATCACATCGTCAATGAGATTCACAGAG	1229
XX	Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P; Thurmond J;	DB	541	AGCCACTGGTGTGTGGGTCCACACAGATGAATCACATCGTCAATGAGATTCACAGAG	600
XX	WPI; 1998-594582/50.	QY	1230	GCCTACCTGACTGTTTCACTAGCAGTGCAGCCACTGCACAGTGCAGTGCAGTGCCTTC	1289
XX	P-PSDB; AAW84155.	DB	601	GCCTACCTGACTGTTTCACTAGCAGTGCAGCCACTGCACAGTGCAGTGCAGTGCCTTC	660
XX	New isolated fatty acid desaturase enzymes - used for the production of polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions, nutritional compositions, cosmetics or animal feed	QY	1290	TTCAACGACTGGTTCAGTGGACACCTTAACTTCCAGATTCAGCACCACCTCTTCCCCACC	1349
XX	Example 12; Pages 116-117; 165pp; English.	DB	661	TTCAACGACTGGTTCAGTGGACACCTTAACTTCCAGATTCAGCACCACCTCTTCCCCACC	720
XX	The present sequence encodes a human desaturase enzyme. The sequence was identified based on homology between human cDNA sequences and Mortierella alpina desaturase gene sequences. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels of a desaturase. The enzyme can be used for desaturating fatty acids. The enzyme can be used to produce polyunsaturated fatty acids, which can be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure. They can also be used to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and inflammatory skin disorders.	QY	1350	ATGCCCGGCAACAATTACAGATTCGCGCGCTGGTGAAGTCTTATGTGCAAGCAT	1409
XX		DB	721	ATGCCCGGCAACAATTACAGATTCGCGCGCTGGTGAAGTCTTATGTGCAAGCAT	780
XX		QY	1410	GSCATTGAATACACAGAGAGCGCTACTGAGGGGCTCTGAGACATCATCAGTCTCCCTG	1469
XX		DB	781	GSCATTGAATACACAGAGAGCGCTACTGAGGGGCTCTGAGACATCATCAGTCTCCCTG	840
XX		QY	1470	AAGAAGTCTGGAAGCTGTGGTGGACGCTTACCTTCAATGAAGCAGCAGCCCCGG	1529
XX		DB	841	AAGAAGTCTGGAAGCTGTGGTGGACGCTTACCTTCAATGAAGCAGCAGCCCCGG	900
XX		QY	1530	GCACCGTGGGAGGGGTGCAGGTGGGTGATGCCAGAGGAATGATGGGCTTTTGTTC	1589
XX		DB	901	GCACCGTGGGAGGGGTGCAGGTGGGTGATGCCAGAGGAATGATGGGCTTTTGTTC	960
XX		QY	1590	TGAGGGGTCTCCGAGAGGCTGTGTATGCTCATGCTCAGGACCCCATGTTGATCTTCT	1649
XX		DB	961	TGAGGGGTCTCCGAGAGGCTGTGTATGCTCATGCTCAGGACCCCATGTTGATCTTCT	1020
XX		QY	1650	CCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1709
XX		DB	1021	CCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1080
XX		QY	1710	CTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1769
XX		DB	1081	CTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1140
XX		QY	1770	TTCCAAAGAGCAGAGAGGTGGCGACCGGGGTGGCTGTCTCTCTCTCTCTCTCTCTCTCT	1829
XX		DB	1141	TTCCAAAGAGCAGAGAGGTGGCGACCGGGGTGGCTGTCTCTCTCTCTCTCTCTCTCTCT	1200
XX		QY	1830	CTAAAGATGGGAGAGACACAGCGGTCCATGGGTCTGGGCTGTGGGCTGTGGGCTGTGGG	1889
XX		DB	1201	CTAAAGATGGGAGAGACACAGCGGTCCATGGGTCTGGGCTGTGGGCTGTGGGCTGTGGG	1260

Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Query Match 57.5%; Score 1830.4; DB 19; Length 1843;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

630 GTCTCTACTTTGGCAATGGCTGGATTCCTACCTCATCAGCGCTTTGTCTTGTCTAC 689
 TACTTTGGCAATGGCTGGATTCCTACCTCATCAGCGCTTTGTCTTGTCTTGTCTAC 60

GGCCCAAGCTGGATGGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 749
 GGCCCAAGCTGGATGGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

AGTGGAACCACTGTGTCCACAAATTCGTCATTGGCCACTTAAAGGGTGCCTCTGCC 809
 AGTGGAACCACTGTGTCCACAAATTCGTCATTGGCCACTTAAAGGGTGCCTCTGCC 180

Thu De

PR 11-APR-1997; 97US-0834033.
PR 11-APR-1997; 97US-0834655.
XX (ABBO) ABBOTT LAB.
PA (CALB) CALGOTT LLC.
XX
XX Chaudhary S, Huang Y, Knutzen D, Leonard AB, Mukerji P;
PI Thurmond J;
XX
XX WZ1; 1989-080739/07.
DR P-FSDB; AAWS5513.
XX
XX Nucleic acid construct able to express fatty acid desaturase in
PT plants - useful in human or animal nutrition, as cosmetics and
PT therapeutically, e.g. for restenosis, cancer and diabetes
XX
XX Claim 48; Page 160-161; 210pp; English.
XX
XX The invention relates to a nucleic acid construct that contains at least
CC one of the nucleotide sequences (AAW00389 to AAW00831) encoding
CC Mortierella alpina delta 6, delta 12 and delta 5 desaturases (AAW95504 to
CC AAW95505) respectively coupled to an expression control sequence
CC functional in plants. Recombinant plant cells containing at least one DNA
CC encoding a M. alpina fatty acid desaturase (FAD), can be used for the
CC production of polyunsaturated fatty acid (PUFA). These recombinant cells
CC or plants containing them are used to produce oils such as linoleic
CC acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic
CC acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils
CC are used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
CC dietary supplements or substitutes, for use in humans or animals; (iii)
CC for treating disorders associated with inadequate consumption or
CC production of PUFA (or their metabolites such as prostaglandins), e.g.
CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics,
CC and (v) as animal feeds. Fragments of the DNA are used as probes to
CC isolate related coding sequences. Recombinant plants can produce high
CC yields of PUFA, since new pathways can be created and unwanted ones
CC suppressed. Plants can be engineered to express oils of particular PUFA
CC composition, e.g. one similar to that in human milk, and product recovery
CC is simpler than with e.g. fish. Sequences AAW00904-910 represent DNA
CC sequences of various contigs of human desaturase genes which are similar
CC to the M. alpina desaturase sequences.
XX
XX Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

AA000909

301 AAGAAAGCTGAAATACCTGCCCTACAATCA

301

QY	990	CGCGCGTCTGCTCATCCCCATGATATTTTCCAGTACCAAGATCATCATGACCAAGATGCTCCAT	1049
DB	361	CGCGCGTCTCATCCCCATGATATTTTCCAGTACCAAGATCATCATGACCAAGTACGCTCCAT	420
QY	1050	AAGAACTGGGTGGAACTGGCTGGCGCGTCAGCTACTACATCCGGTCTTCATCACTAC	1109
DB	421	AAGAACTGGGTGGAACTGGCTGGCGCGTCAGCTACTACATCCGGTCTTCATCACTAC	480
QY	1110	ATCCCTTTTACCGGCATCTCTGGAGAGCCCTCTCTTCTCAACTCATCAGGTTCCCTGGAG	1169
DB	481	ATCCCTTTTACCGGCATCTCTGGAGAGCCCTCTCTTCTCAACTCATCAGGTTCCCTGGAG	540
QY	1170	AGCACTGGTTTGTGTGGTTCACACAGATGAATCATCGTCAATGAGATTCGACCAAGAG	1229
DB	541	AGCACTGGTTTGTGTGGTTCACACAGATGAATCATCGTCAATGAGATTCGACCAAGAG	600
QY	1230	GCCTACCGTACCTGGTTTCAGTAGCCAGCTGCAGAGCCACCTGCACGTGGAGAGTCTCTTC	1289
DB	601	GCCTACCGTACCTGGTTTCAGTAGCCAGCTGCAGAGCCACCTGCACGTGGAGAGTCTCTTC	660
QY	1290	TTCAAGCACTGGTTTCAGTGAGACACCTTAATTCAGATTGAGCACCACTCTTCCCCACC	1349
DB	661	TTCAAGCACTGGTTTCAGTGAGACACCTTAATTCAGATTGAGCACCACTCTTCCCCACC	720
QY	1350	ATGCCCGGCACAACTTTACAAAGATCGCCCCCTGTGTGAAGTCTCTATGTGCCAAGCAT	1409
DB	721	ATGCCCGGCACAACTTTACAAAGATCGCCCCCTGTGTGAAGTCTCTATGTGCCAAGCAT	780
QY	1410	GGCATTGAATPACAGGAGAAAGCCGTACTGAGGGCCCTGTGTGACATCATCAGTGCCTG	1469
DB	781	GGCATTGAATPACAGGAGAAAGCCGTACTGAGGGCCCTGTGTGACATCATCAGTGCCTG	840
QY	1470	AAGAGTCTCGGAGAGCTGTGCTGGAGCGCCTACTCTCACAAATGAAGCCACAGCCCCCGG	1529
DB	841	AAGAGTCTCGGAGAGCTGTGCTGGAGCGCCTACTCTCACAAATGAAGCCACAGCCCCCGG	900
QY	1530	GACACCGTGGGGAAGGGGTCCAGTGGGGTGAATGGCCAGAGGAATGATGGGCTTTTGTTC	1589
DB	901	GACACCGTGGGGAAGGGGTCCAGTGGGGTGAATGGCCAGAGGAATGATGGGCTTTTGTTC	960
QY	1590	TGAGGGGTGTCGAGAGGCTGGTATGCACTGCTCACGACCCCACTGTTTGGATCTTTCT	1649
DB	961	TGAGGGGTGTCGAGAGGCTGGTATGCACTGCTCACGACCCCACTGTTTGGATCTTTCT	1020
QY	1650	CCCTTTCTCCTCTCCCTTTTCTCTTCACTCTCCCCATAGACCCCTGCCTCATGGAC	1709
DB	1021	CCCTTTCTCCTCTCCCTTTTCTCTTCACTCTCCCCATAGACCCCTGCCTCATGGAC	1080
QY	1710	CTGCCCTCCCTCAGCCGTCAGCCATCAGCCATGSCCCTCCAGTGCCCTCTAGCCCTTC	1769
DB	1081	CTGCCCTCCCTCAGCCGTCAGCCATCAGCCATGSCCCTCCAGTGCCCTCTAGCCCTTC	1140
QY	1770	TTCCAAAGGAGCAGAGAGTGCCACCCGGGGTGGCTCTGTCTTCACTTCCACTCTCTGCC	1829
DB	1141	TTCCAAAGGAGCAGAGAGTGCCACCCGGGGTGGCTCTGTCTTCACTTCCACTCTCTGCC	1200
QY	1830	CTAAAGATGGGAGGAGACCGCGTCCAATGGGTCGTGCCCTGTGAGTCTCCCTTGCAGCC	1889
DB	1201	CTAAAGATGGGAGGAGACCGCGTCCAATGGGTCGTGCCCTGTGAGTCTCCCTTGCAGCC	1260
QY	1890	TGGTCACTAGGCATCACCCCCGCTTTGGTCTTCAGATGCTCTTGGGGTTCATAGGGGCA	1949
DB	1261	TGGTCACTAGGCATCACCCCCGCTTTGGTCTTCAGATGCTCTTGGGGTTCATAGGGGCA	1320
QY	1950	GGTCTTAGTGGGAGGAGCCCTGACCCCTCCCGGCTGGCTTCACTCTCCCTGACGCTG	2009
DB	1321	GGTCTTAGTGGGAGGAGCCCTGACCCCTCCCGGCTGGCTTCACTCTCCCTGACGCTG	1380
QY	2010	CCATTGGTCCACCTTTTCATAGAGAGGCTGCTTTGTTTACAAAGCTGGGTCCTCCCTCCT	2069
DB	1381	CCATTGGTCCACCTTTTCATAGAGAGGCTGCTTTGTTTACAAAGCTGGGTCCTCCCTCCT	1440
QY	2070	GCAGCTCGGTTAAGTACCCGAGGCGCTCTCTTAAAGATGTCAGGGCCCCAGGCCCGCGGC	2129

Db	1441	GCAGCTCGGTAAAGTACCGAGGCCCTCTTTAAGATGTCCAGGGCCCGGCGCGGC	1500
Qy	2130	ACAGCCAGGCCAAACCTTGGGCCCTGGAAGAGTCTCCACCCCATCACTAGATGCTCTG	2189
Db	1501	ACAGCCAGGCCAAACCTTGGGCCCTGGAAGAGTCTCCACCCCATCACTAGATGCTCTG	1560
Qy	2190	ACCTGGGCTTTCACGGGCCCATTCACCGCTCCCACTTTGAGCGCTGTGACCTTGGG	2249
Db	1561	ACCTGGGCTTTCACGGGCCCATTCACCGCTCCCACTTTGAGCGCTGTGACCTTGGG	1620
Qy	2250	ACCAAGGGGGAGTCCCTCGTCTCTTGTGACTCAGCAGAGCAGTGCACGTTTCAGGGA	2309
Db	1621	ACCAAGGGGGAGTCCCTCGTCTCTTGTGACTCAGCAGAGCAGTGCACGTTTCAGGGA	1680
Qy	2310	GGGGCCGGCTGGCTTGAGAGCTCAGCCACCTTCAGCTTTTCTCAGGGTGTCTCTGAGG	2369
Db	1681	GGGGCCGGCTGGCTTGAGAGCTCAGCCACCTTCAGCTTTTCTCAGGGTGTCTCTGAGG	1740
Qy	2370	TCCAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTATTACAGCTGGGCAGTGC	2429
Db	1741	TCCAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTATTACAGCTGGGCAGTGC	1800
Qy	2430	CAGCCAACTCCCTGGCCATTGGGCCCGGAGGAGCTGGGCCCTG	2473
Db	1801	CAGCCAACTCCCTGGCCATTGGGCCCGGAGGAGCTGGGCCCTG	1843

RESULT 21

AAV82641
ID AAV82641 standard; DNA; 1843 BP.
XX
XX
AC AAV82641;
XX
DT 11-FEB-1999 (first entry)
XX
XX
XX Contig 2535 encoding a desaturase enzyme.
XX
XX Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.
XX
XX Homo sapiens.
XX
XX WO9846765-A1.
PN
XX
PD 22-OCT-1998.
XX
XX
PF 10-APR-1998; 98WO-US07422.
XX
XX
PR 11-APR-1997; 97US-0833610.
XX
XX (ABEO) ABBOTT LAB.
PA (CALJ) CALGENE LLC.
PA
XX
XX Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
PI Thurmond J;
PI
XX
DR WPI; 1999-009334/01.
DR P-PSDB; AAW85134.
XX
XX New nucleic acid encoding delta5 and other desaturase enzymes -
PT useful in production of oils of increased arachidonic acid content,
PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
XX
XX Claim 86; Pages 110-111; 153pp; English.
PS
XX
XX The present sequence encodes a human desaturase enzyme. The enzyme
CC sequence is used in the methods of the invention. The specification
CC describes methods for desaturating a fatty acid and for producing a

CC desaturated fatty acid by expressing increased levels of a desaturase.
 CC The enzyme can be used for desaturating fatty acids. The enzyme can be
 CC used to produce polyunsaturated fatty acids, which can be used for
 CC treating malnutrition, in pharmaceutical compositions, in cosmetics or
 CC in animal feed. The polyunsaturated fatty acids can be used for treating
 CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,
 CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.
 CC They can also be used to inhibit platelet aggregation, cause
 CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
 CC wall smooth muscle and fibrous tissue, reduce or prevent
 CC gastro-intestinal bleeding and other side effects caused by non-steroidal
 CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual
 CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after
 CC viral infections, treat AIDS, multiple sclerosis, acute respiratory
 CC syndrome, hypertension and inflammatory skin disorders.
 XX
 SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;
 Query Match 57.5%; Score 1830.4; DB 20; Length 1843;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 630 GTCTTCTACTTTGGCAATGGCTGGATCTCTACCTCTCAACGCGCTTTGTCCTGTAC 689
 DB 1 GTCTTTTACTTTGGCAATGGCTGGATCTCTACCTCTCAACGCGCTTTGTCCTGTAC 60
 QY 690 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAGAAA 749
 DB 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAGAAA 120
 QY 750 CCCAAGTGAACCACTTTGTGTCAAAATTCGTATTTGGCCACTTAAAGGTGCTCTGCC 809
 DB 121 CCCAAGTGAACCACTTTGTGTCAAAATTCGTATTTGGCCACTTAAAGGTGCTCTGCC 180
 QY 810 AACTGTGGAATCATCGCCACTTCCAGACCAACGCGCTCAACTTCCACAGGAT 869
 DB 181 AACTGTGGAATCATCGCCACTTCCAGACCAACGCGCTCAACTTCCACAGGAT 240
 QY 870 CCGATGTGAACATCGCTGCACTGTGTTGTTCTGGGCGAATGGAGCCCATCGATAGCGC 929
 DB 241 CCGATGTGAACATCGCTGCACTGTGTTGTTCTGGGCGAATGGAGCCCATCGATAGCGC 300
 QY 930 AAGAAGACTGAATACCTGCGCTTACAAATCAGCAGCAGCAATACCTTCTTCTGATTTGG 989
 DB 301 AAGAAGACTGAATACCTGCGCTTACAAATCAGCAGCAGCAATACCTTCTTCTGATTTGG 360
 QY 990 CCGCGCTGCTCATCCCATGATTTTCCAGTACAGATCATCATGACCATGATGCTCCAT 1049
 DB 361 CCGCGCTGCTCATCCCATGATTTTCCAGTACAGATCATCATGACCATGATGCTCCAT 420
 QY 1050 AAGAAGCTGGTGGACCTGGGCGCTGAGTACTACATCCGCTTCTTCAACCTAC 1109
 DB 421 AAGAAGCTGGTGGACCTGGGCGCTGAGTACTACATCCGCTTCTTCAACCTAC 480
 QY 1110 ATCCCTTTCTAGGGCATCTGGAGCCCTCTTTTCTCACTTCATCAGTTCTGGAG 1169
 DB 481 ATCCCTTTCTAGGGCATCTGGAGCCCTCTTTTCTCACTTCATCAGTTCTGGAG 540
 QY 1170 AGCACTGGTTTGTGTGGGTCAACAGATGAATCAGATCGTCAATGGAGATTGACAGGAG 1229
 DB 541 AGCACTGGTTTGTGTGGGTCAACAGATGAATCAGATCGTCAATGGAGATTGACAGGAG 600
 QY 1230 GCTACCGTGTGCTGTAGTACGAGCTGACGCACTGCTCAACCTGGAGGAGTCTTTC 1289
 DB 601 GCTACCGTGTGCTGTAGTACGAGCTGACGCACTGCTCAACCTGGAGGAGTCTTTC 660
 QY 1290 TTCAAGACTGGTTGAGTGGACACCTTAACTTCCAGATTTAGACACCACTCTTCCCAACC 1349
 DB 661 TTCAAGACTGGTTGAGTGGACACCTTAACTTCCAGATTTAGACACCACTCTTCCCAACC 720
 QY 1350 ATGCCCGGCGACACTTACAGAGATCGCCCGCTGTGTGATCTATGTGCGCAGCAT 1409
 DB 721 ATGCCCGGCGACACTTACAGAGATCGCCCGCTGTGTGATCTATGTGCGCAGCAT 780

QY 1410 GGCAATTGAATACAGAGGAGCGGCTTACTGAGGCGCTGCTGGACATCATCAGGTCCCTG 1469
 DB 781 GGCAATTGAATACAGAGGAGCGGCTTACTGAGGCGCTGCTGGACATCATCAGGTCCCTG 840
 QY 1470 AAGAAGTCTGGGAAGCTGTGGTGGAGCGCTTACCTTCAAAATGAAGGACACAGCCCGG 1529
 DB 841 AAGAAGTCTGGGAAGCTGTGGTGGAGCGCTTACCTTCAAAATGAAGGACACAGCCCGG 900
 QY 1530 GACACCTGGGGAAGGCGTGGAGTGGGCTGATGGCAGAGGAATGATGGGCTTTTGTTC 1589
 DB 901 GACACCTGGGGAAGGCGTGGAGTGGGCTGATGGCAGAGGAATGATGGGCTTTTGTTC 960
 QY 1590 TGAGGGGTGTCAGAGAGGCTGTGTATGACATGCTACAGGACCCCATGTTGATCTTCT 1649
 DB 961 TGAGGGGTGTCAGAGAGGCTGTGTATGACATGCTACAGGACCCCATGTTGATCTTCT 1020
 QY 1650 CCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1709
 DB 1021 CCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
 QY 1710 CTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1769
 DB 1081 CTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
 QY 1770 TTCAAAGGAGCAGAGAGGTGGCCACCGGGGGTGGCTCTCTCTCTCTCTCTCTCTCTCT 1829
 DB 1141 TTCAAAGGAGCAGAGAGGTGGCCACCGGGGGTGGCTCTCTCTCTCTCTCTCTCTCTCT 1200
 QY 1830 CTAAGATGGAGAGAGCAGCGGTCTGAGTCTGGGCTGTGAGTCTCTCTCTCTCTCTCTCTCT 1889
 DB 1201 CTAAGATGGAGAGAGCAGCGGTCTGAGTCTGGGCTGTGAGTCTCTCTCTCTCTCTCTCT 1260
 QY 1890 TGGTCACTAGGCACTACCCCGCTTTGGTCTTTCAGATGCTCTTGGGGTTCATAGGGCA 1949
 DB 1261 TGGTCACTAGGCACTACCCCGCTTTGGTCTTTCAGATGCTCTTGGGGTTCATAGGGCA 1320
 QY 1950 GGTCTTGTGGGAGGCGGCGCTGACCTCCCGGCTGGCTTCACTCTCTCTCTCTCTCTCTCT 2009
 DB 1321 GGTCTTGTGGGAGGCGGCGCTGACCTCCCGGCTGGCTTCACTCTCTCTCTCTCTCTCTCT 1380
 QY 2010 CCATTGTCTCAACCCCTTTTCATAGAGAGCGCTGTCTTTGTTTAAAGCTCTGGGTCTCTCTCT 2069
 DB 1381 CCATTGTCTCAACCCCTTTTCATAGAGAGCGCTGTCTTTGTTTAAAGCTCTGGGTCTCTCTCT 1440
 QY 2070 GCAGCTCGTCTTAAAGTACCGAGCGCTCTTAAAGTCTCCAGGCGCCAGGCGCCGCGGCG 2129
 DB 1441 GCAGCTCGTCTTAAAGTACCGAGCGCTCTTAAAGTCTCCAGGCGCCAGGCGCCGCGGCG 1500
 QY 2130 ACAGCCAGCCCAACCTTTGGGCGCTGGAAGAGTCTTCAACCCCATCATCTAGAGTCTCTG 2189
 DB 1501 ACAGCCAGCCCAACCTTTGGGCGCTGGAAGAGTCTTCAACCCCATCATCTAGAGTCTCTG 1560
 QY 2190 ACCCTGGGCTTTCAGGCGGCGGCTTCCAGCGCTCTCCCACTTGAAGCTGTGAGCTGTGG 2249
 DB 1561 ACCCTGGGCTTTCAGGCGGCGGCTTCCAGCGCTCTCCCACTTGAAGCTGTGAGCTGTGG 1620
 QY 2250 ACCAAAGGGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2309
 DB 1621 ACCAAAGGGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1680
 QY 2310 GGGGCGGCTTGGGCTGAGGCTCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2369
 DB 1681 GGGGCGGCTTGGGCTGAGGCTCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740
 QY 2370 TCCAAAGTCTGGAGCAATCTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2429
 DB 1741 TCCAAAGTCTGGAGCAATCTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800
 QY 2430 CAGCCCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2473
 DB 1801 CAGCCCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1843

RESULT 22

AAA49938
ID AAA49938 standard; cDNA; 1843 BP.

XX AC AAA49938;

XX DT 10-OCT-2000 (first entry)

XX DE Human delta-5-desaturase-related contig 2535.

XX KW Delta-5-desaturase; human; polyunsaturated fatty acid;
XX KW arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;
XX KW docosahexaenoic acid; nutrition; feedstuff; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT 1..885
XX CDS /*tag= a

XX PN WO200040705-A2.

XX PD 13-JUL-2000.

XX PF 29-DEC-1999; 99WO-US31163.

XX PR 08-JAN-1999; 99US-0227613.

XX PA (ABBO) ABBOTT LAB.

XX PI Mukerji P, Leonard AEY, Huang Y, Parker-Barnes JM;

XX DR WPI; 2000-465975/40.
XX P-PSDB; AA95448.

XX PT New polypeptide useful for preparation of nutritional supplements based
XX PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids
XX PT at carbon 5 -

XX PS Example 1; Fig 7; 127pp; English.

XX CC The present sequence is that of contig 2535, a contig produced
XX CC from overlapping contigs 2511785 (see AAA49937) and 3506132 (see
XX CC AAA49935), which were isolated from the Incyte Lifeseq database on
XX CC the basis of homology to Mortierella alpina delta-5-desaturase and
XX CC delta-6-desaturase cDNA sequences. The contig includes a partial
XX CC open reading frame. It overlaps with another isolated contig,
XX CC 3854933 (see AAA49936), creating a final contig, 253538a (see
XX CC AAA49939), that contains a partial open reading frame which aligns
XX CC with M. alpina delta-5 and delta-6-desaturase sequences. The
XX CC contig was utilised in the isolation of cDNA (see AAA49932) encoding
XX CC human delta-5-desaturase (see AA95445). Delta-5-desaturase
XX CC catalyzes the conversion of dihydro-gamma-linolenic acid to
XX CC arachidonic acid and of 20:4n-3 to eicosapentaenoic acid.
XX CC Recombinant enzyme, expressed in prokaryotic or eukaryotic hosts
XX CC using the isolated human delta-5-desaturase cDNA, can be used in
XX CC the production of polyunsaturated fatty acids that may be added to
XX CC nutritional, veterinary and pharmaceutical compositions.

XX SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Query Match 57.5%; Score 1830.4; DB 21; Length 1843;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 630 GTCTCTACTTTGGCAATGGGTGGATTCCTACCCCTCATACGGGCTTTGTCTGTGTACC 689
DB 1 GTCTTTTACTTTGGCAATGGGTGGATTCCTACCCCTCATACGGGCTTTGTCTGTGTACC 60

QY 690 TCTCAGGCCCAAGCTGGATGGCTGCAATGATTATGGCCACCTGTCTGTCTACAGHAAA 749
DB 61 TCTCAGGCCCAAGCTGGATGGCTGCAATGATTATGGCCACCTGTCTGTCTACAGHAAA 120

QY 750 CCCAAGTGGACACCTTTGTCACAAATTCGTTCATTTGGCCACTTAAAGGTCCTCTGCC 809
DB 121 CCCAAGTGGACACCTTTGTCACAAATTCGTTCATTTGGCCACTTAAAGGTCCTCTGCC 180
QY 810 AACTGGTGGAAATCATGCCCATTTCCAGCACCAAGCCCAAGCCTTAACATCTTCCACAGGAT 869
DB 181 AACTGGTGGAAATCATGCCCATTTCCAGCACCAAGCCCAAGCCTTAACATCTTCCACAGGAT 240
QY 870 CCCGATGTGAACATGCTGCACGTTTGTCTGGGCGAATGGCAGCCCATCCAGTACGGC 929
DB 241 CCCGATGTGAACATGCTGCACGTTTGTCTGGGCGAATGGCAGCCCATCCAGTACGGC 300
QY 930 AAGAAGAAGCTGAAATACCTGCCCTACAATCACCAACAGCAATCTTCTTCTGATGGG 989
DB 301 AAGAAGAAGCTGAAATACCTGCCCTACAATCACCAACAGCAATCTTCTTCTGATGGG 360
QY 990 CCGCGCTGTCTATCCCATGTTATTTCCAGTACCAATCATATGACCATGATCGTCCAT 1049
DB 361 CCGCGCTGTCTATCCCATGTTATTTCCAGTACCAATCATATGACCATGATCGTCCAT 420
QY 1050 AAGAACTGGGTGGACCTGGGCTGGGCGCTCAGTACTATACATCCGGTCTTCACTAC 1109
DB 421 AAGAACTGGGTGGACCTGGGCTGGGCGCTCAGTACTATACATCCGGTCTTCACTAC 480
QY 1110 ATCCCTTTCTACGGCATCTCTGGGAGCCCTCTTTTCTCAACTTTCATCAGGTTCTCTGGAG 1169
DB 481 ATCCCTTTCTACGGCATCTCTGGGAGCCCTCTTTTCTCAACTTTCATCAGGTTCTCTGGAG 540
QY 1170 AGCCACTGGTTTGTGTGGGTCAACAGATGAATCATCTGTCTATGGAGATTGACCAAGAG 1229
DB 541 AGCCACTGGTTTGTGTGGGTCAACAGATGAATCATCTGTCTATGGAGATTGACCAAGAG 600
QY 1230 GCCTACCGTGACTGTTTCACTAGCCAGTACAGAGCCACCTGCAACCTGGAGCAGTCTTTC 1289
DB 601 GCCTACCGTGACTGTTTCACTAGCCAGTACAGAGCCACCTGCAACCTGGAGCAGTCTTTC 660
QY 1290 TTCAACAGCTGGTTTCACTAGGACACCTTAACTTCCAGATTGAGCACCCTCTTCCGCCAC 1349
DB 661 TTCAACAGCTGGTTTCACTAGGACACCTTAACTTCCAGATTGAGCACCCTCTTCCGCCAC 720
QY 1350 ATGCCCCGGGCACAACTTACACAAGATCGCCCCCTGGTGAAGTCTCTATGTGCCAAGCAT 1409
DB 721 ATGCCCCGGGCACAACTTACACAAGATCGCCCCCTGGTGAAGTCTCTATGTGCCAAGCAT 780
QY 1410 GGCATTGAATACCAAGAGAGCCCTACTAGAGGCCCTGCTGGACATCATCAGGTCCTTG 1469
DB 781 GGCATTGAATACCAAGAGAGCCCTACTAGAGGCCCTGCTGGACATCATCAGGTCCTTG 840
QY 1470 AAGAAGTCTGGGAAGCTGTGGCTGGAGCGCTACCTTCACAAAATGAAGCCACAGCCCCGG 1529
DB 841 AAGAAGTCTGGGAAGCTGTGGCTGGAGCGCTACCTTCACAAAATGAAGCCACAGCCCCGG 900
QY 1530 GACACCGTGGGAAGGGGTGAGTGGGGTGATGGCCAGAGGATGATGGGCTTTGTTC 1589
DB 901 GACACCGTGGGAAGGGGTGAGTGGGGTGATGGCCAGAGGATGATGGGCTTTGTTC 960
QY 1590 TGAGGGGTGTCCGAGAGGGCTGTGTATGCACTGTCTACGGACCCCATGTGTGATCTTCT 1649
DB 961 TGAGGGGTGTCCGAGAGGGCTGTGTATGCACTGTCTACGGACCCCATGTGTGATCTTCT 1020
QY 1650 CCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1709
DB 1021 CCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 1710 CTGCCCCCTCTCAGCCGCTCAGCCCATCAGCCCATCGGCCCTCTCCAGTGGCTCTCTAGCCCCCTTC 1769
DB 1081 CTGCCCCCTCTCAGCCGCTCAGCCCATCAGCCCATCGGCCCTCTCCAGTGGCTCTCTAGCCCCCTTC 1140
QY 1770 TTCCAGAGAGCAGAGAGGTGGCCACCGGGGTGGCTGTCTGTCTCTCTCTCTCTCTCTCTCTCT 1829
DB 1141 TTCCAGAGAGCAGAGAGGTGGCCACCGGGGTGGCTGTCTGTCTCTCTCTCTCTCTCTCTCTCT 1200

PS Example 9; Page 147-148; 161pp; English.

XX AAA14588-94 represent contigs of a human desaturase. The specification describes a Mortierella alpina delta5-desaturase. The protein is involved in the biosynthesis of poly-unsaturated long chain fatty acids (PUFAs). The polynucleotide is to produce PUFAs, especially arachidonic acid. The oils produced by the invention are used in pharmaceutical compositions, infant formulas, dietary supplements, dietary substitutes, and cosmetics. The nutritional compositions can be used to treat normal individuals temporally exposed to stress, or individuals having specialized needs due to chronic or acute diseases (e.g. metabolic disorders such as gastrointestinal difficulties and/or malabsorption, and other disorders such as restenosis after angioplasty, symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis, osteoporosis, kidney stones, tract stones, cancer, cachexia associated with cancer, diabetes, eczema, endometriosis, premenstrual syndrome, myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis, acute respiratory syndrome, hypertension, inflammatory skin disorders, as well as reduce blood score, inhibit platelet aggregation, cause vasodilatation, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, prevent or reduce gastro-intestinal bleeding, and for geriatric treatments).

SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Query Match 57.5%; Score 1830.4; DB 21; Length 1843;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 630 GTCTTTCTACTTTGGCAATGGCTGATTCCTACCTCATCAGCGCCCTTGTCTCTGCTAC 689
DB 1 GTCTTTTACTTTGGCAATGGCTGATTCCTACCTCATCAGCGCCCTTGTCTCTGCTAC 60

QY 690 TCTCAGGCCCAAGCTGGATGGTGCACATGATATGCGCACCTGTCTGTCTACAGAAA 749
DB 61 TCTCAGGCCCAAGCTGGATGGTGCACATGATATGCGCACCTGTCTGTCTACAGAAA 120

QY 750 CCCAAGTGGAAACCACTGTGCCAAATTCGTATTGGCCACTTAAAGGGTGCCCTGCGC 809
DB 121 CCCAAGTGGAAACCACTGTGCCAAATTCGTATTGGCCACTTAAAGGGTGCCCTGCGC 180

QY 810 AACTGTGTGAATCATGCCCACTTCCAGCACCAAGCCCAAGCTTAACTTCCACAGGAT 869
DB 181 AACTGTGTGAATCATGCCCACTTCCAGCACCAAGCCCAAGCTTAACTTCCACAGGAT 240

QY 870 CCGGATGTGAATCATGCCCACTTCCAGCACCAAGCCCAAGCTTAACTTCCACAGGAT 929
DB 241 CCGGATGTGAATCATGCCCACTTCCAGCACCAAGCCCAAGCTTAACTTCCACAGGAT 300

QY 930 AAGAAGAGCTGAATACCTGCCCTAACAATCCAGCAGCAATATCTTCTCTGATGGG 989
DB 301 AAGAAGAGCTGAATACCTGCCCTAACAATCCAGCAGCAATATCTTCTCTGATGGG 360

QY 990 CCGCGCTGTCTATCCCACTGATTTCCAGTACCATCATATGACCATGATCGTCCAT 1049
DB 361 CCGCGCTGTCTATCCCACTGATTTCCAGTACCATCATATGACCATGATCGTCCAT 420

QY 1050 AAGAATCTGGGTGGACCTGGCGGTGAGTACTTACATCCGGTCTTCTCATCACTAC 1109
DB 421 AAGAATCTGGGTGGACCTGGCGGTGAGTACTTACATCCGGTCTTCTCATCACTAC 480

QY 1110 ATCCCTTTTACGGCATCTGGAGCCCTCTTTTCTTCTCACTTCATCAGTTCCTGGAG 1169
DB 481 ATCCCTTTTACGGCATCTGGAGCCCTCTTTTCTTCTCACTTCATCACTTCCTGGAG 540

QY 1170 AGCCACTGGTGTGGGTGCACACAGATGAATACATCGTATGAGATGACACAGGAG 1229
DB 541 AGCCACTGGTGTGGGTGCACACAGATGAATACATCGTATGAGATGACACAGGAG 600

QY 1230 GCCTACCGTGTGATGGTTCAGTACCGACTGACAGCCACTTGGACGTGGAGGAGTCTTTC 1289
DB 601 GCCTACCGTGTGATGGTTCAGTACCGACTGACAGCCACTTGGACGTGGAGGAGTCTTTC 660

QY 1290 TTCAACGACTGGTTCAGTGGACACACCTTAACCTTCCAGATTGAGCACCACCTTCTTCCCCACC 1349
DB 661 TTCAACGACTGGTTCAGTGGACACACCTTAACCTTCCAGATTGAGCACCACCTTCTTCCCCACC 720

QY 1350 ATGCCCGGCGACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTCCAGGAT 1409
DB 721 ATGCCCGGCGACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTCCAGGAT 780

QY 1410 GGCATTGAATATACACAGAGAACCGCTTACTGAGGGCCCTCTCTGACATCATCAGGTCCCTG 1469
DB 781 GGCATTGAATATACACAGAGAACCGCTTACTGAGGGCCCTCTCTGACATCATCAGGTCCCTG 840

QY 1470 AAGAAGTCTGGAGAGCTGTGGCTGGAGCGCTACTTCAAAATGAGCCACAGCCCCCGG 1529
DB 841 AAGAAGTCTGGAGAGCTGTGGCTGGAGCGCTACTTCAAAATGAGCCACAGCCCCCGG 900

QY 1530 GACACCGTGGGGAAGGGGTGCAGGTGGGTGTATGGCCAGAGGAATGATGGGCTTTGTTC 1589
DB 901 GACACCGTGGGGAAGGGGTGCAGGTGGGTGTATGGCCAGAGGAATGATGGGCTTTGTTC 960

QY 1590 TGAGGGGTGTCCAGAGAGGTGTGTATGACATGCTCAGGACCCCATGTGATCTTCT 1649
DB 961 TGAGGGGTGTCCAGAGAGGTGTGTATGACATGCTCAGGACCCCATGTGATCTTCT 1020

QY 1650 CCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1709
DB 1021 CCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080

QY 1710 CTGCCCCCTCCAGCGCTGAGCCATCAGCCATGGCCCTCCAGTGCCTCTAGCCCCCTTC 1769
DB 1081 CTGCCCCCTCCAGCGCTGAGCCATCAGCCATGGCCCTCCAGTGCCTCTAGCCCCCTTC 1140

QY 1770 TTCCAGAGGACAGAGAGGTGGCCACCGGGGTGGCTCTGTCTCTCTCTCTCTCTCTCTCTCT 1829
DB 1141 TTCCAGAGGACAGAGAGGTGGCCACCGGGGTGGCTCTGTCTCTCTCTCTCTCTCTCTCTCT 1200

QY 1830 CTAAAGATGGAGAGAGACAGCGGTCCATGGGTCTGGCTGTGAGTCTCCCTCTGAGCC 1889
DB 1201 CTAAAGATGGAGAGAGACAGCGGTCCATGGGTCTGGCTGTGAGTCTCCCTCTGAGCC 1260

QY 1890 TGGTCACTAGGCATCACCCCGCTTTGGTCTTTCAGATGCTCTTGGGTTCATAGGGGCA 1949
DB 1261 TGGTCACTAGGCATCACCCCGCTTTGGTCTTTCAGATGCTCTTGGGTTCATAGGGGCA 1320

QY 1950 GGTCTCTAGTCCGGCAGGGCCCTGACCCCTCCCGGCTGGCTTCACTCTCCCTGACGGCTG 2009
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QY 2010 CCATTTGGTCCACCCCTTTTCATAGAGAGCGCTTGTGTTTACAAAGCTCGGCTCTCCCTCTCT 2069
DB 1381 CCATTTGGTCCACCCCTTTTCATAGAGAGCGCTTGTGTTTACAAAGCTCGGCTCTCCCTCTCT 1440

QY 2070 GCAGCTCGGTAAAGTACCCGAGGCTCTCTTAAAGATCTCAGGGCCCGCAGGGCCCGGGCC 2129
DB 1441 GCAGCTCGGTAAAGTACCCGAGGCTCTCTTAAAGATCTCAGGGCCCGCAGGGCCCGGGCC 1500

QY 2130 ACAGCCAGCCCAAACTTTGGCCCTTGGAGAGTCTCCACCCCATCACTAGAGTCTCTG 2189
DB 1501 ACAGCCAGCCCAAACTTTGGCCCTTGGAGAGTCTCCACCCCATCACTAGAGTCTCTG 1560

QY 2190 ACCCTGGGCTTTACGGGGCCCTTTCACCGCCCTCCCAAACTTGAGCCTGTGACCTTGGG 2249
DB 1561 ACCCTGGGCTTTACGGGGCCCTTTCACCGCCCTCCCAAACTTGAGCCTGTGACCTTGGG 1620

QY 2250 ACCAAAGGGGAGTCTCTGCTCTCTGACTCAGCAGGAGCAGTGGCCAGGTCAGGGA 2309
DB 1621 ACCAAAGGGGAGTCTCTGCTCTCTGACTCAGCAGGAGCAGTGGCCAGGTCAGGGA 1680

QY 2310 GGGGCGGCTGGCTGGAGGCTCAGCCCATCCCTCCAGCTTTTCTCAGGGTGTCTCTGAGG 2369
DB 1681 GGGGCGGCTGGCTGGAGGCTCAGCCCATCCCTCCAGCTTTTCTCAGGGTGTCTCTGAGG 1740

QY 2370 TCCAAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTTATCAGCTGGGCGAGTGC 2429

Db	1741	TCCAAGATTCTGGAGCAATCTGACCTTCTCCAAAGGCTCTGTATACAGCTGGGAGTGC	1800
Qy	2430	CAGCCAAATCCCTGGCCATTGGCCCGCCAGGGGACGTGGGCCCTG	2473
Db	1801	CAGCCAAATCCCTGGCCATTGGCCCGCCAGGGGACGTGGGCCCTG	1843
RESULT 25			
ABS71825			
ID	ABS71825	standard; DNA; 1843 BP.	
XX	ABS71825;		
AC	ABS71825;		
XX	02-DEC-2002	(first entry)	
DT	02-DEC-2002	(first entry)	
XX	Human	deltas-desaturase gene #7.	
DE	Human;	deltas-desaturase; polyunsaturated fatty acid; DGLA;	
XX	Human;	deltas-desaturase; polyunsaturated fatty acid; DGLA;	
KW	dihomo-gamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;		
KW	eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;		
KW	gene; ds.		
XX	Homo sapiens.		
OS	US6432684-B1.		
XX	13-AUG-2002.		
PD	08-JAN-1999;	99US-0227613.	
XX	11-APR-1997;	97US-0833610.	
XX	10-APR-1998;	98WO-US07422.	
PR	(ABBO)	ABBOTT LAB.	
PA	Mukerji P, Leonard AE, Huang Y, Das T;		
XX	WPI; 2002-689761/74.		
PI	Nucleic acids encoding human DELTAS-desaturase, useful for catalysing		
XX	the conversion of dihomogamma-linolenic acid to arachidonic acid and		
PT	in the conversion of 20:4n-3 to eicosapentaenoic acid -		
XX	Example 1; Figure 7; 88pp; English.		
PS	The invention relates to an isolated human deltas-desaturase nucleotide		
XX	sequence (I) which desaturates polyunsaturated fatty acids at		
CC	carbon 5. The nucleotide sequence (I) may be used in the recombinant		
CC	production of vectors and host cells for the production of deltas-		
CC	desaturase. Deltas-desaturase may be utilised in the conversion of		
CC	dihomo-gamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the		
CC	conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA Or		
CC	polyunsaturated fatty acids produced from it may be added to		
CC	pharmaceutical compositions, nutritional compositions, animal feeds, as		
CC	well as other products such as cosmetics. ABS71819-ABS71854		
CC	represent human deltas-desaturase coding sequences and PCR primers of		
CC	the invention.		
XX	Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;		
SQ			
Query Match 57.5%; Score 1830.4; DB 24; Length 1843;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
Qy	630	GTCTTCTACTTTGGCAATGGCTGGATTCTTACCTCATCAGGCTTGTCTGTCTTAC	689
Db	1	GTCTTCTACTTTGGCAATGGCTGGATTCTTACCTCATCAGGCTTGTCTGTCTTAC	60
Qy	690	TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGCCACCTGTCTGTCTACAGAAA	749
Db	61	TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGCCACCTGTCTGTCTACAGAAA	120

Qy	750	CCCAAGTGGAAACCACTTGTCTCCAAATTCGTTCATTTGGCCACTTAAAGGGTCTCTCTGCC	809
Db	121	CCCAAGTGGAAACCACTTGTCTCCAAATTCGTTCATTTGGCCACTTAAAGGGTCTCTCTGCC	180
Qy	810	AACGTGTGAATCATCGCCACTTCCAGCACCAGCCCAAGCCTAAACATCTTCCAAAGGAT	869
Db	181	AACGTGTGAATCATCGCCACTTCCAGCACCAGCCCAAGCCTAAACATCTTCCAAAGGAT	240
Qy	870	CCCGATGTGAACATGTGCACGTGTTTGTCTCTGGGGAATGGCAGCCCATCGAGTACGGC	929
Db	241	CCCGATGTGAACATGTGCACGTGTTTGTCTCTGGGGAATGGCAGCCCATCGAGTACGGC	300
Qy	930	AAGAAGAGCTGAAATACCTTGCCTCAATCAATCAACAGCAGGAATCTTCTTCTGATTGGG	989
Db	301	AAGAAGAGCTGAAATACCTTGCCTCAATCAATCAACAGCAGGAATCTTCTTCTGATTGGG	360
Qy	990	CCGCCGTCTCATCCCATGTAATTTCCAGTACAGATCATCATGACCATGATGCTCCAT	1049
Db	361	CCGCCGTCTCATCCCATGTAATTTCCAGTACAGATCATCATGACCATGATGCTCCAT	420
Qy	1050	AAGAACTGGGTGACCTGGCGCTGGCGCTGAGTACTACATCCGGTTCTTTCATCAGCTAC	1109
Db	421	AAGAACTGGGTGACCTGGCGCTGGCGCTGAGTACTACATCCGGTTCTTTCATCAGCTAC	480
Qy	1110	ATCCCTTTCTACGGCATCTGGAGCCCTCTTCTTCTCACTTCACTCATGAGTTCTCTGGAG	1169
Db	481	ATCCCTTTCTACGGCATCTGGAGCCCTCTTCTTCTCACTTCACTCATGAGTTCTCTGGAG	540
Qy	1170	AGCCACTGTTTGTGTGGGTACACAGATCAATCAATCATCTGTATGGAGATTGACCCAGGAG	1229
Db	541	AGCCACTGTTTGTGTGGGTACACAGATCAATCAATCATCTGTATGGAGATTGACCCAGGAG	600
Qy	1230	GCCTACCTGTGATGGTTTCACTAGCAGCTGACAGCCACTGTCGAACTGTCGAGTCTTTC	1289
Db	601	GCCTACCTGTGATGGTTTCACTAGCAGCTGACAGCCACTGTCGAACTGTCGAGTCTTTC	660
Qy	1290	TTCAACGACTGTTTGTGTGGGTACACAGATCAATCAATCATCTGTATGGAGATTGACCCAGG	1349
Db	661	TTCAACGACTGTTTGTGTGGGTACACAGATCAATCAATCATCTGTATGGAGATTGACCCAGG	720
Qy	1350	ATGCCCCGGGCAAACTTACAAAGATCGCCCGCTGTGTGAAGTCTTATGTGCCAAGAT	1409
Db	721	ATGCCCCGGGCAAACTTACAAAGATCGCCCGCTGTGTGAAGTCTTATGTGCCAAGAT	780
Qy	1410	GGCAATTGATACCAAGAGAGCCCTTACTGAGGGCCCTGTGAGCATCATCAGTCTCTG	1469
Db	781	GGCAATTGATACCAAGAGAGCCCTTACTGAGGGCCCTGTGAGCATCATCAGTCTCTG	840
Qy	1470	AAGAAGTCTGGGAAGCTGTGCTGGAGCCCTTACCTTCAAAATGAAGCCACAGCCCGCG	1529
Db	841	AAGAAGTCTGGGAAGCTGTGCTGGAGCCCTTACCTTCAAAATGAAGCCACAGCCCGCG	900
Qy	1530	GACACCGTGGGAAGGGGTGAGTGGGTGATGGCCAGAGGAATGATGGCTTTTGTTC	1589
Db	901	GACACCGTGGGAAGGGGTGAGTGGGTGATGGCCAGAGGAATGATGGCTTTTGTTC	960
Qy	1590	TGAGGGGTGTCGAGAGGCTGTGTATGCTACCTGTCTCAGGACCCCATGTTGGATCTTCT	1649
Db	961	TGAGGGGTGTCGAGAGGCTGTGTATGCTACCTGTCTCAGGACCCCATGTTGGATCTTCT	1020
Qy	1650	CCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1709
Db	1021	CCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1080
Qy	1710	CTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1769
Db	1081	CTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1140
Qy	1770	TTCCAAAGGAGCAGAGAGTGGCCACCGGGGGTGGTCTGTCTCTCTCTCTCTCTCTCTCT	1829
Db	1141	TTCCAAAGGAGCAGAGAGTGGCCACCGGGGGTGGTCTGTCTCTCTCTCTCTCTCTCTCT	1200
Qy	1830	CTAAAGATGGGAGGAGACCGGGGTCCATGGGTCTGGGCTGTGAGTCTCTCTCTCTCTCT	1889

QY 870 CCGATGTGAACATGCTGACAGTGTGTTGTTCTGGGGAATGACGCCATCGAGTACGGC 929
Db 241 CCGATGTGAACATGCTGACAGTGTGTTGTTCTGGGGAATGACGCCATCGAGTACGGC 300
QY 930 AAGAAGAGCTGAATACCTGCGCTCAATACACAGACAGAAATCTTCTCTGATTTGG 989
Db 301 AAGAAGAGCTGAATACCTGCGCTCAATACACAGACAGAAATCTTCTCTGATTTGG 360
QY 990 CCGCGCTGCTCATCCCATGATTTCCAGTACCCAGATCATCATGACATGATCTCCAT 1049
Db 361 CCGCGCTGCTCATCCCATGATTTCCAGTACCCAGATCATCATGACATGATCTCCAT 420
QY 1050 AAGAAGCTGGTGGACCTGCGCTGCGCTGAGTACTACATCCGCTTCTTCACTAC 1109
Db 421 AAGAAGCTGGTGGACCTGCGCTGCGCTGAGTACTACATCCGCTTCTTCACTAC 480
QY 1110 ATCCCTTTCTACGGCATCTGGAGGCCCTCTTCTCACTCATCAGGTTCTGGAG 1169
Db 481 ATCCCTTTCTACGGCATCTGGAGGCCCTCTTCTCACTCATCAGGTTCTGGAG 540
QY 1170 AGCCACTGGTGTGTTGTTGGTTCACACAGATGAATCACATGTCATGAGATTGACAGGAG 1229
Db 541 AGCCACTGGTGTGTTGTTGGTTCACACAGATGAATCACATGTCATGAGATTGACAGGAG 600
QY 1230 GCCTACGCTGACTGGTTCAGTAGCCAGCTGACAGCCACCTGCAACGCTGAGAGTCTTC 1289
Db 601 GCCTACGCTGACTGGTTCAGTAGCCAGCTGACAGCCACCTGCAACGCTGAGAGTCTTC 660
QY 1290 TTCAAAGACTGGTTCAGTGACACCTTAACTTCCAGATTGACACCACTCTTCCCA 1349
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QY 1410 GGCAATTGAATACAGAGAGCGCTACTGAGGCGCTGCTGACATCATCAGTCTCCCTG 1469
Db 781 GGCAATTGAATACAGAGAGCGCTACTGAGGCGCTGCTGACATCATCAGTCTCCCTG 840
QY 1470 AAGAAGTCTGGAGTCTGGCTGGAGCGCTACCTTCAAAATGAAGCCACAGCCCGG 1529
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QY 1530 GACACCTGGGAGGGGTGACGTGGGTGATGGCCAGAGGAATCATGGCTTTTGTTC 1589
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QY 1590 TGAGGGGTGTCGAGAGGGTGGTGTATGCACTGCTCAAGACCCCATGTTGATCTTCT 1649
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QY 1650 CCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1709
Db 1021 CCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
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QY 1770 TTCAAGAGCAGAGAGTGGCCACCGGGGTGGCTGTCTCTCTCTCTCTCTCTCTCTCT 1829
Db 1141 TTCAAGAGCAGAGAGTGGCCACCGGGGTGGCTGTCTCTCTCTCTCTCTCTCTCTCT 1200
QY 1830 CTAAGATGGAGAGACAGCGCTCACTGGGCTGTGGCTGTGAGTCTCTCTCTCTCTCT 1889
Db 1201 CTAAGATGGAGAGACAGCGGTCACTGGGCTGTGGCTGTGAGTCTCTCTCTCTCTCT 1260
QY 1890 TGGTCACTAGGCATCAACCCCGCTTTGGTCTTTCAGATGCTCTTGGGTTTCATAGGGCA 1949
Db 1261 TGGTCACTAGGCATCAACCCCGCTTTGGTCTTTCAGATGCTCTTGGGTTTCATAGGGCA 1320

RESULT 27
AAS32517

ID AAS32517 standard; DNA; 29521 BP.

XX AAS32517;

AC AAS32517;

DT 17-DEC-2001 (first entry)

XX Human genomic DNA for novel endocrine antigen, SEQ ID No 471.
XX Human; endocrine antigen; ds; cytostatic; antiinfertility; antidiabetic;
KW thyroid-active; adrenal-active; androgenic; gastric; gene therapy;
KW antisenescence-therapeutic; antibody; endocrine disorder; hormone imbalance;
KW reproductive disorder; endocrine cancer; pancreatic disorder;
KW diabetes mellitus; adrenal gland disorder; hirsutism; thyroid disorder;
KW hyperthyroidism; hypothalamic disorder; vanishing testes syndrome.

XX Homo sapiens.

XX WO20015319-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01335.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

condition or a susceptibility to a pathological condition. The DNAs, antigens and antibodies raised against the antigens useful for treating, preventing and/or prognosing disorders related to the endocrine system or hormone imbalance or reproductive disorders, cancers of endocrine tissues, disorders of the pancreas (e.g. diabetes mellitus), the adrenal glands (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the hypothalamus and testes (e.g. vanishing testes syndrome), many examples of diseases and disorders are given in the specification. The present sequence is genomic DNA fragment form a gene encoding an endocrine antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct/sequences](http://wipo.int/pub/published/pct/sequences).

Sequence 29521 BP: 6369 A: 8019 C: 7628 G: 7505 T: 0 other;

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Query Match      53.5%; Score 1703.4; DB 22; Length 29521;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
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DB Human genomic DNA for novel endocrine antigen, SEQ ID No 470.
XX Human; endocrine antigen; ds; cytostatic; antifertility; antidiabetic;
KW thyroid-active; adrenal-active; androgenic; gastric; gene therapy;
KW antisense-therapy; antibody; endocrine disorder; hormone imbalance;
KW reproductive disorder; endocrine cancer; pancreatic disorder;
KW diabetes mellitus; adrenal gland disorder; hirsutism; thyroid disorder;
KW hyperthyroidism; hypothalamic disorder; vanishing testes syndrome.
OS Homo sapiens.
XX WO200155319-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01335.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
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PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
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PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
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 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-457726/49.
 DR
 XX Isolated polypeptide for treating, preventing and prognosing disorders
 PT related to the endocrine system including endocrine disorders,
 PT reproductive disorders, and gastrointestinal disorders and also for
 PT testing and detection e.g. diagnosis -
 XX
 PS Disclosure; SEQ ID No 470; 558pp; English.
 XX
 CC The invention relates to cDNAs encoding novel human endocrine
 CC antigens or a fragment having biological activity, a domain, an epitope,
 CC full length protein, variant, allelic variant or a species homologue of
 CC the cDNA/antigen. The DNAs and polypeptides are useful for preventing,
 CC treating or ameliorating a medical condition when administered
 CC (e.g. by gene therapy or antisense-therapy). Identifying mutations in
 CC the genes coding for the antigens is useful for diagnosing a pathological
 CC condition or a susceptibility to a pathological condition. The DNAs,
 CC antigens and antibodies raised against the antigens useful for treating,
 CC preventing and/or prognosing disorders related to the endocrine system
 CC or hormone imbalance or reproductive disorders, cancers of endocrine
 CC tissues, disorders of the pancreas (e.g. diabetes mellitus), the adrenal
 CC glands (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the
 CC hypothalamus and testes (e.g. vanishing testes syndrome), many examples
 CC of diseases and disorders are given in the specification. The present
 CC sequence is genomic DNA fragment form a gene encoding an endocrine
 CC antigen of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 29543 BP; 6367 A; 8023 C; 7634 G; 7519 T; 0 other;
 Query Match 53.5%; Score 1703.4; DB 22; Length 29543;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1721; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
 QY 1442 GGCCCTGTGGACATCATCAGTCCCTGAAGAAGTCTGGGAAGCTGTGGCTGGACGCTA 1501
 DB GTTCCATCCCCAATTTCAGGTCCCTGAAGAGTCTGGGAAGCTGTGGCTGGACGCTA 27865
 QY 1502 CTTTCAAAATGAAGCCACAGCCCCCGGGACACCGTGGGGAAGGGGTGACGTTGGGTGA 1561
 DB CTTTCAAAATGAAGCCACAGCCCCCGGGACACCGTGGGGAAGGGGTGACGTTGGGTGA 27925
 QY 1562 TGGCCAGAGGAATGATGGCTTTTCTGTGAGGGGTGTCCAGAGGCTGGGTATGCACT 1621
 DB TGGCCAGAGGAATGATGGCTTTTCTGTGAGGGGTGTCCAGAGGCTGGGTATGCACT 27985
 QY 1622 GCTACGAGACCCCATGTTGGATCTTCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1681
 DB GCTACGAGACCCCATGTTGGATCTTCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 27986
 QY 1682 CCCCCTATGACCCCTGCTCATGGAGCTGCTCCCTCCCTCAGCCGTGAGCCATCAGCCAT 1741
 DB CCCCCTATGACCCCTGCTCATGGAGCTGCTCCCTCCCTCAGCCGTGAGCCATCAGCCAT 28045
 QY 1742 GGCCTTCCAGTGCCTCTAGCCCTTCTTCCAGAGGACAGAGAGGTGGCCACCGGGGGT 1801
 DB GGCCTTCCAGTGCCTCTAGCCCTTCTTCCAGAGGACAGAGAGGTGGCCACCGGGGGT 28105
 QY 28106 GGCCTTCCAGTGCCTCTAGCCCTTCTTCCAGAGGACAGAGAGGTGGCCACCGGGGGT 28165

QY 1802 GGCTCTGTCTACCTCCACTCTCTGCCCTTAAGATGGAGGAGACCAAGCGTGCATGGG 1861
 DB GGCTCTGTCTACCTCCACTCTCTGCCCTTAAGATGGAGGAGACCAAGCGTGCATGGG 28166
 QY 1862 TCTGGCCTGTGAGTCTCCCTTTTCAGACCTGGTCACTAGGCATCAACCCCGCTTTGGTTCT 1921
 DB TCTGGCCTGTGAGTCTCCCTTTTCAGACCTGGTCACTAGGCATCAACCCCGCTTTGGTTCT 28226
 QY 1922 TCAGATGCTCTTGGGGTTCATAGGGGCGAGTCTAGTGGGCGAGGCGCCCTGACCTCC 1981
 DB TCAGATGCTCTTGGGGTTCATAGGGGCGAGTCTAGTGGGCGAGGCGCCCTGACCTCC 28286
 QY 1982 GGCTCTGGCTTCACTCTCCCTGACGGCTGCACTTGGTCCACCTTTTCATAGAGAGGCTGC 2041
 DB GGCTCTGGCTTCACTCTCCCTGACGGCTGCACTTGGTCCACCTTTTCATAGAGAGGCTGC 28345
 QY 2042 TTTGTTACAAAGCTCGGGTCTCCCTCTGACGCTGGTTAAGTACCGAGGGCTCTCTTTA 2101
 DB TTTGTTACAAAGCTCGGGTCTCCCTCTGACGCTGGTTAAGTACCGAGGGCTCTCTTTA 28405
 QY 2102 AGATGTCCAGGGGCCCGGCGGCGACAGCCAGCCCAACCTTTGGGCCCTTGAAGAG 2161
 DB AGATGTCCAGGGGCCCGGCGGCGACAGCCAGCCCAACCTTTGGGCCCTTGAAGAG 28466
 QY 2162 TCTTCCACCCCATCACTAGAGTGTCTGACCTGGCTTTTCAGGGGCCCTTTCACCGC 2221
 DB TCTTCCACCCCATCACTAGAGTGTCTGACCTGGCTTTTCAGGGGCCCTTTCACCGC 28525
 QY 2222 CTCCCAACTTGGACCTGTGACCTTGGGACCAAGGGGAGTCCCTGCTCTTGTGACT 2281
 DB CTCCCAACTTGGACCTGTGACCTTGGGACCAAGGGGAGTCCCTGCTCTTGTGACT 28585
 QY 2282 CAGCAGAGGAGTGGCCACGTTTCAGGGAGGGCGCGCTGGCTGAGGCTCAGCCACCC 2341
 DB CAGCAGAGGAGTGGCCACGTTTCAGGGAGGGCGCGCTGGCTGAGGCTCAGCCACCC 28645
 QY 2342 TCCAGCTTTTCTCAGGGTGTCTGAGGTGCCAAGATTTCTGAGCAATCTGACCTTCTCC 2401
 DB TCCAGCTTTTCTCAGGGTGTCTGAGGTGCCAAGATTTCTGAGCAATCTGACCTTCTCC 28705
 QY 2402 AAAGGCTCTGTTATCAGCTGGGACGTCAGCAATTCCTGGCCATTTGGCCCCAGGGGG 2461
 DB AAAGGCTCTGTTATCAGCTGGGACGTCAGCAATTCCTGGCCATTTGGCCCCAGGGGG 28765
 QY 2462 ACCTGGGCCCTGACGCTCAGAGGGGCTGAGGCTGGAGGTCTCGTCCAGCCCTCC 2521
 DB ACCTGGGCCCTGACGCTCAGAGGGGCTGAGGCTGGAGGTCTCGTCCAGCCCTCC 28824
 QY 2522 CCATCTCGGGGCTGTGTGTGGACGGCGCTGCTCAGGCACCTCTCTGTCTGAACTGCTC 2581
 DB CCATCTCGGGGCTGTGTGTGGACGGCGCTGCTCAGGCACCTCTCTGTCTGAACTGCTC 28884
 QY 2582 CTTTACTGTGTTAACTGTGTCTCAGGATGATTTCTGATAGAGGGGGCGGAGGCTG 2641
 DB CTTTACTGTGTTAACTGTGTCTCAGGATGATTTCTGATAGAGGGGGCGGAGGCTG 28944
 QY 2642 GGCTTTGTGACCAATCTGCTCTTTCACCAATGCTGCTCGGTGGCCCTGCTGCTGCTGCT 2701
 DB GGCTTTGTGACCAATCTGCTCTTTCACCAATGCTGCTCGGTGGCCCTGCTGCTGCTGCT 29004
 QY 2701 GAGGGCCAGGAGGACAGCGGAGTCTCAGAGAGGCTGCTCAGAGGAGGCTGCTGAGGGCTG 2761
 DB GAGGGCCAGGAGGACAGCGGAGTCTCAGAGAGGCTGCTCAGAGGAGGCTGCTGAGGGCTG 29064
 QY 2762 GAGGGGCTACCTCATGAGGACCAAGGGTGGAGCTGAGAGAGGAGGAGTGGGGGCTGGAG 2814
 DB GAGGGGCTACCTCATGAGGACCAAGGGTGGAGCTGAGAGAGGAGGAGTGGGGGCTGGAG 29184
 QY 2814 GTGCTGCTGAGTGAAGGGACGGGCAAGTGAAGGGAGGAGGAGGAGTCTCTGGAGGATC 2881
 DB GTGCTGCTGAGTGAAGGGACGGGCAAGTGAAGGGAGGAGGAGGAGTCTCTGGAGGATC 29185
 QY 2882 CTGAGCTGTGTTGAGTCTAACCCACTAATCAGTTCTTTAGATTTCAGGGGAGGAGGCT 2941

D _b	29245	CTGAGCTGCTGTTGTCAGTCTAAACCCCACTAATCAGTCTCTTAGATTGAGGGGAAGGCGCAGGC	29304
Q _Y	2942	ACCAACAACCTCAGAAATGGGGGGCTTTTCGGGGAGGGCGCCCTAGTCCCCCGCAGCTCTAAGCAG	3001
D _b	29305	ACCAACAACCTCAGAAATGGGGGGCTTTTCGGGGAGGGCGCCCTAGTCCCCCGCAGCTCTAAGCAG	29364
Q _Y	3002	CCAGGAGGAGCACCTGTCATCTAAAGCATCTCGGTGTTGCCATGGCAATGSCATGCCCCCGCAGCTA	3061
D _b	29365	CCAGGAGGAGCACCTGTCATCTAAGCATCTCGGTGTTGCCATGGCAATGSCATGCCCCCGCAGCTA	29424
Q _Y	3062	CTGTATGCCCGCCGACCCCGCGAGGCGAGAGAAATGAACCCATAGGGAGCTGATCGTAAATGTT	3121
D _b	29425	CTGTATGCCCGCCGACCCCGCGAGGCGAGAGAAATGAACCCATAGGGAGCTGATCGTAAATGTT	29484
Q _Y	3122	TATCATGTTACTTCCCAACCCCTACATTTTTTTGAAATAAAATAAGGAATTTTA	3174
D _b	29485	TATCATGTTACTTCCCAACCCCTACATTTTTTTGAAATAAAATAAGGAATTTTA	29537

RESULT 29
ABT10147/C
ID ABT10147 standard; CDNA; 185035 BP.
XX
XX ABT10147;
XX AC
XX DT
XX 04-DEC-2002 (first entry)
XX
DE Human breast cancer associated coding sequence SEQ ID NO: 281.

xx The present invention relates to methods of diagnosing breast cancer in a
cc patient, which comprise detecting the level of expression in a tissue
cc sample of two or more genes selected from those shown in ABR09867.
cc ABR1112, where a differential expression of the genes indicates breast
cc cancer. The methods are useful in diagnosing, treating, detecting the
cc progression, and in monitoring treatment of breast cancer in patients.
cc The methods are also useful as a screening tool for agents that modulate
cc the onset or progression of breast cancer. The breast cancer genes may be
cc used as diagnostic markers for the prediction or identification of the
cc malignant state of breast tissue, for confirming the type and progression
cc of cancer, and for drug screening and assays. The present sequence is a
cc coding sequence of the invention.
cc Note: The sequence data for this patent did not form part of the printed
cc specification, but was obtained in electronic format directly from WIPO
cc at ftp.wipo.int/pub/published/pct sequences.

[illegible]

or plants containing them are used to produce oils such as linoleic acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are used: (i) to treat malnutrition; (ii) in infant feeding formulas, or dietary supplements or substitutes, for use in humans or animals; (iii) for treating disorders associated with inadequate consumption or production of PUFA (or their metabolites such as prostaglandins), e.g. restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis, psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and (v) as animal feeds. Fragments of the DNA are used as probes to isolate related coding sequences. Recombinant plants can produce high yields of PUFA, since new pathways can be created and unwanted ones suppressed. Plants can be engineered to express oils of particular PUFA composition, e.g. one similar to that in human milk, and product recovery is simpler than with e.g. fish. Sequences AAX00904-910 represent DNA sequences of various contigs of human desaturase genes which are similar to the M. alpina desaturase sequences.

Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;

Query Match	52.6%	Score 1675;	DB 20;	Length 1686;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1686;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
QY	787	GCACCTTAAAGGGTCCCTCTGCCAACTGGTGGAAATCATCGCCACTTCGCACTCCAGCACCAACGCCCA	846	
Db	1	GCACCTTAAAGGGTCCCTCTGCCAACTGGTGGAAATCATCGCCACTTCGCACTCCAGCACCAACGCCCA	60	
QY	847	AGCCTAACTCTTCCACAAGGATCCCGATGTGAACATGCTGCACGTGTTTGTCTTGGGCG	906	
Db	61	AGCCTAACTCTTCCACAAGGATCCCGATGTGAACATGCTGCACGTGTTTGTCTTGGGCG	120	
QY	907	AATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAAATACCTGCCCTACATCATCACCAGC	966	
Db	121	AATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAAATACCTGCCCTACATCATCACCAGC	180	
QY	967	ACGAATACTTCTTCCTGATTGGGCGCGCTGCTCATCCCCATCTATTTCAGTACCAGA	1026	
Db	181	ACGAATACTTCTTCCTGATTGGGCGCGCTGCTCATCCCCATCTATTTCAGTACCAGA	240	
QY	1027	TCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCTGGCGCGCTCAGCTACT	1086	
Db	241	TCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCTGGCGCGCTCAGCTACT	300	
QY	1087	ACATCCGGTCTTCATCACCTACATCCCTTCTACGGCATCCTGGGAGCCCTCCTTTTCC	1146	
Db	301	ACATCCGGTCTTCATCACCTACATCCCTTCTACGGCATCCTGGGAGCCCTCCTTTTCC	360	
QY	1147	TCAACTTCATCAGGTTCCTGGAGAGCCACTGTTTGTGTGGTGCACACAGATGAATCACA	1206	
Db	361	TCAACTTCATCAGGTTCCTGGAGAGCCACTGTTTGTGTGGTGCACACAGATGAATCACA	420	
QY	1207	TCGTCATGGAGATTGACAGAGAGCCCTACCGTGACTGGTTCAGTAGCCAGCTGCACGCCA	1266	
Db	421	TCGTCATGGAGATTGACAGAGAGCCCTACCGTGACTGGTTCAGTAGCCAGCTGCACGCCA	480	
QY	1267	CCTGCACGTGGGAGCTCTCTTTCACAGACTGGTTTCAGTGGACACTTAACTTCAGA	1326	
Db	481	CCTGCACGTGGGAGCTCTCTTTCACAGACTGGTTTCAGTGGACACTTAACTTCAGA	540	
QY	1327	TTGAGCACCACTCTTCCCCACCATGCCCCGGGCACAACTTACACAAAGTCGCCCGCTGG	1386	
Db	541	TTGAGCACCACTCTTCCCCACCATGCCCCGGGCACAACTTACACAAAGTCGCCCGCTGG	600	
QY	1387	TGAAGTCTTATGTGCCAAGCATGGCATTTGAATACCAAGGAGAGCCGCTACTGAGGGCCC	1446	
Db	601	TGAAGTCTTATGTGCCAAGCATGGCATTTGAATACCAAGGAGAGCCGCTACTGAGGGCCC	660	
QY	1447	TGCTGGACATCATCAGTCCCTGAAGAAGTCTGGGAAGCTGTGGCTGGAGCGCTACCTTC	1506	
Db	661	TGCTGGACATCATCAGTCCCTGAAGAAGTCTGGGAAGCTGTGGCTGGAGCGCTACCTTC	720	
QY	1507	ACAAATGAAGCCACAGCGCCCCGGGACACCGTGGGGAAGGGGTGCAGGTGGGGTGAATGCC	1566	

XX	11-FEB-1999	(first entry)	
DT	Contig 2511785	encoding a desaturase enzyme.	
DE			
XX			
XX			
KW	Fatty acid; desaturase; polyunsaturated fatty acid;		
KW	malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;		
KW	cancer; diabetes; eczema; platelet aggregation; vasodilation;		
KW	cholesterol level; endometriosis; premenstrual syndrome;		
KW	myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;		
KW	acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.		
OS	Homo sapiens.		
XX			
XX	WO9846765-A1.		
XX	22-OCT-1998.		
XX	10-APR-1998;	98WO-US07422.	
XX	11-APR-1997;	97US-0833610.	
XX	(ABBO) ABBOTT LAB.		
PA	(CALJ) CALGENE LLC.		
XX	Chaudhary S, Huang Y, Knutzon D, Leonard AB, Mukerji P;		
PI	Thurmond J;		
XX	WPI: 1999-009334/01.		
DR	P-PSDB; AAW85133.		
XX	New nucleic acid encoding deltas and other desaturase enzymes -		
PT	useful in production of oils of increased arachidonic acid content,		
PT	used, e.g. for treating cancer, as foods, animal feeds and cosmetics		
XX	Claim 86; Pages 109-110; 153pp; English.		
XX	The present sequence encodes a human desaturase enzyme. The enzyme		
CC	sequence is used in the methods of the invention. The specification		
CC	describes methods for desaturating a fatty acid and for producing a		
CC	desaturated fatty acid by expressing increased levels of a desaturase.		
CC	The enzyme can be used for desaturating fatty acids. The enzyme can be		
CC	used to produce polyunsaturated fatty acids, which can be used for		
CC	treating malnutrition, in pharmaceutical compositions, in cosmetics or		
CC	in animal feed. The polyunsaturated fatty acids can be used for treating		
CC	e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,		
CC	asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.		
CC	They can also be used to inhibit platelet aggregation, cause		
CC	vasodilation, lower cholesterol levels, inhibit proliferation of vessel		
CC	wall smooth muscle and fibrous tissue, reduce or prevent		
CC	gastro-intestinal bleeding and other side effects caused by non-steroidal		
CC	anti-inflammatory drugs, prevent or treat endometriosis and premenstrual		
CC	syndrome, treat myalgic encephalomyelitis and chronic fatigue after		
CC	viral infections, treat AIDS, multiple sclerosis, acute respiratory		
CC	syndrome, hypertension and inflammatory skin disorders.		
XX			
SQ	Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;		
	Query Match	52.6%; Score 1675; DB 20; Length 1686;	
	Best Local Similarity	99.9%; Pred. No. 0;	
	Matches 1686; Conservative	0; Mismatches	0; Indels
		1; Gaps	1;
QY	787	GCCACTTAAAGGGTGCCCTCTGCCAACTGGTGGAAATCATCGGCACCTTCAGCACCA	846
Db	1	GCCACTTAAAGGGTGCCCTCTGCCAACTGGTGGAAATCATCGGCACCTTCAGCACCA	60
QY	847	AGCCTTAACATCTTCACAGAGATCCGATGTGAACATCTCAGCTGTCTTCTGGCG	906
Db	61	AGCCTTAACATCTTCACAGAGATCCGATGTGAACATCTCAGCTGTCTTCTGGCG	120
QY	907	AATGGCAGCCCATCGAGTACGGCAAGAGAAAGCTGAAATACCTGCCCTTACCAATCACCAGC	966
Db	121	AATGGCAGCCCATCGAGTACGGCAAGAGAAAGCTGAAATACCTGCCCTTACCAATCACCAGC	180

2047	Qy	TACAAAGCTCGGGTCTCCCTCTGAGCTCGGTTAAGTACCGAGGCGCTCTCTTAAGATG	2106
1261	Db	TACAAAGCTCGGGTCTCCCTCTGAGCTCGGTTAAGTACCGAGGCGCTCTCTTAAGATG	1320
2107	Qy	TCCAGGGCCCCAGCGCGGGGACAGCCAGCCAAACCTTTGGCGCCTGGAAGAGTCCTC	2166
1321	Db	TCCAGGGCCCCAGCGCGGGGACAGCCAGCCAAACCTTTGGCGCCTGGAAGAGTCCTC	1380
2167	Qy	CACCCCATCTAGAGTGCTCTGACCTGGCTTTTCACGGGCCCCATTCCACCGCCTCCC	2226
1381	Db	CACCCCATCTAGAGTGCTCTGACCTGGCTTTTCACGGGCCCCATTCCACCGCCTCCC	1440
2227	Qy	CACATTGAGCCTGTGACCTTTGGGACCAAGGGGGAGTCCCTCGTCTCTTGTACTCAGCA	2286
1441	Db	CACATTGAGCCTGTGACCTTTGGGACCAAGGGGGAGTCCCTCGTCTCTTGTACTCAGCA	1500
2287	Qy	GAGGCAGTGCCACGTTTCAGGGAGGGGCCGGCTGGCTGGAGGCTCAGCCCCACCTCCAG	2346
1501	Db	GAGGCAGTGCCACGTTTCAGGGAGGGGCCGGCTGGCTGGAGGCTCAGCCCCACCTCCAG	1560
2347	Qy	CTTTTCCTCAGGTTGCTCAGGTCCAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGG	2406
1561	Db	CTTTTCCTCAGGTTGCTCAGGTCCAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGG	1620
2407	Qy	CTCTGTATCAGCTGGGCAGTGCCAGGCCAATCCCTGGCCCAATTTGGCCCCCAGGGGACGTG	2466
1621	Db	CTCTGTATCAGCTGGGCAGTGCCAGGCCAATCCCTGGCCCAATTTGGCCCCA-GGGAGCTG	1679
2467	Qy	GGCCCTG 2473	
1680	Db	GGCCCTG 1686	

RESULT 33

AAA49937
ID AAA49937 standard: cDNA: 1686 bp.

XX
AC AAA49937;

DT 10-OCT-2000 (first entry)

DE Human delta-5-desaturase-related contig 2511785.

Delta-5-desaturase; human; polyunsaturated fatty acid;
KW
XX

arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid; KW
docosahexaenoic acid; nutrition; feedstuff; ss. KW

XX
SO
Homo sapiens

XX
PN WO200040705-A2.

XX
PD 13-JUL-2000.

XX 29-DEC-1999; 99WO-US3

XX
PR 08-JAN-1999; 99US-022761

XX PA (ABBO) ABBOTT LAB.

XX
PI Mukerji P, Leonard AEY, Huang Y, Parker-Barnes JM;
vv

(see AAA49935). These were combined to produce contig 2535 (see AAA49937). Full-length cDNA (see AAA49932) for human delta-5-desaturase (see AA935445) was subsequently obtained. Delta-5-desaturase catalyzes the conversion of dihomogamma-linolenic acid to arachidonic acid and of 20:4n-3 to eicosapentaenoic acid. Recombinant enzyme, expressed in prokaryotic or eukaryotic hosts using the isolated human delta-5-desaturase cDNA, can be used in the production of polyunsaturated fatty acids that may be added to nutritional, veterinary and pharmaceutical compositions.

XX
SQ Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;

847 QY AGCCTAACATCTTCCACAGGATCCCGATGTAACATGCTGCACTGTTTCTTGGGCG 906
Db AGCCTAACATCTTCCACAGGATCCCGATGTAACATGCTGCACTGTTTCTTGGGCG 120
907 QY AATGCGACCCATCGAGTACGCGACAGAGAGCTCAATACCTGCGCTACCAATCACCAGC 966
Db AATGCGACCCATCGAGTACGCGACAGAGAGCTCAATACCTGCGCTACCAATCACCAGC 180
967 QY ACGAATACCTTCTCTGATTTGGGCGCGCGCTCTCATCCCATGATTTCCAGTACCAGA 1026
Db ACGAATACCTTCTCTGATTTGGGCGCGCGCTCTCATCCCATGATTTCCAGTACCAGA 240
1027 QY TCATCATGACCATGATCGTCCATAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1086
Db TCATCATGACCATGATCGTCCATAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
1087 QY ACATCCGGTCTTCTCATCACTACCTATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTCC 1146
Db ACATCCGGTCTTCTCATCACTACCTATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTCC 360
1147 QY TCNACTTCATCAGTCTTCTGGAGAGCCACTGTTTGTGGTGCACAGATGATACACA 1206
Db TCNACTTCATCAGTCTTCTGGAGAGCCACTGTTTGTGGTGCACAGATGATACACA 420
1207 QY TCGTCATGAGATGACACGAGGCGCTACCGTGACTGGTTCACTAGCCAGCTGACAGCCA 1266
Db TCGTCATGAGATGACACGAGGCGCTACCGTGACTGGTTCACTAGCCAGCTGACAGCCA 480
1267 QY CCGTCAAGCTGGAGCAGTCTTCTCAAGACTGGTTCAGTGGACACCTTAACTTCCAGA 1326
Db CCGTCAAGCTGGAGCAGTCTTCTCAAGACTGGTTCAGTGGACACCTTAACTTCCAGA 540
1327 QY TTGAGCACCACTCTTCCCAACCATGCGCGGACAACTTACAGAGATCGCGCGCTGG 1386
Db TTGAGCACCACTCTTCCCAACCATGCGCGGACAACTTACAGAGATCGCGCGCTGG 600
1387 QY TGAAGTCTCATGTGCAAGCATGCGCATTAACAGGAGAGCGCGTACTAGAGGCC 1446
Db TGAAGTCTCATGTGCAAGCATGCGCATTAACAGGAGAGCGCGTACTAGAGGCC 660
1447 QY TGTGAGACATCATCAGTCTCCCTCAAGAGTCTGGAGAGTGTGGTGGAGCTGACCTTC 1506
Db TGTGAGACATCATCAGTCTCCCTCAAGAGTCTGGAGAGTGTGGTGGAGCTGACCTTC 720
1507 QY ACAATGAAGCCACAGCCCCCGGACACCGTGGGAGAGGGTGCAGTGGGTGATGGCC 1566
Db ACAATGAAGCCACAGCCCCCGGACACCGTGGGAGAGGGTGCAGTGGGTGATGGCC 780
1567 QY AGAGGATGATGGCTTTTGTCTGAGGGGTGCGAGAGGCTGGTATGCACTGCTCA 1626
Db AGAGGATGATGGCTTTTGTCTGAGGGGTGCGAGAGGCTGGTATGCACTGCTCA 840
1627 QY CGGACCCCATGTTGGATCTTCTCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1686
Db CGGACCCCATGTTGGATCTTCTCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
1687 QY ATAGCACCTCCCTCATGAGACCTGCGCTCCCTCAGCGTACGACCATGAGCCATGGCCC 1746
Db ATAGCACCTCCCTCATGAGACCTGCGCTCCCTCAGCGTACGACCATGAGCCATGGCCC 960
1747 QY TCCAGTGCCTCTAGCCCTTTCTTCCAGGAGCAGAGAGTGGCCACCGGGGGTGGCTC 1806
Db TCCAGTGCCTCTAGCCCTTTCTTCCAGGAGCAGAGAGTGGCCACCGGGGGTGGCTC 1020
1807 QY TGTCTTACCTCCACTCTCTGCGCGCTTAAAGATGGAGGAGACACCGGTTCATGGTCTGG 1866
Db TGTCTTACCTCCACTCTCTGCGCGCTTAAAGATGGAGGAGACACCGGTTCATGGTCTGG 1080
1867 QY CCTGTGAGTCTCCCTTTGAGCCTGGTCACTAGGCATCACCCCGCTTTGGTTCCTCAGA 1926
Db CCTGTGAGTCTCCCTTTGAGCCTGGTCACTAGGCATCACCCCGCTTTGGTTCCTCAGA 1140
1927 QY TGCTCTTGGGGTTCATAGGGGAGGTCCTAGTGGGCGAGGGGCCCTGACCCCTCCCGGCT 1986

1141 Db TGCTCTTGGGGTTCATAGGGGAGGTCCTAGTGGGCGAGGCCCTTGAACCTTCCCGGCT 1200
1987 QY GGCTTCACTCTCTCCCTGACCGGCTGCCATTGGTCCACCTTTTCATAGAGAGGCTGCTTGT 2046
Db GGCTTCACTCTCTCCCTGACCGGCTGCCATTGGTCCACCTTTTCATAGAGAGGCTGCTTGT 1260
2047 QY TACAAGAGCTGGGTCTCCCTCCCTGAGCTCGGTAACTAGTACCGAGGCTCTCTTAAGATG 2106
Db TACAAGAGCTGGGTCTCCCTCCCTGAGCTCGGTAACTAGTACCGAGGCTCTCTTAAGATG 1320
2107 QY TCCAGGGCCCCAGGCGCGGCGGACAGCCAGCCCAAACTTGGGCCCTTGGAGAGTCCCT 2166
Db TCCAGGGCCCCAGGCGCGGCGGACAGCCAGCCCAAACTTGGGCCCTTGGAGAGTCCCT 1380
2167 QY CACCCCATCACTAGAGTCTCTGACCTGGGCTTTCACGGGCCCATTCACCGGCTCC 2226
Db CACCCCATCACTAGAGTCTCTGACCTGGGCTTTCACGGGCCCATTCACCGGCTCC 1440
2227 QY CAACCTTGAGCTGTGACCTTTGGGACCAAGGGGAGTCCCTCGTCTCTTGTGACTCAGCA 2286
Db CAACCTTGAGCTGTGACCTTTGGGACCAAGGGGAGTCCCTCGTCTCTTGTGACTCAGCA 1500
2287 QY GAGCAGTGCCACGTTTCAGGAGGGCGGCTGGCTGGAGGCTCAGCCACGCTCCAG 2346
Db GAGCAGTGCCACGTTTCAGGAGGGCGGCTGGCTGGAGGCTCAGCCACGCTCCAG 1560
2347 QY CTCTTCTCAGGGTGTCTCTGAGGTCCAAGATTCTGGAGCAATCTGACCTTCTCCAAAG 2406
Db CTCTTCTCAGGGTGTCTCTGAGGTCCAAGATTCTGGAGCAATCTGACCTTCTCCAAAG 1620
2407 QY CTCTGTTATCAGCTGGGACGTGCCAGCAATCTCTGGCCATTTGGGCCAGGGAGCTG 2466
Db CTCTGTTATCAGCTGGGACGTGCCAGCAATCTCTGGCCATTTGGGCCAGGGAGCTG 1679
2467 QY GGCCCTG 2473
Db GGCCCTG 1686

RESULT 35
AAAA14592
ID AAA14592 standard; DNA; 1686 BP.
XX
AC AAA14592;
XX
DT 08-AUG-2000 (first entry)
XX
DE Nucleotide sequence of a contig of a human desaturase enzyme.
XX
KW Delta5-desaturase; poly-unsaturated long chain fatty acid; PUPA;
KW arachidonic acid; infant formula; dietary supplement; dietary substitute;
KW cosmetic; stress; metabolic disorder; gastrointestinal difficulty;
KW malabsorption; restenosis; angioplasty; inflammation; kidney stone;
KW rheumatoid arthritis; asthma; psoriasis; osteoporosis; tract stone;
KW cancer; cachexia; diabetes; eczema; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder;
KW blood score; platelet aggregation; vasodilatation;
KW gastro-intestinal bleeding; ss.
XX
OS Homo sapiens.
XX
PN WO200020603-A1.
XX
PD 13-APR-2000.
XX
PF 29-SEP-1999; 99WO-US22692.
XX
PR 05-OCT-1998; 98US-0103109.
XX
PA (ABSO) ABBOTT LAB.
XX

PI Mukerji P, Huang Y, Parker-Barnes JH, Das T;
XX WPI: 2000-364599/31.
DR P-PSDB; AAY84701.
XX
PT Novel transgenic insect cell with modified delta-5-desaturase
PT production, useful for altering fatty acid biosynthesis -
XX
XX Example 9; Page 146-147; 161pp; English.
XX
XX AAA14588-94 represent contigs of a human desaturase. The specification
CC describes a Mortierella alpina delta5-desaturase. The protein is
CC involved in the biosynthesis of poly-unsaturated long chain fatty
CC acids (PUFAs). The polynucleotide is to produce PUFAs, especially
CC arachidonic acid. The oils produced by the invention are used in
CC pharmaceutical compositions, infant formulas, dietary supplements,
CC dietary substitutes, and cosmetics. The nutritional compositions can be
CC used to treat normal individuals temporally exposed to stress, or
CC individuals having specialized needs due to chronic or acute diseases
CC (e.g. metabolic disorders such as gastrointestinal difficulties and/or
CC malabsorption, and other disorders such as restenosis after angioplasty,
CC symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis,
CC osteoporosis, kidney stones, tract stones, cancer, cachexia associated
CC with cancer, diabetes, eczema, endometriosis, premenstrual syndrome,
CC myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis,
CC acute respiratory syndrome, hypertension, inflammatory skin disorders,
CC as well as reduce blood score, inhibit platelet aggregation, cause
CC vasodilation, inhibit proliferation of vessel wall smooth muscle and
CC fibrous tissue, prevent or reduce gastro-intestinal bleeding, and for
CC geriatric treatments).
XX
XX Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;

Query Match 52.6%; Score 1675; DB 21; Length 1686;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 787 GCACCTTAAAGGGTCCCTGCGCACTGGTGGGAATACGCCACTTCCAGCACACGCCCA 846
DB 1 GCACCTTAAAGGGTCCCTGCGCACTGGTGGGAATACGCCACTTCCAGCACACGCCCA 60
QY 847 AGCCTAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCACGTTTGTCTGGGG 906
DB 61 AGCCTAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCACGTTTGTCTGGGG 120
QY 907 AATGGAGCCCATCGAGTACGGCAAGAGCTGAATACCTGCCCTCAATCAATCACCAGC 966
DB 121 AATGGAGCCCATCGAGTACGGCAAGAGCTGAATACCTGCCCTCAATCAATCACCAGC 180
QY 967 ACGAATACCTTCTCTGATTGGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGA 1026
DB 181 ACGAATACCTTCTCTGATTGGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGA 240
QY 1027 TCATCATGACATGATGTCTCATAGAACTGGGTGGACCTGGCTGGCGGTGAGCTACT 1086
DB 241 TCATCATGACATGATGTCTCATAGAACTGGGTGGACCTGGCTGGCGGTGAGCTACT 300
QY 1087 ACATCCGGTCTTCTCATCACTACATCCCTTTCTACGGCATCTCTGGGAGCCCTCTTTTC 1146
DB 301 ACATCCGGTCTTCTCATCACTACATCCCTTTCTACGGCATCTCTGGGAGCCCTCTTTTC 360
QY 1147 TCAATTCATGAGTTCTCTGAGAGCCACTGGTTGTGGGTGACAGATGATCACA 1206
DB 361 TCAATTCATGAGTTCTCTGAGAGCCACTGGTTGTGGGTGACAGATGATCACA 420
QY 1207 TCGTCATGAGATTGACAGAGGCTACCGTGTACTGGTTTCAGTAGCCAGCTGACAGCCA 1266
DB 421 TCGTCATGAGATTGACAGAGGCTACCGTGTACTGGTTTCAGTAGCCAGCTGACAGCCA 480
QY 1267 CTTGCAACGTGAGAGCTCTTTTCAACAGCTGGTTTCAGTGGACACTTTAACTTCCAGA 1326
DB 481 CTTGCAACGTGAGAGCTCTTTTCAACAGCTGGTTTCAGTGGACACTTTAACTTCCAGA 540

QY 1327 TTGAGCACCACTCTTCCCAACCATGCCCCGCGACAACTTACACAGATGCCCGCGTGG 1386
DB 541 TTGAGCACCACTCTTCCCAACCATGCCCCGCGACAACTTACACAGATGCCCGCGTGG 600
QY 1387 TGAAGTCTCTATGTGCCAAGCATGGCATTGAATACAGGAGAACCGCTACTAGGGCCC 1446
DB 601 TGAAGTCTCTATGTGCCAAGCATGGCATTGAATACAGGAGAACCGCTACTAGGGCCC 660
QY 1447 TGCTGGACATCATCAGGTCCCTGAAGAACTCTGGGAAGCTGTGGCTGGAGCCCTACCTTC 1506
DB 561 TGCTGGACATCATCAGGTCCCTGAAGAACTCTGGGAAGCTGTGGCTGGAGCCCTACCTTC 720
QY 1507 ACAAATGAAGCCACAGCCCCCGGAGACACCTGTGGGAAAGGGGTGAGTGGGTGATGGCC 1566
DB 721 ACAAATGAAGCCACAGCCCCCGGAGACACCTGTGGGAAAGGGGTGAGTGGGTGATGGCC 780
QY 1567 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGGTGTATGCACTGTCA 1626
DB 781 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGGTGTATGCACTGTCA 840
QY 1627 CGGACCCCATGTTGGATCTTTCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1686
DB 841 CGGACCCCATGTTGGATCTTTCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
QY 1687 ATAGCACCTGCTCATGGGACCTGCCCTCCCTCAGCGCTCAGCCATCAGCCATGAGCCC 1746
DB 901 ATAGCACCTGCTCATGGGACCTGCCCTCCCTCAGCGCTCAGCCATCAGCCATGAGCCC 960
QY 1747 TCCAGTGCCTCTAGGCCCTTTCTTCAAGAGCAGAGAGTGGCCACCGGGGGTGGCTC 1806
DB 961 TCCAGTGCCTCTAGGCCCTTTCTTCAAGAGCAGAGAGTGGCCACCGGGGGTGGCTC 1020
QY 1807 TGTCTACTCCACTCTCTGCCCTTAAAGATGGGAGGAGACAGCGTCCATGGGTCTGG 1866
DB 1021 TGTCTACTCCACTCTCTGCCCTTAAAGATGGGAGGAGACAGCGTCCATGGGTCTGG 1080
QY 1867 CTTGTAGTCTCCCTTTCAGCCTGGTCACTAGGATCAACCCCGCTTGTGTTCTTCTCAGA 1926
DB 1081 CTTGTAGTCTCCCTTTCAGCCTGGTCACTAGGATCAACCCCGCTTGTGTTCTTCTCAGA 1140
QY 1927 TGCTCTGGGTTCATAGGGGACGTCTAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1986
DB 1141 TGCTCTGGGTTCATAGGGGACGTCTAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
QY 1987 GCTCTCACTCTCCCTGACGGTGCATTTGTCACCTTTTCATAGAGAGGCTCTTTGT 2046
DB 1201 GCTCTCACTCTCCCTGACGGTGCATTTGTCACCTTTTCATAGAGAGGCTCTTTGT 1260
QY 2047 TACAAGCTCGGTCTCTCTGAGTCTGGTTAAGTACCGGAGGCTCTCTTAAGATG 2106
DB 1261 TACAAGCTCGGTCTCTCTGAGTCTGGTTAAGTACCGGAGGCTCTCTTAAGATG 1320
QY 2107 TCCAGGGCCCCAGGGCCCCGGGACAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 2166
DB 1321 TCCAGGGCCCCAGGGCCCCGGGACAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1380
QY 2167 CACCCCATCATAGAGTCTGACCTTGGGGTTTTCAGGGGCCCCATTCACCGCTCCC 2226
DB 1381 CACCCCATCATAGAGTCTGACCTTGGGGTTTTCAGGGGCCCCATTCACCGCTCCC 1440
QY 2227 CAACCTTGAGCTGTGACCTTGGGACCAAGGGGGAGTCCCTGCTCTTTGTGACTCAGCA 2286
DB 1441 CAACCTTGAGCTGTGACCTTGGGACCAAGGGGGAGTCCCTGCTCTTTGTGACTCAGCA 1500
QY 2287 GAGGAGTGGCCACGTTTCAGGAGGGGGGGTGGCTTGGAGGCTCAGCCACCCCTCCAG 2346
DB 1501 GAGGAGTGGCCACGTTTCAGGAGGGGGGGTGGCTTGGAGGCTCAGCCACCCCTCCAG 1560
QY 2347 CTTTCTCAGGGTGTCTCTGAGTCCAAGATTTCTGGAGCAATCTCACCTTTCTCCAAAGG 2406
DB 1561 CTTTCTCAGGGTGTCTCTGAGTCCAAGATTTCTGGAGCAATCTCACCTTTCTCCAAAGG 1620
QY 2407 CTTCTGTTATCAGTGGGAGTGCACAGCAATCCCTTGGGCAATTTTGGCCCCAGGGGACGTG 2466

Db 1621 CTCCTGTATCAGCTGGGAGTCCGAGCAATCCCTGGCCATTTGGCCCA-GGGACCTG 1679

QY 2467 GGCCCTG 2473

Db 1680 GGCCCTG 1686

RESULT 36

ABS71824

ID ABS71824 standard; DNA; 1686 BP.

XX AC

XX ABS71824;

DT 02-DSC-2002 (first entry)

XX DE Human delta5-desaturase gene #6.

XX KW Human; delta5-desaturase; polyunsaturated fatty acid; DGLA;

KW dihomogamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;

KW eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;

XX KW gene; ds.

XX OS Homo sapiens.

XX US6432684-B1.

XX 13-AUG-2002.

XX 08-JAN-1999; 99US-0227613.

XX 11-APR-1997; 97US-0833610.

XX 10-APR-1998; 98WO-US07422.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Leonard AE, Huang Y, Das T;

XX WFI; 2002-689761/74.

XX XX

XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing

PT the conversion of dihomogamma-linolenic acid to arachidonic acid and

PT in the conversion of 20:4n-3 to eicosapentaenoic acid -

XX XX

XX Example 1; Figure 6; 88pp; English.

XX XX

CC The invention relates to an isolated human delta5-desaturase nucleotide

CC sequence (I) which desaturates polyunsaturated fatty acids at

CC carbon 5. The nucleotide sequence (I) may be used in the recombinant

CC production of vectors and host cells for the production of delta5-

CC desaturase. Delta5-desaturase may be utilised in the conversion of

CC dihomogamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the

CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA Or

CC polyunsaturated fatty acids produced from it may be added to

CC pharmaceutical compositions, nutritional compositions, animal feeds, as

CC well as other products such as cosmetics. ABS71819-ABS71854

CC represent human delta5-desaturase coding sequences and PCR primers of

CC the invention.

XX XX

XX Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;

XX XX

Query Match 52.6%; Score 1675; DB 24; Length 1686;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 787 GCACCTAAAGGGTGCCCTGCGCAACTGGTGGGAATCATGCCACTTCCAGCACCGCCA 846

Db 1 GCACCTAAAGGGTGCCCTGCGCAACTGGTGGGAATCATGCCACTTCCAGCACCGCCA 60

QY 847 AGCCTAACATCTTCCCAAGGATCCCGATGTGAACATGTGACATGTCGTTGTTCGGCG 906

Db 61 AGCCTAACATCTTCCCAAGGATCCCGATGTGAACATGTGACATGTCGTTGTTCGGCG 120

QY 907 AATGGAGCCCATCGAGTACGCGCAAGAAGCTGAATACCTTCGCTCAATCACCAGC 966

Db 121 AATGGAGCCCATCGAGTACGCGCAAGAAGCTGAATACCTTCGCTCAATCACCAGC 180

QY 967 ACGAATACCTTCTTCCTGATTTGGCCCGCGCTGCTCATCCCATGTTATTTCCAGTACGAG 1026

Db 181 ACGAATACCTTCTTCCTGATTTGGCCCGCGCTGCTCATCCCATGTTATTTCCAGTACGAG 240

QY 1027 TCATCATGACCATGATCGTCCATAAAGACTGGGTGACCTGGCTGGCGCTCAGCTACT 1086

Db 241 TCATCATGACCATGATCGTCCATAAAGACTGGGTGACCTGGCTGGCGCTCAGCTACT 300

QY 1087 ACATCCGGTTCTTCATCACTACCTATCCCTTTCTACGGCATCTCGGAGCGCTCTTTTC 1146

Db 301 ACATCCGGTTCTTCATCACTACCTATCCCTTTCTACGGCATCTCGGAGCGCTCTTTTC 360

QY 1147 TCAACTTTCATCAGTTCTCGAGAGCACTGGTTTGTGGGTCAACAGATGAATCACA 1206

Db 361 TCAACTTTCATCAGTTCTCGAGAGCACTGGTTTGTGGGTCAACAGATGAATCACA 420

QY 1207 TCGTCAATGAGATGACCGAGAGCGCTACCGTGACTGGTTCACTAGCGAGCTGACAGCCA 1266

Db 421 TCGTCAATGAGATGACCGAGAGCGCTACCGTGACTGGTTCACTAGCGAGCTGACAGCCA 480

QY 1267 CCTGCAACGTGGAGAGCTCTTCTTCAACGACTGGTTCACTGACACCTTTAACTTCAGA 1326

Db 481 CCTGCAACGTGGAGAGCTCTTCTTCAACGACTGGTTCACTGACACCTTTAACTTCAGA 540

QY 1327 TTGAGCAACCACTTCTTCCCACTGCCCCGCGCAACTTTACAAAGATCGCCCGCTGG 1386

Db 541 TTGAGCAACCACTTCTTCCCACTGCCCCGCGCAACTTTACAAAGATCGCCCGCTGG 600

QY 1387 TGAAGTCTCTATGTCGCAAGCATGGCATTTGAATACAGGAGAGCGCTACTAGGAGGCC 1446

Db 601 TGAAGTCTCTATGTCGCAAGCATGGCATTTGAATACAGGAGAGCGCTACTAGGAGGCC 660

QY 1447 TGCTGACATCATCAGTCCCTGAAAGAGTCTGGAGAGTGTGGCTGGAGCGCTACCTTC 1506

Db 661 TGCTGACATCATCAGTCCCTGAAAGAGTCTGGAGAGTGTGGCTGGAGCGCTACCTTC 720

QY 1507 ACAATGAAGCCACAGCCCCCGGAGACACCGTGGGAGAGGGTGCAGTGGGGTGGTGGCC 1566

Db 721 ACAATGAAGCCACAGCCCCCGGAGACACCGTGGGAGAGGGTGCAGTGGGGTGGTGGCC 780

QY 1567 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGGTGTATGCACTGTCTCA 1626

Db 781 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGGTGTATGCACTGTCTCA 840

QY 1627 CGGACCCCATGTTGGATCTTTCTCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1686

Db 841 CGGACCCCATGTTGGATCTTTCTCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900

QY 1687 ATAGCACCCCTGCTCATGGAGCTGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 1746

Db 901 ATAGCACCCCTGCTCATGGAGCTGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 960

QY 1747 TCCAGTGCCTCTTAGGCCCTCTTTTCCAAAGAGAGAGAGTGGCCACCGGGGGTGGCTC 1806

Db 961 TCCAGTGCCTCTTAGGCCCTCTTTTCCAAAGAGAGAGAGTGGCCACCGGGGGTGGCTC 1020

QY 1807 TGTCTACCTCCACTCTCTGCCCCCTTAAAGATGGGAGAGAGACAGCGGTCCATGGGTCTGG 1866

Db 1021 TGTCTACCTCCACTCTCTGCCCCCTTAAAGATGGGAGAGAGACAGCGGTCCATGGGTCTGG 1080

QY 1867 CCTGTGAGTCTCCCTTTGAGCCTGGTCACTPAGGCATCACCCCCGCTTTGGTCTTTCAGA 1926

Db 1081 CCTGTGAGTCTCCCTTTGAGCCTGGTCACTPAGGCATCACCCCCGCTTTGGTCTTTCAGA 1140

QY 1927 TGCTCTTGGGGTTTATAGGGGAGGTCTCTAGTGGGAGAGGCCCTCTACCTCCCGGCT 1986

Db 1141 TGCTCTTGGGGTTTATAGGGGAGGTCTCTAGTGGGAGAGGCCCTCTACCTCCCGGCT 1200

QY 1987 GGCTTCACTCTCCCTGACGGCTGCCATTTGGTCCACCTTTTCATAGAGAGGGCTCTTGT 2046

Db 1201 GGGTTCACTCTCCCTGACGGTGCATGGTCAACCCCTTCATAGAGAGGCGCTGTTGT 1260
 QY 2047 TACAAAGCTCGGTCTCCCTCTGACAGCTCGGTAAAGTACCGAGGCGCTCTCTTAAGATG 2106
 Db 1261 TACAAAGCTCGGTCTCCCTCTGACAGCTCGGTAAAGTACCGAGGCGCTCTCTTAAGATG 1320
 QY 2107 TCCAGGCGCCAGGCGCGGGGACAGCCAGGCGCCAAACCTTGGGCGCTGGAAAGTCTCTC 2166
 Db 1321 TCCAGGCGCCAGGCGCGGGGACAGCCAGGCGCCAAACCTTGGGCGCTGGAAAGTCTCTC 1380
 QY 2167 CACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTCACGGGCGCCATTCACCGCTCTCC 2226
 Db 1381 CACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTCACGGGCGCCATTCACCGCTCTCC 1440
 QY 2227 CAACCTGAGCTGTGACCTTGGACCAAGAGGGGAGTCCCTGCTCTGTGACTCAGCA 2286
 Db 1441 CAACCTGAGCTGTGACCTTGGACCAAGAGGGGAGTCCCTGCTCTGTGACTCAGCA 1500
 QY 2287 GAGGCACTGCCACGTTTCAGGAGGGGCGGCTGGAGCTCAGCCACCTCCAG 2346
 Db 1501 GAGGCACTGCCACGTTTCAGGAGGGGCGGCTGGAGCTCAGCCACCTCCAG 1560
 QY 2347 CTTTCTCAGGTGCTCTGAGTCCAGATTCGAGCAATCTGACCTTCTCCAAAGG 2406
 Db 1561 CTTTCTCAGGTGCTCTGAGTCCAGATTCGAGCAATCTGACCTTCTCCAAAGG 1620
 QY 2407 CTCTGTATCAGCTGGGAGTGCAGCCAACTCCCTGGCCATTGGGCCAGGGGACGCTG 2466
 Db 1621 CTCTGTATCAGCTGGGAGTGCAGCCAACTCCCTGGCCATTGGGCCAGGGGACGCTG 1679
 QY 2467 GGCCCTG 2473
 Db 1680 GGCCCTG 1686

RESULT 37

ABS76711
 ID ABS76711 standard; cDNA; 1686 BP.

AC ABS76711;

DT 12-DEC-2002 (first entry)

DE Human desaturase cDNA edited contig 2511785.

XX Human; ss; delta5 desaturase; polyunsaturated fatty acid;
 KW PUFA; nutritional; animal feed; cosmetic; skin aging; burn; angioplasty;
 KW inflammation; rheumatoid arthritis; asthma; psoriasis; osteoporosis;
 KW kidney stone; urinary tract stone; cancer; cachexia; diabetes; eczema;
 KW AIDS; multiple sclerosis; blood pressure; platelet aggregation;
 KW vasodilation; cholesterol; proliferation of fibrous tissue;
 KW endometriosis; myalgic encephalomyelitis; human breast milk;
 KW dietary supplement; chromosome 11q12.

XX Homo sapiens.

XX US6428990-B1.

XX 06-AUG-2002.

XX 12-NOV-1999; 99US-0439261.

XX 11-APR-1997; 97US-0833610.

XX 10-APR-1998; 98WO-US07422.

XX 08-JAN-1999; 99US-0227613.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;

XX WPI; 2002-730518/79.

PT Producing a polyunsaturated fatty acid (PUFA), useful in dietary
 PT supplements and in treating diseases e.g., cancer, comprises expressing
 PT human delta 5-desaturase enzyme and exposing enzyme to substrate PUFA
 PS to convert to product PUFA -
 PS Example 1; Fig 6; 104pp; English.

CC The invention relates to producing (M1) a polyunsaturated fatty acid
 CC (PUFA), comprising: (i) isolating a fully defined human Delta5-desaturase
 CC gene sequence (I); (ii) constructing a vector comprising (I);
 CC (iii) introducing the vector into a host cell for expression of the
 CC human Delta5-desaturase enzyme (II); and (iv) exposing (II) to a
 CC substrate PUFA (III) such that it is converted to a product PUFA (IV).
 CC The method is useful for producing a polyunsaturated fatty acid
 CC such as arachidonic acid (AA), eicosapentaenoic acid (EPA), adrenic
 CC acid, (n-3)-docosapentaenoic acid, (n-6)-docosapentaenoic acid and/or
 CC as arachidonic acid (AA), eicosapentaenoic acid (EPA) and/or
 CC docosahexaenoic acid (DHA) acid. The PUFAs produced by the method, such
 CC as arachidonic acid (AA), eicosapentaenoic acid (EPA) and/or
 CC docosahexaenoic acid (DHA) acid, are useful for replicating the PUFA content
 CC of human breast milk or to alter the presence of PUFAs normally found
 CC in a non-human mammal's milk. PUFAs produced by (M1) may be added to a
 CC dietary substitute or supplement, particularly an infant formula, for
 CC patients undergoing intravenous feeding or for preventing or treating
 CC malnutrition or other conditions or disease states. The PUFAs are
 CC useful for producing nutritional compositions e.g., any food or
 CC preparation for human consumption including for enteral or parenteral
 CC consumption, which when taken into the body serve to nourish or build
 CC up tissues or supply energy and/or maintain, restore or support
 CC adequate nutritional status or metabolic function. The PUFAs are also
 CC useful in animal feed supplements to alter an animal tissue or milk
 CC fatty acid composition to one or more desirable for human or animal
 CC consumption, in animal feed substitutes, animal vitamins or in animal
 CC topical ointments. The PUFAs produced by this method are useful in
 CC producing pharmaceutical compositions for treating rough or aging skin,
 CC injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,
 CC asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,
 CC cachexia associated with cancer, diabetes, eczema, AIDS, multiple
 CC sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting
 CC platelet aggregation, inducing vasodilation, reducing cholesterol
 CC levels, inhibiting proliferation of fibrous tissue, treating
 CC endometriosis, and myalgic encephalomyelitis. The gene for delta5
 CC desaturase is located on chromosome 11q12. The present sequence
 CC is a partial cDNA for a human delta5 desaturase.

XX Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;

SQ Query Match 52.6%; Score 1675; DB 24; Length 1686;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 787 GCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATGCCACTTCCAGCACACGCCCA 846
 Db 1 GCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATGCCACTTCCAGCACACGCCCA 60
 QY 847 AGCCTAACATCTTCCAAAGGATCCGATGTGAACATGCTGCAGCTGTTTCTGGCG 906
 Db 61 AGCCTAACATCTTCCAAAGGATCCGATGTGAACATGCTGCAGCTGTTTCTGGCG 120
 QY 907 AATGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACATCACCAGC 966
 Db 121 AATGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACATCACCAGC 180
 QY 967 ACGAATATCTTCTCTGATTGGCGCGCGCTGCTCATCCCGCATGATTTCAGTACCAGA 1026
 Db 181 ACGAATATCTTCTCTGATTGGCGCGCGCTGCTCATCCCGCATGATTTCAGTACCAGA 240
 QY 1027 TCATCATGACCATGATCTGTCATTAAGAACTGGGTGGACCTGGCTGGGCGCTGAGTACT 1086
 Db 241 TCATCATGACCATGATCTGTCATTAAGAACTGGGTGGACCTGGCTGGGCGCTGAGTACT 300
 QY 1087 ACATCCGGTCTTTCATCACCTACATCCCTTTCTACGGCATCTCGGAGCGCTCTTTTC 1146
 Db 301 ACATCCGGTCTTTCATCACCTACATCCCTTTCTACGGCATCTCGGAGCGCTCTTTTC 360

PT detection, prevention, and treatment of various disorders such as
 XX cancer and immune system disorders -
 XX
 XX Claim 1; Page 351-352; 442pp; English.
 CC The polynucleotide sequences given in AAC60025-C60071 encode the human
 CC secreted proteins represented in AAB34854-B34900. Sequences
 CC AAB34901-B34976 are fragments of proteins encoded by the genes, and also
 CC proteins with which they share sequence homology. The proteins have
 CC activities based on the tissues in which their encoding genes are
 CC expressed. Examples of the proteins activities include: neuroprotective;
 CC cytostatic; cardioactive; immunomodulatory; general muscular activity;
 CC vulnary; general gastrointestinal activity; nephrotoxic;
 CC antiinfective; gynaecological; and antibacterial. The human secreted
 CC proteins, polynucleotides, antagonists and antagonists of the invention
 CC may be useful in treating, preventing and/or diagnosing various
 CC diseases, disorders and conditions such as neural, immune, muscular,
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal and
 CC proliferative disorders and cancer. They may also be used in the
 CC treatment of wounds, and infectious diseases. The polypeptides may be
 CC used as a food additive or preservative to increase storage capabilities.
 CC Sequences AAC60016-C60024 and AAB34853 are used in the course of the
 CC invention during the identification and characterisation of the protein
 CC and nucleotide sequences.
 XX
 SQ Sequence 1536 BP; 306 A; 464 C; 456 G; 310 T; 0 other;

	Query Match	44.2%	Score 1408.4	DB 21	Length 1536;
	Best Local Similarity	98.7%	Pred. No. 0		
	Matches 1494	Conservative 0	Mismatches 11	Indels 9	Gaps 7
Qy	1671	TCCTTCACATCTCCCCCATAGCACCCCTGCCTCATGGGACCTGCCTCCCTCAGCCGTCAG	1730		
Db	8	TCGCGACATCTCCCCCATAGCACCCCTGCCTCATGGGACCTGCCTCCCTCAGCCGTCAG	67		
Qy	1731	CCATCAGGCATGGCCCTCCGAGTGCCTCTAGCCCTCTTCCAGGAGCAGAGAGTGG	1790		
Db	68	CCATCAGGCATGGCCCTCCGAGTGCCTCTAGCCCTCTTCCAGGAGCAGAGAGTGG	127		
Qy	1791	CCACCGGGGGTGGTCTGTCTACTCCACTCTCTGCCCCCTAAAGATGGGAGGAGCCAG	1850		
Db	128	CCACCGGGGGT-GTCTGTCTCTACTCCACTCTCTGCCCCCTAAAGATGGGAGGAGCCAG	186		
Qy	1851	CGGTCCATGGGTCTGGGCTGTGAGTCTCCCTCTTGAGCGCTGGTCACTAGGCATCACCCCC	1910		
Db	187	CGGTCCATGGGTCTGGGCTGTGAGTCTCCCTCTTGAGCGCTGGTCACTAGGCATCACCCCC	246		
Qy	1911	GCTTTGTTCTTCAGATGCTCTTGCGGTTCATAGGGCAGTCCCTAGTCGGGAGGGCCC	1970		
Db	247	GCTTTGTTCTTCAGATGCTCTTGCGGTTCATAGGGCAGTCCCTAGTCGGGAGGGCCC	306		
Qy	1971	CTGACCTCCGGCTGGCTTCACTCTCCCTGACGGTGCATATGGTCCACCTTTTCATA	2030		
Db	307	CTGACCTCCGGCTGGCTTCACTCTCCCTGACGGTGCATATGGTCCACCTTTTCATA	366		
Qy	2031	GAGAGGCTGCTTTGTACAAAGCTCGGTCTCCCTCTCTCAGCTCGTTAAGTACCCTGA	2090		
Db	367	GAGAGGCTGCTTTGTACAAAGCTCGGTCTCCCTCTCTCAGCTCGTTAAGTACCCTGA	426		
Qy	2091	GGCCTCTCTTAAAGATGTCAGGGCCCCCAGAGCCCCGGGCGCAGCCAGCCAAACCTTGGG	2150		
Db	427	GGCCTCTCTTAAAGATGTCAGGGCCCCCAGAGCCCCGGGCGCAGCCAGCCAAACCTTGGG	486		
Qy	2151	CCCTGGGAAGAGTCTCCACCCCATCATCTAGAGTGCCTCTGACCTTGGGCTTTCAGGGCCC	2210		
Db	487	CCCTGGGAAGA-TCTCCACCCCATCTAGAGTGCCTCTGACCTTGGGCTTTCAGGGCCC	545		
Qy	2211	CATTCCACCGCTCCCAACTTGAAGCTGTGACCTTGGGACCAAGGGGAGTCCCTCGT	2270		
Db	546	CATTCCACCGCTCCCAACTTGAAGCTGTGACCTTGGGACCAAGGGGAGTCCCTCGT	604		
Qy	2271	CTCTTGTGACTCAGCAGGCGAGTGGCCACGTTTCAGGGAGGGGCCGCTGCTCGTGGAGC	2330		

KW Human; secreted protein; cancer; tumour; hyperproliferative disorder;
 KW autoimmune disorder; inflammation; angiogenic diseases; AIDS;
 KW acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing;
 KW drug screening; chromosome identification; chromosome mapping;
 KW cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV;
 KW antianaemic; vulnary; chromosome 11q12-13.1; gene; ss.
 XX Homo sapiens.
 XX MO200277013-A2.
 XX 03-OCT-2002.
 XX 26-MAR-2002; 2002WO-US09370.
 XX 27-MAR-2001; 2001US-278650P.
 XX 12-SEP-2001; 2001US-0950882.
 XX 12-SEP-2001; 2001US-0950883.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Ruben SM;
 XX WPI; 2003-040578/03.
 XX P-PSDB; ABR01027.
 XX New human secreted proteins and nucleic acids, useful for detecting or
 PT treating cancer or other hyperproliferative disorders, autoimmune
 PT disorders, inflammatory disorders, HIV disease, hepatitis or anemia -
 XX Claim 21; Page 1206; 247app; English.
 XX ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted
 CC protein genes, and ABP00947-ABP01363 represent the proteins they encode.
 CC ABZ73698-ABZ74687 represent human secreted protein genomic fragments. The
 CC invention also encompasses antibodies specific for the secreted proteins,
 CC the use of the secreted proteins in drug screening and recombinant
 CC vectors and host cells comprising a nucleic acid of the invention. The
 CC secreted proteins are thought to be involved in biological activities
 CC associated with cellular signalling, cellular differentiation, cell
 CC migration, prothrombin activation and neurotransmitter activity. The
 CC secreted proteins, nucleic acids encoding them, antibodies or antibody
 CC fragments specific for the secreted proteins, and modulators of protein
 CC activity are useful for diagnosing or treating cancers or other
 CC hyperproliferative disorders. Additionally, the secreted proteins and
 CC their nucleic acids may also be used in the treatment of autoimmune
 CC disorders, inflammatory disorders, diseases involving angiogenesis, AIDS
 CC (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote
 CC wound healing. Nucleic acids of the invention may be used for chromosome
 CC identification, chromosome mapping, in gene therapy, for identifying
 CC individuals from minute biological samples, as hybridisation probes, and
 CC as molecular weight markers. The present sequence represents a human
 CC secreted protein-encoding cDNA clone of the invention.
 XX SQ Sequence 1536 BP; 306 A; 464 C; 456 G; 310 T; 0 other;
 Query Match 44.2%; Score 1408.4; DB 25; Length 1536;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 1494; Conservative 0; Mismatches 11; Indels 9; Gaps 7;
 QY 1671 TCTTCACATCTCCGCAATAGACACCTGCTCCCTATGGAGCTGCTCCCTCCCTCAGCCGTCAG 1730
 DB 8 TCCGCAATCTCCGCAATAGACACCTGCTCCCTATGGAGCTGCTCCCTCCCTCAGCCGTCAG 67
 QY 1731 CCATCAGCCATGCGCTCCGAGTCCCTCTAGCCCTTTCTTCCAGGAGCAGAGAGTGG 1790
 DB 68 CCATCAGCCATGCGCTCCGAGTCCCTCTAGCCCTTTCTTCCAGGAGCAGAGAGTGG 127
 QY 1791 CCACCGGGGTGCTCTGCTCCTACTCTCTGCTCCCTTAAAGATGGAGGAGACCCAG 1850
 DB 128 CCACCGGGGTGCTCTGCTCCTACTCTCTGCTCCCTTAAAGATGGAGGAGACCCAG 186
 QY 1851 CGGTCCATGGTCTGGGCTGTGAGTCTCCCTTGGAGCTGGTCACTAGGCATCACCCCC 1910

DB 187 CGGTCCATGGTCTGGCCTGTGAGTCTCCCTTGGAGCCTGGTCACTAGGCATCACCCCC 246
 QY 1911 GCTTTGGTCTTCCAGATGCTCTTTGGGGTTCAATAGGGGAGGCTCTAGTTCGGGAGGGCCC 1970
 DB 247 GCTTTGGTCTTCCAGATGCTCTTTGGGGTTCAATAGGGGAGGCTCTAGTTCGGGAGGGCCC 306
 QY 1971 CTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCCATTGGTCCACCCCTTTTCA 2030
 DB 307 CTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCCATTGGTCCACCCCTTTTCA 366
 QY 2031 GAGAGGCTGCTTTGTTTAAAGTCTGGGTCTCCCTCTCTGACGCTCGTCTTAAGTACCGGA 2090
 DB 367 GAGAGGCTGCTTTGTTTAAAGTCTGGGTCTCCCTCTCTGACGCTCGTCTTAAGTACCGGA 426
 QY 2091 GGCCTCTCTTAAAGTCTCAGAGGCCCGGCGGCGGACAGCCAGCCCAACCTTTGGG 2150
 DB 427 GGCCTCTCTTAAAGTCTCAGAGGCCCGGCGGCGGACAGCCAGCCCAACCTTTGGG 486
 QY 2151 CCCTGGAAGAGTCTCTCAACCCCTCACTAGAGTGTCTGACCTCGGCTTTTCAAGGGCCC 2210
 DB 487 CCCTGGAAGA-TCTCCACCCCTCACTAGAGTGTCTGACCTCGGCTTTTCAAGGGCCC 545
 QY 2211 CATTCACCGCTCCCTCCCACTTGGAGCTGTGACCTTTGGGACCAAGGGGAGTCCCTCGT 2270
 DB 546 CATTCACCGCTCCCTCCCACTTGGAGCTGTGACCTTTGGGACCAAGGGGAGT-CTCTCGT 604
 QY 2271 CTCTTGTGATCTCAGAGGAGTGGCCAGTTTCAAGGAGGGGCGGCTGGCTGAGGCG 2330
 DB 605 CTCTTGTGATCTCAGAGGAGTGGCCAGTTTCAAGGAGGGGCGGCTGGCTGAGGCG 662
 QY 2331 TCAGCCACCTCCCTCAGCTTCTCAGGGTGTCTGAGGTCCCAAGATTCTGGAGCAATCT 2390
 DB 663 TCAGCCACCTCCCTCAGCTTCTCAGGGTGTCTGAGGTCCCAAGATTCTGGAGCAATCT 722
 QY 2391 GACCTCTCTCAAGAGGCTCTGTTATCAGCTGGGAGTGGCCAGCAATCTCTGGCCATTG 2450
 DB 723 GACCTCTCTCAAGAGGCTCTGTTATCAGCTGGGAGTGGCCAGCAATCTCTGGCCATTG 781
 QY 2451 GCGGAGGGGAGCTGGGCGCTCCAGCTCAGAGGGGCACTGAGCTGGGAGGCTCTCGT 2510
 DB 782 GCGGAGGGGAGCTGGGCGCTCCAGCTCAGAGGGGCACTGAGCTGGGAGGCTCTCGT 839
 QY 2511 CCCAGCCCTCCCATCTCGGGGCTGTGTGAGACGCGCTGCTCAGGCACTCTCTCTGT 2570
 DB 840 CCCAGCCCTCCCATCTCGGGGCTGTGTGAGACGCGCTGCTCAGGCACTCTCTCTGT 899
 QY 2571 CTGAACCTGCGCTTACTGTGTTTAACTGTGCTCCAGGATGCAATCTGATAGAGGGG 2630
 DB 900 CTGAACCTGCGCTTACTGTGTTTAACTGTGCTCCAGGATGCAATCTGATAGAGGGG 959
 QY 2631 CGGAGGGCTGGGCGCTTGTGACCAATCTGCGCTTTTCCACCATGCGCTTGGTGGCCC 2690
 DB 960 CGGAGGGCTGGGCGCTTGTGACCAATCTGCGCTTTTCCACCATGCGCTTGGTGGCCC 1018
 QY 2691 TGAATGTGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2750
 DB 1019 TGAATGTGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1078
 QY 2751 GAGGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2810
 DB 1079 GAGGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1138
 QY 2811 GGGGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2870
 DB 1139 GGGGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1198
 QY 2871 CTGGAGGAGTCTCAGCTGTGTTGAGTCTTAACCCCACTAATCAGTCTTCTAGATTCAGGG 2930
 DB 1199 CTGGAGGAGTCTCAGCTGTGTTGAGTCTTAACCCCACTAATCAGTCTTCTAGATTCAGGG 1258
 QY 2931 GAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2990

Db 1259 GAAGGGCAGGCACCAACAACCTCAGAAATGGGGGCTTTCGGGGAGGGCCCTAGTCCCCCA 1318
 Qy 2991 GCTCTAAGCAGCCAGGAGGACCTGCACTCTAAGCATCTGGTTGCCATGGCAATGGCATG 3050
 Db 1319 GCTCTAAGCAGCCAGGAGGACCTGCACTCTAAGCATCTGGTTGCCATGGCAATGGCATG 1378
 Qy 3051 CCCCCCAGCTACTGTATGCCCCCGACCCCGCAGAGGAGCAATGAACCCATAGGGAGCTG 3110
 Db 1379 CCCCCCAGCTACTGTATGCCCCCGACCCCGCAGAGGAGCAATGAACCCATAGGGAGCTG 1438
 Qy 3111 ATCGTAATGTTTATCATGTTTACTTCCCCACCCCTACATTTTGGAAATAAAATAAGGAAT 3170
 Db 1439 ATCGTAATGTTTATCATGTTTACTTCCCCACCCCTACATTTTGGAAATAAAATAAGGAAT 1498
 Qy 3171 TTTAAAAA 3184
 Db 1499 TTTAAAAA 1512

Search completed: December 10, 2003, 13:03:55
 Job time : 574 secs

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CM protein - protein search, using sw model

Run on: December 9, 2003, 10:07:15 ; Search time 46 Seconds

(without alignments)
1532.056 Million cell updates/sec

Title: US-09-719-601-5

Perfect score: 2438

Sequence: 1 MCKGNGQGGAAAEVSVPT.....DIIRSLKSGKLWLDAYLHK 444

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	2438	100.0	444	21	AAV59182 Human oxidoreducta
2	2425	99.5	444	21	AA441810 Human CRFX ORF1574
3	2425	99.5	444	21	AAV97539 Human fatty acid d
4	2425	99.5	444	22	AAE11083 Human delta-6-desa
5	2425	99.5	444	22	AAV93425 Human polypeptide,
6	2425	99.5	473	22	AAE11084 C-terminal tagged
7	2190	89.8	444	22	AAV51801 Rat fatty acid des
8	2190	89.8	444	22	AAE11081 Rat delta-6-desatu
9	2186	89.7	473	22	AAE11082 C-terminal tagged

10	1940.5	79.6	432	23	ABG94691 Human delta5-desat
11	1940.5	79.6	432	23	ABG96508 Human partial desa
12	1940.5	79.6	465	23	ABG94704 Human delta5-desat
13	1940.5	79.6	465	23	ABG96523 Human partial desa
14	1935	79.4	432	21	AAV95446 Human delta-5-desa
15	1935	79.4	746	19	AAW84156 Human desaturase e
16	1935	79.4	746	20	AAW85135 A desaturase enzym
17	1935	79.4	752	21	AAV92618 Human desaturase h
18	1935	79.4	753	20	AAW95514 Amino acid sequenc
19	1935	79.4	753	21	AAV84703 Amino acid sequenc
20	1790	73.4	322	22	AAV93456 Human polypeptide,
21	1646	67.5	294	21	AAV95448 Human delta-5-desa
22	1646	67.5	608	19	AAW84155 Human desaturase e
23	1646	67.5	608	20	AAW85134 A desaturase enzym
24	1646	67.5	614	21	AAV92617 Human desaturase h
25	1646	67.5	615	20	AAW95513 Amino acid sequenc
26	1646	67.5	615	21	AAV84702 Amino acid sequenc
27	1628.5	66.8	356	23	ABG94699 Human delta5-desat
28	1628.5	66.8	356	23	ABG96517 Human partial desa
29	1594	65.4	286	21	AAV58942 Breast and ovarian
30	1560.5	64.0	445	21	AAV97540 Human fatty acid d
31	1560.5	64.0	445	21	AAV83229 CYB5RP fatty acid
32	1560.5	64.0	445	24	ABU08788 Human delta 6 desa
33	1560.5	64.0	490	22	AAW25786 Human protein sequ
34	1527	62.6	446	22	ABG10281 Novel human diagno
35	1516	62.2	444	21	AAV97538 Human fatty acid d
36	1516	62.2	473	23	AAE14740 C-terminal tagged
37	1515	62.1	444	24	ABU08789 Human delta 6 desa
38	1515	62.1	501	22	AAW93314 Human polypeptide,
39	1512	62.0	444	22	AAV94041 Human protein sequ
40	1508	61.9	444	21	AAV95445 Human delta-5-desa
41	1508	61.9	444	22	AAV31686 Amino acid sequenc
42	1508	61.9	444	23	ABG94694 Human delta5-desat
43	1508	61.9	444	23	ABG96510 Human delta5 desat
44	1508	61.9	445	23	ABG96522 Human delta5 desat
45	1508	61.9	445	23	ABG96528 Human delta5 desat

ALIGNMENTS

- RESULT 1
- AAV59182
- ID AAV59182 standard; Protein; 444 AA.
- XX
- AC AAV59182;
- XX
- DT 28-MAR-2000 (first entry)
- XX
- DE Human oxidoreductase protein (HORP)-5 (clone 008879).
- XX
- DE Human oxidoreductase protein; HORP; neurological; autoimmune; cancer;
- KW Human oxidoreductase protein; HORP; neurological; autoimmune; cancer;
- KW reproduction; cell proliferation; vesicle trafficking; endocrine.
- XX
- OS Homo sapiens.
- XX
- PN WO200000622-A2.
- XX
- PD 06-JAN-2000.
- XX
- PF 29-JUN-1999; 99WO-US14711.
- XX
- PR 30-JUN-1998; 98US-0091177.
- PR 16-JUL-1998; 98US-0155241.
- XX
- XX (INCY-) INCYTE PHARM INC.
- PA Bandman O, Hillman JL, Tang YT, Lal P, Corley NC, Guegler KJ;
- PI Gorgone GA, Baughn MR;
- XX C-terminal tagged
- DR WPI; 2000-117171/10.
- DR N-PSDB; AAZ48247.
- XX

PT New polypeptide, its antagonist useful for treatment and prevention of
 PT neurological, inflammatory, reproductive, endocrine, cell proliferative
 PT and smooth muscle disorders -
 XX Claim 1; Page 80-81; 88pp; English.

XX The invention provides human oxidoreductase proteins (HORP)
 CC (RAY59178-133) and nucleic acid sequences (AAZ8243-248) encoding HORP-1
 CC to HORP-6. The HORP proteins can be expressed by standard recombinant
 CC methodology. Pharmaceutical compositions comprising the HORP proteins are
 CC useful for preventing or treating disorders associated with decreased
 CC expression or activity of HORP while HORP antagonists are useful for
 CC preventing or treating disorders associated with increased expression of
 CC HORP. Such disorders include neurological, autoimmune, reproductive,
 CC cell proliferative, vesicle trafficking, endocrine disorders and cancer
 CC in mammal, especially in humans. HORP is useful for producing antibodies
 CC and for drug screening using libraries of compounds. HORP polynucleotides
 CC and their antibodies are useful for diagnosis of disorders associated
 CC with HORP expression. The present sequence represents the HORP-5
 CC protein.

XX Sequence 444 AA;
 Query Match 100.0%; Score 2438; DB 21; Length 444;
 Best Local Similarity 100.0%; Pred. No. 4.3e-238;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKGNQGEAAREVSVPTFSWEEIQKHLRTDGLVDRKVNITKWSIQHFGQORVI 60
 DB 1 MGKGNQGEAAREVSVPTFSWEEIQKHLRTDGLVDRKVNITKWSIQHFGQORVI 60
 QY 61 GHVAGEDATDAFRAHFDLEFVGKFLKPLLGELAPEPSODHGKSKITDFRALRKA 120
 DB 61 GHVAGEDATDAFRAHFDLEFVGKFLKPLLGELAPEPSODHGKSKITDFRALRKA 120
 QY 121 EDNLFKTNHVPFLLLAHIIALESIAWTFVYFGNGWIPITLITAFVLATSQAQAGLQH 180
 DB 121 EDNLFKTNHVPFLLLAHIIALESIAWTFVYFGNGWIPITLITAFVLATSQAQAGLQH 180
 QY 181 DYGHLSVYRKPKNHLVHFVIGHLKAGSANWNRHFFQHAKEPIPHKDPVKNLHVFF 240
 DB 181 DYGHLSVYRKPKNHLVHFVIGHLKAGSANWNRHFFQHAKEPIPHKDPVKNLHVFF 240
 QY 241 LGEWQIEYGVKKLKYLPYNHQHEVFFLGPPLLPYFQYQIIMTMIVHKNVVDLAWAV 300
 DB 241 LGEWQIEYGVKKLKYLPYNHQHEVFFLGPPLLPYFQYQIIMTMIVHKNVVDLAWAV 300
 QY 301 SYVIRPFITYIPYGLGALLFNIRFLESWFWVWVQMNHIVMEIDQRAYRDFWSSQL 360
 DB 301 SYVIRPFITYIPYGLGALLFNIRFLESWFWVWVQMNHIVMEIDQRAYRDFWSSQL 360
 QY 361 TATCNVEQFFNDWFSGHNFQIEHLLPPTMPRNLHKLAPLVKSLCAKHGIEYQEKPL 420
 DB 361 TATCNVEQFFNDWFSGHNFQIEHLLPPTMPRNLHKLAPLVKSLCAKHGIEYQEKPL 420
 QY 421 RALLDIIRSLKSKGLWLDAYLHK 444
 DB 421 RALLDIIRSLKSKGLWLDAYLHK 444

RESULT 2
 AAB41810
 ID AAB41810 standard; Protein; 444 AA.

XX AAB41810;
 AC AAB41810;
 XX AAB41810;

DT 08-FEB-2001 (first entry)

XX Human ORFX ORF1574 polypeptide sequence SEQ ID NO:3148.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnery; antiproliferative; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;

KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

OS Homo sapiens.

PN WO200058473-A2.

XX 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US08621.

PR 31-MAR-1999; 93US-0127607.

PR 02-APR-1999; 93US-0127636.

PR 05-APR-1999; 93US-0127728.

PR 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach M;

PI WPI; 2000-602362/57.

DR N-PSDB; AAC76019.

XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

PS Claim 11; Page 2367-2368; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antiproliferative; antiparkinsonian; neurotropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 444 AA;

Query Match 99.5%; Score 2425; DB 21; Length 444;
 Best Local Similarity 99.5%; Pred. No. 1.1e-256;
 Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGKGNQGEAAREVSVPTFSWEEIQKHLRTDGLVDRKVNITKWSIQHFGQORVI 60
 DB 1 MGKGNQGEAAREVSVPTFSWEEIQKHLRTDGLVDRKVNITKWSIQHFGQORVI 60

QY 61 GHVAGEDATDAFRAHFDLEFVGKFLKPLLGELAPEPSODHGKSKITDFRALRKA 120
 DB 61 GHVAGEDATDAFRAHFDLEFVGKFLKPLLGELAPEPSODHGKSKITDFRALRKA 120

QY 121 EDMNLFKTNHVFLLAHIALESIAWFTVYFGNGWIPTLITAFVLATSOAQAGWLOH 180
DB 121 EDMNLFKTNHVFLLAHIALESIAWFTVYFGNGWIPTLITAFVLATSOAQAGWLOH 180
QY 181 DYGHLSVYRKPKWNHVLVHKFVIGHLKGSANWNNHRHFQHHAKPNIPHKDPDNNMLHVFV 240
DB 181 DYGHLSVYRKPKWNHVLVHKFVIGHLKGSANWNNHRHFQHHAKPNIPHKDPDNNMLHVFV 240
QY 241 LGWQPIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAV 300
DB 241 LGWQPIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAV 300
QY 301 SYIRPFITYIPFYGILGALLFLNFIREFSHWFWVTOMNHIWETDQAYRDWFSQ 360
DB 301 SYIRPFITYIPFYGILGALLFLNFIREFSHWFWVTOMNHIWETDQAYRDWFSQ 360
QY 361 TATCNVEOSFNDWFSGHLNFOIEHLLPPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLL 420
DB 361 TATCNVEOSFNDWFSGHLNFOIEHLLPPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLL 420
QY 421 RALDDIIRSLKXSGKMLDAYLHK 444
DB 421 RALDDIIRSLKXSGKMLDAYLHK 444

RESULT 3

AA97539
ID AA97539 standard; Protein; 444 AA.
AC AA97539;
DT 15-JAN-2001 (first entry)
DE Human fatty acid desaturase 2 protein sequence.
XX Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;
KW liver disease; coronary artery disease; cancer.
XX Homo sapiens.
XX EP1035207-A1.
XX 13-SEP-2000.
XX 09-MAR-1999; 99EP-0104664.
XX 09-MAR-1999; 99EP-0104664.
XX (MULT-) MULTIGENE BIOTECH GMBH.
XX Weber BHF, Marquardt A;
XX WPI: 2000-559875/52.
XX N-PSDB; AAA90953.
XX Novel cDNA molecules encoding three human fatty acid desaturases,
PT FADS1, FADS2 and FADS3, useful in the treatment of liver disease,
PT coronary artery disease and cancer.
XX Claim 1; Page 41-43; 72pp; English.

CC This sequence is the human fatty acid desaturase, FADS2, of the
CC invention. An antibody directed against the 3 FADS molecule of the
CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or
CC therapeutic purposes. The FADS coding sequences are useful in gene
CC therapy. The polypeptide and antibodies are useful in screening for
CC modulating drugs. The polypeptides are also useful for treating liver
CC disease, coronary artery disease and cancer.
CC Note: Two copies of the sequence listing are present within this
CC patent, which contain different sequences. AAA90952 and AAA90955 are
CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are
CC stated as being SEQ ID's 7-22.

XX SQ Sequence 444 AA;
Query Match 99.5%; Score 2425; DB 21; Length 444;
Best Local Similarity 99.5%; Pred. No. 1.1e-256;
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGKGNQGEAGAAAEVSVPTFSWEEIQHNLRTDGLVIDRKVYNTKWSIQHPGQORVI 60
DB 1 MGKGNQGEAGAAAEVSVPTFSWEEIQHNLRTDGLVIDRKVYNTKWSIQHPGQORVI 60
QY 61 GHVAGEDATDAFRAPHPDLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDFALRKT 120
DB 61 GHVAGEDATDAFRAPHPDLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDFALRKT 120
QY 121 EDMNLFKTNHVFLLAHIALESIAWFTVYFGNGWIPTLITAFVLATSOAQAGWLOH 180
DB 121 EDMNLFKTNHVFLLAHIALESIAWFTVYFGNGWIPTLITAFVLATSOAQAGWLOH 180
QY 181 DYGHLSVYRKPKWNHVLVHKFVIGHLKGSANWNNHRHFQHHAKPNIPHKDPDNNMLHVFV 240
DB 181 DYGHLSVYRKPKWNHVLVHKFVIGHLKGSANWNNHRHFQHHAKPNIPHKDPDNNMLHVFV 240
QY 241 LGWQPIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAV 300
DB 241 LGWQPIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAV 300
QY 301 SYIRPFITYIPFYGILGALLFLNFIREFSHWFWVTOMNHIWETDQAYRDWFSQ 360
DB 301 SYIRPFITYIPFYGILGALLFLNFIREFSHWFWVTOMNHIWETDQAYRDWFSQ 360
QY 361 TATCNVEOSFNDWFSGHLNFOIEHLLPPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLL 420
DB 361 TATCNVEOSFNDWFSGHLNFOIEHLLPPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLL 420
QY 421 RALDDIIRSLKXSGKMLDAYLHK 444
DB 421 RALDDIIRSLKXSGKMLDAYLHK 444

RESULT 4

AAE11083
ID AAE11083 standard; Protein; 444 AA.
XX AAE11083;
DT 18-DEC-2001 (first entry)
XX Human delta-6-desaturase (hD6D-1).
XX Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema;
KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;
KW gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;
KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;
KW cardiovascular disease; Crohn's disease; congenital liver disease;
KW schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;
KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;
KW autoimmune disorder; hypercholesterolemia; atopic disorder; hD6D-1;
KW gene therapy; human.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Domain 53..76 /note= "Cytochrome b5 motif"
FT Region 180..184 /note= "His II box"
FT Region 217..221 /note= "His II box"
FT Region 382..386 /note= "His III box"
XX WO200170993-A2.

XX PD 27-SEP-2001.

XX PF 26-MAR-2001; 2001WO-CA00398.

XX PR 24-MAR-2000; 2000CA-2301158.

XX PA (SCOT-) SCOTIA HOLDINGS PLC.

XX PI Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;

XX DR WPI; 2001-611507/70.

XX DR N-PSDB; RAD19403.

XX PT Nucleic acid encoding delta-6-desaturase gene useful for treating

XX PT atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,

XX PT gastrointestinal disorders, viral infections and post viral fatigue -

XX PS Example 4; Fig 6; 164pp; English.

XX CC The invention relates to polynucleotides that control delta-6

XX CC desaturase genes (D6D) and methods useful for identifying compounds

XX CC which inhibit or promote the activity of mammalian D6D. Compounds

XX CC which modulate D6D gene segments are useful for treating lipid

XX CC metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid

XX CC arthritis, Sjogren's syndrome, gastrointestinal disorders, viral

XX CC infections and post viral fatigue, pre-menstrual syndrome,

XX CC endometriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,

XX CC cardiovascular disease, Crohn's disease, cancer, congenital liver

XX CC disease, schizophrenia, diabetes and diabetic complications including

XX CC diabetic neuropathy, nephropathy and retinopathy. Compounds of the

XX CC invention are also useful for inhibiting progressive and acute

XX CC disorders such as arterial hypertension, atherosclerosis, chronic

XX CC inflammatory and autoimmune disorders, hypercholesterolaemia and

XX CC other atopic disorders. D6D genes are useful in gene therapy. The

XX CC present sequence is human delta-6-desaturase (hD6D-1).

XX SQ Sequence 444 AA;

Query Match 99.5%; Score 2425; DB 22; Length 444;

Best Local Similarity 99.5%; Pred. No. 1.1e-256;

Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGKGNQGEAAREVSVPTFSWEEIQKHLRTDGLVIDRKVNITKWSIQHPGQORVI 60

DB 1 MGKGNQGEAAREVSVPTFSWEEIQKHLRTDGLVIDRKVNITKWSIQHPGQORVI 60

QY 61 GHYAGEDATDAFRAHPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKA 120

DB 61 GHYAGEDATDAFRAHPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKA 120

QY 121 EDNMLFKTNHVFLLLAHIIALESIAWFTVFYFGNGWIPFTLITAFVLATSAQAGWLQH 180

DB 121 EDNMLFKTNHVFLLLAHIIALESIAWFTVFYFGNGWIPFTLITAFVLATSAQAGWLQH 180

QY 181 DYGHLSVYRKPKNNHLVHKFVIGHLKGASANNWNHRHFQHKAPNIFHKDPDVMNMLHVFV 240

DB 181 DYGHLSVYRKPKNNHLVHKFVIGHLKGASANNWNHRHFQHKAPNIFHKDPDVMNMLHVFV 240

QY 241 LGWQPTIEYKGLKYLIPYNQHEYPFLIGPPLIIPMYFOYQIIMTMIVHKWVDLAWAV 300

DB 241 LGWQPTIEYKGLKYLIPYNQHEYPFLIGPPLIIPMYFOYQIIMTMIVHKWVDLAWAV 300

QY 301 SYITRPFITIPFYGILGALLFNFINRFLSHVFWVWVTQNNHIVMEIDQEAAYRDFSSQL 360

DB 301 SYITRPFITIPFYGILGALLFNFINRFLSHVFWVWVTQNNHIVMEIDQEAAYRDFSSQL 360

QY 361 TATCNVQSPFNDWFSGLHNFQIEHLLFPTMPRNHLKIAPLVKSCAKHGIEYQKPL 420

DB 361 TATCNVQSPFNDWFSGLHNFQIEHLLFPTMPRNHLKIAPLVKSCAKHGIEYQKPL 420

QY 421 RALLDIIIRSLKSGKWLDAYLHK 444

DB 421 RALLDIIIRSLKSGKWLDAYLHK 444

RESULT 5

AAM93425

ID AAM93425 standard; Protein; 444 AA.

XX AAM93425;

XX 06-NOV-2001 (first entry)

XX Human polypeptide, SEQ ID NO: 3050.

DE Human; full length cDNA; cDNA synthesis; oligo-capping.

XX Homo sapiens.

OS EP1130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-0114089.

XX 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayaashi K, Iehii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

DR N-PSDB; AAK94346.

XX 830 Primers useful for synthesizing full length cDNA clones and their

XX use in genetic manipulation -

XX Claim 8; SEQ ID NO 3050; 1380pp + sequence listing; English.

XX The invention relates to primers for synthesising full length cDNA

XX clones. 830 cDNA molecules encoding a human protein have been

XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA

XX molecules have been determined. Primers for synthesising the full length

XX cDNA are useful for clarifying the function of the protein encoded by

XX the cDNA. The full length clones were obtained by construction of full

XX length enriched cDNA libraries that were synthesised by the oligo-capping

XX method. The primers enable the production of the full length cDNA easily

XX without any special methods. The present sequence is a polypeptide

XX encoded by a full length human cDNA of the invention.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in CD-ROM format directly from EPO.

XX SQ Sequence 444 AA;

Query Match 99.5%; Score 2425; DB 22; Length 444;

Best Local Similarity 99.5%; Pred. No. 1.1e-256;

Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGKGNQGEAAREVSVPTFSWEEIQKHLRTDGLVIDRKVNITKWSIQHPGQORVI 60

DB 1 MGKGNQGEAAREVSVPTFSWEEIQKHLRTDGLVIDRKVNITKWSIQHPGQORVI 60

QY 61 GHYAGEDATDAFRAHPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKA 120

DB 61 GHYAGEDATDAFRAHPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKA 120

QY 121 EDNMLFKTNHVFLLLAHIIALESIAWFTVFYFGNGWIPFTLITAFVLATSAQAGWLQH 180

DB 121 EDNMLFKTNHVFLLLAHIIALESIAWFTVFYFGNGWIPFTLITAFVLATSAQAGWLQH 180

QY 181 DYGHLSVYRKPKNNHLVHKFVIGHLKGASANNWNHRHFQHKAPNIFHKDPDVMNMLHVFV 240

Db 181 DYGLSVYRKPKWNLVHKFVIGHLKGASANWNRHFQHHAKNIFPHKDPDVNMLHVFV 240
QY 241 LGEWQPIEYGGKKLKYLPYNHOFHEFFLIGPPLIPMYFOIIMTVHKWVYDLAWAV 300
Db 241 LGEWQPIEYGGKKLKYLPYNHOFHEFFLIGPPLIPMYFOIIMTVHKWVYDLAWAV 300
QY 301 SYIRFFTYIPFYGILGALLFLNPIRFLSHFWVVTQNMHIWEIDQAYRDWFSQ 360
Db 301 SYIRFFTYIPFYGILGALLFLNPIRFLSHFWVVTQNMHIWEIDQAYRDWFSQ 360
QY 361 TATCNVEQSFNDWFSGLNFOIEHHLPTTPRNHLKIAPLVKSCLKAKGIEYQEKPL 420
Db 361 TATCNVEQSFNDWFSGLNFOIEHHLPTTPRNHLKIAPLVKSCLKAKGIEYQEKPL 420
QY 421 RALLDIIRSLKSKGLWLDAYLHK 444
Db 421 RALLDIIRSLKSKGLWLDAYLHK 444

RESULT 6

AAE11084
ID AAE11084 standard; Protein; 473 AA.

AC AAE11084;

DT 18-DEC-2001 (first entry)

XX C-terminal tagged human delta-6-desaturase (hδ6D-1).

DE Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema;
KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;
KW Gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;
KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;
KW cardiovascular disease; Crohn's disease; congenital liver disease;
KW schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;
KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;
KW autoimmune disorder; hypercholesterolaemia; atopic disorder; hδ6D-1;
KW gene therapy; human.

OS Homo sapiens.

XX Key Location/Qualifiers
FH Region 451..464
FT /note= "v5 tag"
FT Region 468..473
FT /note= "6xHis tag"

XX WO200170993-A2.

XX 27-SEP-2001.

XX 26-MAR-2001; 2001WO-CA00398.

XX 24-MAR-2000; 2000CA-2301158.

XX (SCOT-) SCOTIA HOLDINGS PLC.

XX Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;

XX WPI; 2001-611507/70.

XX Nucleic acid encoding delta-6-desaturase gene useful for treating
PT atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,
PT gastrointestinal disorders, viral infections and post viral fatigue -

XX Example 4; Fig 5; 164pp; English.

XX The invention relates to polynucleotides that control delta-6
CC desaturase genes (D6D) and methods useful for identifying compounds
CC which inhibit or promote the activity of mammalian D6D. Compounds
CC which modulate D6D gene segments are useful for treating lipid
CC metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid
CC arthritis, Sjogren's syndrome, gastrointestinal disorders, viral

CC infections and post viral fatigue, pre-menstrual syndrome,
CC endometriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,
CC cardiovascular disease, Crohn's disease, cancer, congenital liver
CC disease, schizophrenia, diabetes and diabetic complications including
CC diabetic neuropathy, nephropathy and retinopathy. Compounds of the
CC invention are also useful for inhibiting progressive and acute
CC disorders such as arterial hypertension, atherosclerosis, chronic
CC inflammatory and autoimmune disorders, hypercholesterolaemia and
CC other atopic disorders. D6D genes are useful in gene therapy. The
CC present sequence is C-terminal tagged human delta-6-desaturase
CC (hδ6D-1) enzyme.

XX Sequence 473 AA;

QY Query Match 99.5%; Score 2425; DB 22; Length 473;
Db Best Local Similarity 99.5%; Pred. No. 1.3e-256;
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGKGGNQGEAAREVSVPTFSWEEIQKHNLTDSGLVIDRKVYNITKWSIQHGGQQRVI 60
Db 1 MGKGGNQGEAAREVSVPTFSWEEIQKHNLTDRWLVIDRKVYNITKWSIQHGGQQRVI 60
QY 61 GHYAGEDATDAFRAHPDLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDFRALKTA 120
Db 61 GHYAGEDATDAFRAHPDLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDFRALKTA 120
QY 121 EDNLEKTNHVFLLLAHIIAILESTAMFTVFYFGNGWIPTLITAFVLATSOAQAGWLOH 180
Db 121 EDNLEKTNHVFLLLAHIIAILESTAMFTVFYFGNGWIPTLITAFVLATSOAQAGWLOH 180
QY 181 DYGHLSVYRKPKWNLVHKFVIGHLKGASANWNRHFQHHAKPNI FHKDPDVNMLHVFV 240
Db 181 DYGHLSVYRKPKWNLVHKFVIGHLKGASANWNRHFQHHAKPNI FHKDPDVNMLHVFV 240
QY 241 LGEWQPIEYGGKKLKYLPYNHOFHEFFLIGPPLIPMYFOIIMTVHKWVYDLAWAV 300
Db 241 LGEWQPIEYGGKKLKYLPYNHOFHEFFLIGPPLIPMYFOIIMTVHKWVYDLAWAV 300
QY 301 SYIRFFTYIPFYGILGALLFLNPIRFLSHFWVVTQNMHIWEIDQAYRDWFSQ 360
Db 301 SYIRFFTYIPFYGILGALLFLNPIRFLSHFWVVTQNMHIWEIDQAYRDWFSQ 360
QY 361 TATCNVEQSFNDWFSGLNFOIEHHLPTTPRNHLKIAPLVKSCLKAKGIEYQEKPL 420
Db 361 TATCNVEQSFNDWFSGLNFOIEHHLPTTPRNHLKIAPLVKSCLKAKGIEYQEKPL 420
QY 421 RALLDIIRSLKSKGLWLDAYLHK 444
Db 421 RALLDIIRSLKSKGLWLDAYLHK 444

RESULT 7

AA51801
ID AA51801 standard; Protein; 444 AA.

AC AA51801;

XX 29-JAN-2002 (first entry)

XX Rat fatty acid desaturase.

XX Rat; fatty acid desaturase; unsaturated long-chain fatty acid production;
KW fermentation.

XX Rattus norvegicus.

XX WO200175069-A1.

XX 11-OCT-2001.

XX 31-MAR-2000; 2000WO-JP02129.

XX 31-MAR-2000; 2000WO-JP02129.

XX (IDM) IDEMITSU PETROCHEM CO LTD.
 XX Suzuki O, Ono K, Aki T, Shimauchi T, Nakajima T, Kondo A;
 XX WPI; 2001-648552/74.
 XX N-PSDB; AAI66599.
 XX New microorganism for the efficient expression of long-chain
 PT unsaturated fatty acids into the medium, comprises Saccharomyces
 PT transformed by a fatty acid desaturase gene -
 XX Disclosure; Page 26-27; 29pp; Japanese.
 XX The present invention relates to a microorganism transformed by a gene
 CC encoding a fatty acid desaturase and having the ability to secrete lipids
 CC into the medium. This can be used for the efficient production of
 CC unsaturated long-chain fatty acids by fermentation. The present sequence
 CC is the fatty acid desaturase from Rattus norvegicus.
 XX
 SQ Sequence 444 AA;
 Query Match 89.8%; Score 2190; DB 22; Length 444;
 Best Local Similarity 87.8%; Pred. No. 6.7e-231;
 Matches 390; Conservative 26; Mismatches 28; Indels 0; Gaps 0;
 QY 1 MGKGGNQGEGAAREVSVPTFSWEEIQKHNLRDGLVIDRKVNITKWSIQHPGGORVI 60
 Db 1 MGKGGNQGEGSTELQAPMPTFRWEEIQKHNLRDGLVIDRKVNITKWSIQHPGGORVI 60
 QY 61 GHYAGEDATDAFRAHLDLDFVCKFLKPLLIGELAPEPSQDHGKNSKITDFRALRXTA 120
 Db 61 GHYSGEDATDAFRAHLDLDFVCKFLKPLLIGELAPEPSQDHGKNSKITDFRALRXTA 120
 QY 121 EDMNLFKTNHVFFLLLAHIIALESIAWFTVFYFGNGWIPITLITAFVLATSOAQAGWLQH 180
 Db 121 EDMNLFKTNHVFFLLSHIIVNESIAWFTVILSYFGNGWIPITLITAFVLATSOAQAGWLQH 180
 QY 181 DYCHLSVYRKPKWNLVHKVFTVGHILKGSANWNNHRRHFOHAKPNIFHKDPDVMNLHV 240
 Db 181 DYCHLSVYKSIWNHIVHKVFTVGHILKGSANWNNHRRHFOHAKPNIFHKDPDVKSLAV 240
 QY 241 LGSWQIEYKGLKYLPHNQHEHYEFLGPPLLIPMYFYQIIMTIVHKWVDLAWAV 300
 Db 241 LGSWQIEYKGLKYLPHNQHEHYEFLGPPLLIPMYFYQIIMTIVHKWVDLAWAI 300
 QY 301 SYVIRFFTYIPYIGLALLFNFTIRFLESHWFWVWVWQNHIVMEIDOEAYRDWFSQ 360
 Db 301 SYVIRFFTYIPYIGLALLFNFTIRFLESHWFWVWVWQNHIVMEIDOEAYRDWFSQ 360
 QY 361 TATCNVEQSFNDWFSGLNLFQIEHLLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPLL 420
 Db 361 AATCNVEQSFNDWFSGLNLFQIEHLLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPLL 420
 QY 421 RALLDIIRSLKSGKWLDAYLHK 444
 Db 421 RALLDIIRSLKSGKWLDAYLHK 444

RESULT 8
 AAE11081
 ID AAE11081 standard; Protein; 444 AA.
 XX
 AC AAE11081;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Rat delta-6-desaturase (rd6d-1).
 XX
 XX Delta-6-desaturase gene; D6d; lipid metabolism disorder; atopic eczema;
 KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;
 KW gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;
 KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;

KW cardiovascular disease; Crohn's disease; congenital liver disease;
 KW schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;
 KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;
 KW autoimmune disorder; hypercholesterolaemia; atopic disorder; rd6d-1;
 XX Gene therapy; rat.
 OS
 XX Rattus sp.
 XX Key Location/Qualifiers
 XX Domain 53..76
 FT /note= "Cytochrome b5 motif"
 FT Region 180..184
 FT /note= "His II box"
 FT Region 217..221
 FT /note= "His II box"
 FT Misc-difference 240
 FT /note= "Encoded by GCC"
 FT Region 382..386
 FT /note= "His III box"
 XX
 PN W0200170993-A2.
 XX
 XX 27-SEP-2001.
 XX
 XX 26-MAR-2001; 2001WO-CA00398.
 PF
 XX 24-MAR-2000; 2000CA-2301158.
 PR
 XX (SCOT-) SCOTIA HOLDINGS PLC.
 FA
 XX Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;
 PI
 XX WPI: 2001-611507/70.
 DR N-PSDB; AAD19402.
 XX
 XX Nucleic acid encoding delta-6-desaturase gene useful for treating
 PT atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,
 PT gastrointestinal disorders, viral infections and post viral fatigue -
 PT
 XX Example 3; Fig 5; 164pp; English.
 PS
 XX The invention relates to polynucleotides that control delta-6
 CC desaturase genes (D6d) and methods useful for identifying compounds
 CC which inhibit or promote the activity of mammalian D6d. Compounds
 CC which modulate D6d gene segments are useful for treating lipid
 CC metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid
 CC arthritis, Sjogren's syndrome, gastrointestinal disorders, viral
 CC infections and post viral fatigue, pre-menstrual syndrome,
 CC endometriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,
 CC cardiovascular disease, Crohn's disease, cancer, congenital liver
 CC disease, schizophrenia, diabetes and diabetic complications including
 CC diabetic neuropathy, nephropathy and retinopathy. Compounds of the
 CC invention are also useful for inhibiting progressive and acute
 CC disorders such as arterial hypertension, atherosclerosis, chronic
 CC inflammatory and autoimmune disorders, hypercholesterolaemia and
 CC other atopic disorders. D6d genes are useful in gene therapy. The
 CC present sequence is rat delta-6-desaturase (rd6d-1).
 XX
 SQ Sequence 444 AA;
 Query Match 89.8%; Score 2190; DB 22; Length 444;
 Best Local Similarity 87.8%; Pred. No. 6.7e-231;
 Matches 390; Conservative 26; Mismatches 28; Indels 0; Gaps 0;
 QY 1 MGKGGNQGEGAAREVSVPTFSWEEIQKHNLRDGLVIDRKVNITKWSIQHPGGORVI 60
 Db 1 MGKGGNQGEGSTELQAPMPTFRWEEIQKHNLRDGLVIDRKVNITKWSIQHPGGORVI 60
 QY 61 GHYAGEDATDAFRAHLDLDFVCKFLKPLLIGELAPEPSQDHGKNSKITDFRALRXTA 120
 Db 61 GHYSGEDATDAFRAHLDLDFVCKFLKPLLIGELAPEPSQDHGKNSKITDFRALRXTA 120
 QY 121 EDMNLFKTNHVFFLLLAHIIALESIAWFTVFYFGNGWIPITLITAFVLATSOAQAGWLQH 180

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121 EDMKLFKTNLHFPFLLSLHIIWMSIAWFTLSYFGNGWIPVTITAFVLATSOAAGWLQH 180
181 DYGHLSVYRKPNHVLHVKVIGHLKASANWNNHRRHFOHAKPNIHFKDPDVNMLHVFV 240
181 DYGHLSVYKKSINWHIVHKKVIGHLKASANWNNHRRHFOHAKPNIHFKDPDIKSLHVFV 240
241 LGWQPIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAI 300
241 LGWQPIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMIRRRDWDLAWAI 300
301 SYIRPFITYPFYGILGALLFNFIRFLESHWFWVTOMNHIVMEIDQAYEDWESSOL 360
301 SYARPFYTYIPFYGILGALLFNFIRFLESHWFWVTOMNHIVMEIDLDHYRDWESSOL 360
361 TATCNVQSFNDWFSGLHNFQIEHLLFPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLL 420
361 AATCNVQSFNDWFSGLHNFQIEHLLFPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLL 420
421 RALLDIIRSLKSKGKMLDAYLHK 444
421 RALLDIVSSLKSKGKMLDAYLHK 444

RESULT 9
ID AAE11082 standard; Protein; 473 AA.
AC AAE11082;
XX
XX
DT 18-DEC-2001 (first entry)
DE C-terminal tagged rat delta-6-desaturase (rD6D-1).
XX
XX Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema;
KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;
KW gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;
KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;
KW cardiovascular disease; Crohn's disease; congenital liver disease;
KW schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;
KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;
KW autoimmune disorder; hypercholesterolaemia; atopic disorder; rD6D-1;
KW gene therapy; rat.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
XX Region 451..464
XX FT /note= "v5 tag"
XX FT 468..473
XX FT /note= "6xHis tag"
XX
XX WO200170993-A2.
XX
XX 27-SEP-2001.
XX
XX 26-MAR-2001; 2001WO-CA00398.
XX
XX 24-MAR-2000; 2000CA-2301158.
XX
XX (SCOT-) SCOTIA HOLDINGS PLC.
XX
XX Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;
XX WPI; 2001-611507/70.
XX
XX Nucleic acid encoding delta-6-desaturase gene useful for treating
XX atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,
XX gastrointestinal disorders, viral infections and post viral fatigue -
XX Example 3; Fig 5; 164pp; English.
XX
XX The invention relates to polynucleotides that control delta-6
XX

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CC desaturase genes (D6D) and methods useful for identifying compounds
CC which inhibit or promote the activity of mammalian D6D. Compounds
CC which modulate D6D gene segments are useful for treating lipid
CC metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid
CC arthritis, Sjogren's syndrome, gastrointestinal disorders, viral
CC infections and post viral fatigue, pre-menstrual syndrome,
CC endometriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,
CC cardiovascular disease, Crohn's disease, cancer, congenital liver
CC disease, schizophrenia, diabetes and diabetic complications including
CC diabetic neuropathy, nephropathy and retinopathy. Compounds of the
CC invention are also useful for inhibiting progressive and acute
CC disorders such as arterial hypertension, atherosclerosis, chronic
CC inflammatory and autoimmune disorders, hypercholesterolaemia and
CC other atopic disorders. D6D genes are useful in gene therapy. The
CC present sequence is C-terminal tagged rat delta-6-desaturase
CC (rD6D-1) enzyme.
XX
XX Sequence 473 AA;
SQ
Query Match 89.7%; Score 2186; DB 22; Length 473;
Best Local Similarity 87.6%; Fred. No. 2e-230; Indels 0; Gaps 0;
Matches 389; Conservative 26; Mismatches 29;
1 MGKGNQGEAGAEVSVPTFSWEIQRHNLRTDGLVIDRKVYNITKWSIQHGGQRV 60
1 MGKGNQGEAGSTELQAPMPTFRWEIQRHNLRTDGLVIDRKVYNITKWSIQHGGHVI 60
61 GHYAGEDATDAFRAHPDLEFVGKLPKLLIGELAPEPSODHGKNSKITEDFALRKT 120
61 GHYGEDATDAFRAHLDLDFVGKLPKLLIGELAPEPSLDRGKSSQITDFAKKT 120
121 EDMLFKTNHVPFLLSLAHIIAIESIAWFTVYFGNGWIPVTITAFVLATSOAAGWLQH 180
121 EDMLFKTNHVPFLLSLAHIIWMSIAWFTVYFGNGWIPVTITAFVLATSOAAGWLQH 180
181 DYGHLSVYRKPNHVLHVKFVIGHLKASANWNNHRRHFOHAKPNIHFKDPDVNMLHVFV 240
181 DYGHLSVYKKSINWHIVHKKVIGHLKASANWNNHRRHFOHAKPNIHFKDPDIKSLHVF 240
241 LGWQPIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAI 300
241 LGWQPIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMIRRRDWDLAWAI 300
301 SYIRPFITYPFYGILGALLFNFIRFLESHWFWVTOMNHIVMEIDQAYEDWESSOL 360
301 SYARPFYTYIPFYGILGALLFNFIRFLESHWFWVTOMNHIVMEIDLDHYRDWESSOL 360
361 TATCNVQSFNDWFSGLHNFQIEHLLFPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLL 420
361 AATCNVQSFNDWFSGLHNFQIEHLLFPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLL 420
421 RALLDIIRSLKSKGKMLDAYLHK 444
421 RALLDIVSSLKSKGKMLDAYLHK 444

RESULT 10
ABG94691
ID ABG94691 standard; Protein; 432 AA.
XX
XX AC ABG94691;
XX
XX 02-DEC-2002 (first entry)
XX
XX Human delta5-desaturase #1.
XX
XX Human; delta5-desaturase; polyunsaturated fatty acid; DGLA;
XX dihydro-gamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;
XX eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;
XX enzyme.
XX
XX Homo sapiens.
XX

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PN US6432684-B1.
XX 13-AUG-2002.
XX 08-JAN-1999; 99US-0227613.
XX 11-APR-1997; 97US-0833610.
XX 10-APR-1998; 98WO-US07422.
XX (ABBO) ABBOTT LAB.
XX Mukerji P, Leonard AE, Huang Y, Das T;
XX WPI; 2002-689761/74.
XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing
PT the conversion of dihomogamma-linolenic acid to arachidonic acid and
PT in the conversion of 20:4n-3 to eicosapentaenoic acid -
XX
XX Example 1; Figure 9; 89pp; English.
XX The invention relates to an isolated human delta5-desaturase nucleotide
CC sequence (I) which desaturates polyunsaturated fatty acids at
CC carbon 5. The nucleotide sequence (I) may be used in the recombinant
CC production of vectors and host cells for the production of delta5-
CC desaturase. Delta5-desaturase may be utilised in the conversion of
CC dihomogamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the
CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA or
CC polyunsaturated fatty acids produced from it may be added to
CC pharmaceutical compositions, nutritional compositions, animal feeds, as
CC well as other products such as cosmetics. ABG94691-ABG94708 represent
CC human delta5-desaturase amino acid sequences of the invention.
XX
XX Sequence 432 AA;
Query Match 79.6%; Score 1940.5; DB 23; Length 432;
Best Local Similarity 81.8%; Pred. No. 1.4e-203;
Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;
QY 19 PT---FSWEEIQKHNRDGLVIDEKYNIKFSIOHPGGORVIGHYAGDADAPAF 75
DB 3 PTPRYFTWDEVAQSCCEERNLVIDRKVYNISEFTRRHPGGSRVISHAGQADTPFVAF 62
QY 76 HPDLEFVGKFLKLLIGELAPESPDSODHGKNGSKITDFALRKTAEKMLFKTNHVFLL 135
DB 63 HINKGLVKYKMSLLIGELSPQSPFPTKXKELTDFELRATVVERGLMKANHFVLL 122
QY 136 LLAHIIALSIATFTVYFGNGWIPLITAFVLATSOAQAGLQHDYGHLSVYRKPKNH 195
DB 123 YLLHILLDGAALWLTWVFGTSLPFLLCVLLSAVQAQAGLQHDYGHLSVYRKPKNH 182
QY 196 LVHKFVIGHLKGSANWNNHRRHPOHAKPNIHKDPDVMNLHVFLGEPQIEYGGKLLK 255
DB 183 LVKHFVIGHLKGSANWNNHRRHPOHAKPNIHKDPDVMNLHVFLGEPQIEYGGKLLK 242
QY 256 YLPYNHQHEFFLIGPLLPIMYFQYQIIMTVHKNQWDLAWAVSYIRFTITIPYFG 315
DB 243 YLPYNHQHEFFLIGPLLPIMYFQYQIIMTVHKNQWDLAWAVSYIRFTITIPYFG 302
QY 316 ILGALLFLNFIRESHFWVWVQMMHNYEIDQEAIRDFWESSQLTATCNVQSFPNDWF 375
DB 303 ILGALLFLNFIRESHFWVWVQMMHNYEIDQEAIRDFWESSQLTATCNVQSFPNDWF 362
QY 376 SGHLNFQIEHLLFPTPRNHLKIAPLVKSCLKAGHIEYQEKPLRALDLIIRSLKSGK 435
DB 363 SGHLNFQIEHLLFPTPRNHLKIAPLVKSCLKAGHIEYQEKPLRALDLIIRSLKSGK 422
QY 436 LWLDAYLHK 444
DB 423 LWLDAYLHK 431

RESULT 11

ABG96508
ID ABG96508 standard; Protein; 432 AA.
XX
AC ABG96508;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human partial desaturase protein from contig 253538a.
XX
KW Human; enzyme; delta5 desaturase; polyunsaturated fatty acid;
KW PUFA; nutritional; animal feed; cosmetic; skin aging; burn; angioplasty;
KW inflammation; rheumatoid arthritis; asthma; psoriasis; osteoporosis;
KW kidney stone; urinary tract stone; cancer; cachexia; diabetes; eczema;
KW AIDS; multiple sclerosis; blood pressure; platelet aggregation;
KW vasodilatation; cholesterol; proliferation of fibrous tissue;
KW endometriosis; myalgic encephalomyelitis; human breast milk;
XX dietary supplement; chromosome 11q12.
XX
OS Homo sapiens.
XX
XX US6428990-B1.
XX
XX 06-AUG-2002.
XX
XX 12-NOV-1999; 99US-0439261.
XX
XX 11-APR-1997; 97US-0833610.
XX 10-APR-1998; 98WO-US07422.
XX 08-JAN-1999; 99US-0227613.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;
XX
XX WPI; 2002-730518/79.
XX N-PSDB; ABS76713.
XX
XX Producing a polyunsaturated fatty acid (PUFA), useful in dietary
PT supplements and in treating diseases e.g., cancer, comprises expressing
PT human delta 5-desaturase enzyme and exposing enzyme to substrate PUFA
PT to convert to product PUFA -
XX
XX Example 1; Fig 9; 104pp; English.
XX
XX The invention relates to producing (M1) a polyunsaturated fatty acid
CC (PUFA), comprising: (i) isolating a fully defined human Delta5-desaturase
CC gene sequence (I); (ii) constructing a vector comprising (i);
CC (iii) introducing the vector into a host cell for expression of the
CC human Delta5-desaturase enzyme (II); and (iv) exposing (II) to a
CC substrate PUFA (III) such that it is converted to a product PUFA (IV).
CC The method is useful for producing a polyunsaturated fatty acid
CC such as arachidonic acid (AA), eicosapentaenoic acid (EPA), adrenic
CC acid, (n-3)-docosapentaenoic acid, (n-6)-docosapentaenoic acid and/or
CC docosahexaenoic (DHA) acid. The PUFAs produced by the method, such
CC as arachidonic acid (AA), eicosapentaenoic acid (EPA) and/or
CC docosahexaenoic (DHA) acid, are useful for replicating the PUFA content
CC of human breast milk or to alter the presence of PUFAs normally found
CC in a non-human mammal's milk. PUFAs produced by (M1) may be added to a
CC dietary substitute or supplement, particularly an infant formula, for
CC patients undergoing intravenous feeding or for preventing or treating
CC malnutrition or other conditions or disease states. The PUFAs are
CC useful for producing nutritional compositions e.g., any food or
CC preparation for human consumption including for enteral or parenteral
CC consumption, which when taken into the body serve to nourish or build
CC up tissues or supply energy and/or maintain, restore or support
CC adequate nutritional status or metabolic function. The PUFAs are also
CC useful in animal feed supplements to alter an animal tissue or milk
CC fatty acid composition to one or more desirable for human or animal
CC consumption, in animal feed substitutes, animal vitamins or in animal
CC topical ointments. The PUFAs produced by this method are useful in
CC producing pharmaceutical compositions for treating rough or aging skin,
CC injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,
CC asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,

CC cachexia associated with cancer, diabetes, eczema, AIDS, multiple
 CC sclerosis, PUFAs are also useful in reducing blood pressure, inhibiting
 CC platelet aggregation, inducing vasodilation, reducing cholesterol
 CC levels, inhibiting proliferation of fibrous tissue, treating
 CC endometriosis, and myalgic encephalomyelitis. The gene for delta5
 CC desaturase is located on chromosome 11q12. The present sequence
 XX is a partial human delta5 desaturase protein.
 SQ Sequence 432 AA;

Query Match 79.6%; Score 1940.5; DB 23; Length 432;
 Best Local Similarity 81.8%; Pred. No. 1.4e-203;
 Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;

Qy 19 PT---FWEETQKHNLRDGLVDRKVNITKWSIQHGGQVGHYAGEDATDAFRAF 75
 Db 3 PTPRYFTWDEVAQSGGCEERLWIDRVKYNISEFTRRHPGGSRVISHYAGQDATDPFVAF 62

Qy 76 HPDLFVGVKFLPLLIGELAPBEPDQHGKSKITDFRALRKTAEADNMLFKTNHVPFLL 135
 Db 63 HINKGLVKYKYNLSLIGELSPQSPFETPKNLTDFRELRAVTRMGLMKANHVFFLL 122

Qy 136 LLAHIIALESATWTFVFGNGWITLITAFVLATSOAQAGWLQHDYGHLSVYRKPKWNH 195
 Db 123 YLLHILLDGAWLTLVFGTSFLPFLCAVLLSAVQAQAQAGWLQHDYGHLSVYRKPKWNH 182

Qy 196 LVHKEFVIGHLKASANNWNRHFOHAKPNIFHKDPDNNMLHVPVLGEWOPIEYKKKLLK 255
 Db 183 LVHKEFVIGHLKASANNWNRHFOHAKPNIFHKDPDNNMLHVPVLGEWOPIEYKKKLLK 242

Qy 256 YLPYNHGHYFFLLGPPLLIPMYFOYQIIMTVHKWVDLANAVSYVIRFTIYIPFYG 315
 Db 243 YLPYNHGHYFFLLGPPLLIPMYFOYQIIMTVHKWVDLANAVSYVIRFTIYIPFYG 302

Qy 316 ILGALLFLNFIREFLESHWVWVTQNNHIVMEIDQAYRDWFFSQLTATCNVEQSFNDWF 375
 Db 303 ILGALLFLNFIREFLESHWVWVTQNNHIVMEIDQAYRDWFFSQLTATCNVEQSFNDWF 362

Qy 376 SGHNFQIEHLLFPTMPRNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKS GK 435
 Db 363 SGHNFQIEHLLFPTMPRNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKS GK 422

Qy 436 LWLDAYLHK 444
 Db 423 LWLDAYLHK 431

RESULT 12
 ABG94704
 ID ABG94704 standard; Protein; 465 AA.
 AC ABG94704;
 XX
 XX 02-DEC-2002 (first entry)
 DE Human delta5-desaturase #14.
 XX Human; delta5-desaturase; polyunsaturated fatty acid; DGLA;
 XX dihydro-gamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;
 XX eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;
 XX enzyme.
 OS Homo sapiens.
 OS
 OS US6432684-B1.
 FN
 XX
 XX 13-AUG-2002.
 PD
 XX
 XX 08-JAN-1999; 99US-0227613.
 EF
 XX
 XX 11-APR-1997; 97US-0833610.
 PR
 XX 10-APR-1998; 98WO-US07422.
 XX

PA (ABRO) ABBOTT LAB.
 XX Mukerji P, Leonard AE, Huang Y, Das T;
 PI WPI; 2002-689761/74.
 XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing
 PT the conversion of dihydro-gamma-linolenic acid to arachidonic acid and
 PT in the conversion of 20:4n-3 to eicosapentaenoic acid -
 XX Example 1; Figure 29; 88pp; English.
 PS The invention relates to an isolated human delta5-desaturase nucleotide
 XX sequence (i) which desaturates polyunsaturated fatty acids at
 CC carbon 5. The nucleotide sequence (i) may be used in the recombinant
 CC production of vectors and host cells for the production of delta5-
 CC desaturase. Delta5-desaturase may be utilised in the conversion of
 CC dihydro-gamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the
 CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA) AA. Or
 CC polyunsaturated fatty acids produced from it may be added to
 CC pharmaceutical compositions, nutritional compositions, animal feeds, as
 CC well as other products such as cosmetics. ABG94691-ABG94708 represent
 CC human delta5-desaturase amino acid sequences of the invention.
 XX Sequence 465 AA;
 SQ

Query Match 79.6%; Score 1940.5; DB 23; Length 465;
 Best Local Similarity 81.8%; Pred. No. 1.6e-203;
 Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;

Qy 19 PT---FSWEEIQKHNLRDGLVDRKVNITKWSIQHGGQVGHYAGEDATDAFRAF 75
 Db 3 PTPRYFTWDEVAQSGGCEERLWIDRVKYNISEFTRRHPGGSRVISHYAGQDATDPFVAF 62

Qy 76 HPDLFVGVKFLPLLIGELAPBEPDQHGKSKITDFRALRKTAEADNMLFKTNHVPFLL 135
 Db 63 HINKGLVKYKYNLSLIGELSPQSPFETPKNLTDFRELRAVTRMGLMKANHVFFLL 122

Qy 136 LLAHIIALESATWTFVFGNGWITLITAFVLATSOAQAGWLQHDYGHLSVYRKPKWNH 195
 Db 123 YLLHILLDGAWLTLVFGTSFLPFLCAVLLSAVQAQAQAGWLQHDYGHLSVYRKPKWNH 182

Qy 196 LVHKEFVIGHLKASANNWNRHFOHAKPNIFHKDPDNNMLHVPVLGEWOPIEYKKKLLK 255
 Db 183 LVHKEFVIGHLKASANNWNRHFOHAKPNIFHKDPDNNMLHVPVLGEWOPIEYKKKLLK 242

Qy 256 YLPYNHGHYFFLLGPPLLIPMYFOYQIIMTVHKWVDLANAVSYVIRFTIYIPFYG 315
 Db 243 YLPYNHGHYFFLLGPPLLIPMYFOYQIIMTVHKWVDLANAVSYVIRFTIYIPFYG 302

Qy 316 ILGALLFLNFIREFLESHWVWVTQNNHIVMEIDQAYRDWFFSQLTATCNVEQSFNDWF 375
 Db 303 ILGALLFLNFIREFLESHWVWVTQNNHIVMEIDQAYRDWFFSQLTATCNVEQSFNDWF 362

Qy 376 SGHNFQIEHLLFPTMPRNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKS GK 435
 Db 363 SGHNFQIEHLLFPTMPRNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKS GK 422

Qy 436 LWLDAYLHK 444
 Db 423 LWLDAYLHK 431

RESULT 13
 ABG96523
 ID ABG96523 standard; Protein; 465 AA.
 XX
 XX ABG96523;
 XX
 XX 12-DEC-2002 (first entry)
 DT Human partial desaturase from cDNA contig 253538a.
 XX
 XX

KW Human; enzyme; delta5 desaturase; polyunsaturated fatty acid;
 KW PUFA; nutritional; animal feed; cosmetic; skin aging; burn; angioplasty;
 KW inflammation; rheumatoid arthritis; asthma; psoriasis; osteoporosis;
 KW kidney stone; urinary tract stone; cancer; cachexia; diabetes; eczema;
 KW AIDS; multiple sclerosis; blood pressure; platelet aggregation;
 KW vasodilation; cholesterol; proliferation of fibrous tissue;
 KW endometriosis; myalgic encephalomyelitis; human breast milk;
 KW dietary supplement; chromosome 11q2.

OS Homo sapiens.

XX US6428990-B1.

PD 06-AUG-2002.

XX 12-NOV-1999; 99US-0439261.

PR 11-APR-1997; 97US-0833610.

PR 10-APR-1998; 98WO-US07422.

PR 08-JAN-1999; 99US-0227613.

XX (ABBO) ABBOTT LAB.

PI Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;

XX WPI; 2002-730518/79.

PT Producing a polyunsaturated fatty acid (PUFA), useful in dietary
 PT supplements and in treating diseases e.g., cancer, comprises expressing
 PT human delta 5-desaturase enzyme and exposing enzyme to substrate PUFA
 PT to convert to product PUFA.

XX Example 1; Fig 29; 10app; English.

CC The invention relates to producing (M) a polyunsaturated fatty acid
 CC (PUFA), comprising: (i) isolating a fully defined human delta5-desaturase
 CC gene sequence (I); (ii) constructing a vector comprising (I);
 CC (iii) introducing the vector into a host cell for expression of the
 CC human delta5-desaturase enzyme (II); and (iv) exposing (II) to a
 CC substrate PUFA (III) such that it is converted to a product PUFA (IV).
 CC The method is useful for producing a polyunsaturated fatty acid
 CC such as arachidonic acid (AA), eicosapentaenoic acid (EPA), adrenic
 CC acid, (n-3)-docosapentaenoic acid, (n-6)-docosapentaenoic acid and/or
 CC docosahexaenoic (DHA) acid. The PUFAs produced by the method, such
 CC as arachidonic acid (AA), eicosapentaenoic acid (EPA) and/or
 CC docosahexaenoic (DHA) acid, are useful for replicating the PUFA content
 CC of human breast milk or to alter the presence of PUFAs normally found
 CC in a non-human mammal's milk. PUFAs produced by (M) may be added to a
 CC dietary substitute or supplement, particularly an infant formula, for
 CC patients undergoing intravenous feeding or for preventing or treating
 CC malnutrition or other conditions or disease states. The PUFAs are
 CC useful for producing nutritional compositions e.g., any food or
 CC preparation for human consumption including for enteral or parenteral
 CC consumption, which when taken into the body serve to nourish or build
 CC up tissues or supply energy and/or maintain, restore or support
 CC adequate nutritional status or metabolic function. The PUFAs are also
 CC useful in animal feed supplements to alter an animal tissue or milk
 CC fatty acid composition to one or more desirable for human or animal
 CC consumption, in animal feed substitutes, animal vitamins or in animal
 CC topical ointments. The PUFAs produced by this method are useful in
 CC producing pharmaceutical compositions for treating rough or aging skin,
 CC injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,
 CC asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,
 CC cachexia associated with cancer, diabetes, eczema, AIDS, multiple
 CC sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting
 CC platelet aggregation, inducing vasodilation, reducing cholesterol
 CC levels, inhibiting proliferation of fibrous tissue, treating
 CC endometriosis, and myalgic encephalomyelitis. The gene for delta5
 CC desaturase is located on chromosome 11q2. The present sequence
 CC is a partial human delta5 desaturase protein.

XX Sequence 465 AA;

Query Match 79.6%; Score 1940.5; DB 23; Length 465;
 Best Local Similarity 81.8%; Pred. No. 1.6e-203;
 Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;
 QY 19 PT---FSNEEIOKHNLRDGLVIDRKVYNTTKWSIOHPGQCRVIGHVAGEDATDAFRAF 75
 DB 3 PTPRFTWDEVAQRSGCERWLVDRKVNISESTRHRPGGSRVISHVAGQDADPFAF 62
 QY 76 HPDLFVGVKFLKPLILIGELAPBEPSSQHGKNSKITEDFRALRKTAEDMNLFKTNHVPFLL 135
 DB 63 HINKGLVKYNNLSLIGLSPESFETQNKELTDFRELRATVERMGLMKANHVFFLL 122
 QY 136 LLAHIIALESIAWFTVPVFGNGWPTLITAFVLTASQAQGLQHDYGHLSVYRKPKWNH 195
 DB 123 YLLHILLDGAWLTWVFGTSFLPFLCAVLLSVAQAQAGWLDYGHLSVYRKPKWNH 182
 QY 196 LVHKFVIGHLKGSANWNNRHFQHKAPNIFHKDPDNNMLHVFVLGEWQPIEYKKKLLK 255
 DB 183 LVHKFVIGHLKGSANWNNRHFQHKAPNIFHKDPDNNMLHVFVLGEWQPIEYKKKLLK 242
 QY 256 YLPYNHQHEYFELIGPPLIPMYFOYQIIMTWIHKWVDLAWAVSYVIRFFIYIPFYG 315
 DB 243 YLPYNHQHEYFELIGPPLIPMYFOYQIIMTWIHKWVDLAWAVSYVIRFFIYIPFYG 302
 QY 316 ILGALLFINFIRFLESNHFVWVQNHVMEIDQEAAYDRWFSSQLTATCNVEQSFNDWF 375
 DB 303 ILGALLFINFIRFLESNHFVWVQNHVMEIDQEAAYDRWFSSQLTATCNVEQSFNDWF 362
 QY 376 SGHLNFQIEHFLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPLRLALDIIIRSLKSGK 435
 DB 363 SGHLNFQIEHFLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPLRLALDIIIRSLKSGK 422
 QY 436 LMLDAYLHK 444
 DB 423 LMLDAYLHK 431

RESULT 14

AAAY95446

ID AAY95446 standard; Protein; 432 AA.

AC AAY95446;

XX 10-OCT-2000 (first entry)

DE Human delta-5-desaturase-related contig 253538a-encoded protein.

XX Delta-5-desaturase; human; polyunsaturated fatty acid;

XX arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;

XX docosahexaenoic acid; nutrition; feedstuff.

OS Homo sapiens.

XX WO2000040705-A2.

XX 13-JUL-2000.

XX 29-DEC-1999; 99WO-US31163.

XX 08-JAN-1999; 99US-0227613.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Leonard AEY, Huang Y, Parker-Barnes JM;

XX WPI; 2000-465975/40.

XX N-PSDB; AAA49939.

XX New polypeptide useful for preparation of nutritional supplements based
 XX upon human delta5-desaturase, desaturates polyunsaturated fatty acids
 XX at carbon 5 -
 XX Example 1; Fig 9; 127pp; English.

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XX The present sequence is that of the polypeptide encoded by the
CC partial open reading frame of contig 253538a (see A449939). The
CC translated sequence shows homology to Mortierella alpina
CC delta-5-desaturase and delta-6-desaturase sequences, suggesting a
CC human desaturase-like protein. The contig was utilised in the
CC isolation of cDNA (see A449932) encoding human delta-5-desaturase
CC (see A495445). Delta-5-desaturase catalyzes the conversion of
CC dihomogamma-linolenic acid to arachidonic acid and of 20:4n-3 to
CC eicosapentaenoic acid. Recombinant enzyme, expressed in prokaryotic
CC or eukaryotic hosts using the isolated human delta-5-desaturase
CC cDNA, can be used in the production of polyunsaturated fatty acids
CC that may be added to nutritional, veterinary and pharmaceutical
CC compositions.
XX
XX Sequence 432 AA;
XX
XX Query Match 79.4%; Score 1935; DB 21; Length 432;
XX Best Local Similarity 81.9%; Pred. No. 5.8e-203;
XX Matches 352; Conservative 30; Mismatches 44; Indels 4; Gaps 2;
XX
Qy 19 FT---FSWEEIOKHNLTDSGLVIDRKVNITKWS:QHPGGQRVIGHYAGEDATDAFRAF 75
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 3 PTPRYFTWDEVAQRSGCEERWLVIDRKVNISBFTRRHPGGSRVISHYAGQDATDPFVAF 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 76 HPDLFVGVKFLKPLIGELAPEEPSQDHGKNSKITEDFRALRKTADNMLFKTNHVFLL 135
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 63 HINKGLVKKNYNSLLIGELSPQSPFPTKKNKLTDFRELATVERMGLMKANHVFFLL 122
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 136 LLAHIIALESIAFWTFYFGNGWIPITLITAFVL-ATSOAQAGWLQHDYGHLSYVRKPKWN 194
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 123 YLLHILLDGAALWLTWVFGTSFLPFLCAVLLSAVQQAQAGWLQHDYGHLSYVRKPKWN 182
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 195 HLHVKFVGHILKGSANWNNHRRHFQHAKEPNIFHKDPDVMNLHVFLGEMQPIEYKCKKL 254
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 183 HLHVKFVGHILKGSANWNNHRRHFQHAKEPNIFHKDPDVMNLHVFLGEMQPIEYKCKKL 242
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 255 KYLPNYHQHEYFFLIGPPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFIYIPFY 314
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 243 KYLPNYHQHEYFFLIGPPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFIYIPFY 302
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 315 GILGALLFLNPIRFLSHFWVWQMHVMEIDQEAIRYDFSSQLTATCNVQSFNDW 374
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 303 GILGALLFLNPIRFLSHFWVWQMHVMEIDQEAIRYDFSSQLTATCNVQSFNDW 362
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 375 FSGHLNFOIEHHLPTWPRNHLKIAPLVKSCLAKHGIEYOEKPLLRALLDIIRSLKSG 434
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 435 KLWLDAYLHK 444
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 423 KLWLDAYLHK 432
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 15
AAW84156
ID AAW84156 standard; Protein; 746 AA.
XX
XX AAW84156;
XX
XX 15-FEB-1999 (first entry)
XX
XX Human desaturase enzyme encoded by contig 253538a.
XX
XX Fatty acid; desaturase; polyunsaturated fatty acid;
XX malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
XX cancer; diabetes; eczema; platelet aggregation; vasodilation;
XX cholesterol level; endometriosis; premenstrual syndrome; human;
XX myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
XX acute respiratory syndrome; hypertension; inflammatory skin disorder.
XX
XX Homo sapiens.
XX
XX

```

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FH Key Location/Qualifiers
FT Misc-difference 746 /note= "not specified"
XX
XX WO9846763-A1.
XX
XX 22-OCT-1998.
XX
XX 10-APR-1998; 98WO-US071126.
XX
XX 11-APR-1997; 97US-0834655.
XX
XX (ABBO ) ABBOTT LAB.
XX (CALJ ) CALGENE LLC.
XX
XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;
XX Thurmond J;
XX
XX WPI; 1998-594582/50.
XX N-PSDB; AAV63643.
XX
XX New isolated fatty acid desaturase enzymes - used for the production
XX of polyunsaturated fatty acids for use in, e.g. pharmaceutical
XX compositions, nutritional compositions, cosmetics or animal feed
XX
XX Example 12; Pages 124-126; 165pp; English.
XX
XX The present sequence is a human desaturase enzyme. The cDNA sequence was
XX identified based on homology between human cDNA sequences and Mortierella
XX alpina desaturase gene sequences. The specification describes methods for
XX desaturating a fatty acid and for producing a desaturated fatty acid by
XX expressing increased levels of a desaturase. The enzyme can be used for
XX desaturating fatty acids. The enzyme can be used to produce
XX polyunsaturated fatty acids, which can be used for treating malnutrition,
XX in pharmaceutical compositions, in cosmetics or in animal feed. The
XX polyunsaturated fatty acids can be used for treating e.g. restenosis
XX after angioplasty, inflammation, rheumatoid arthritis, asthma,
XX psoriasis, cancer, diabetes or eczema or reduce blood pressure. They
XX can also be used to inhibit platelet aggregation, cause vasodilation,
XX lower cholesterol levels, inhibit proliferation of vessel wall smooth
XX muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
XX and other side effects caused by non-steroidal anti-inflammatory drugs
XX prevent or treat endometriosis and premenstrual syndrome, treat myalgic
XX encephalomyelitis and chronic fatigue after viral infections, treat
XX AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
XX inflammatory skin disorders.
XX
XX Sequence 746 AA;
XX
XX Query Match 79.4%; Score 1935; DB 19; Length 746;
XX Best Local Similarity 81.9%; Pred. No. 1.3e-202;
XX Matches 352; Conservative 30; Mismatches 44; Indels 4; Gaps 2;
XX
Qy 19 FT---FSWEEIOKHNLTDSGLVIDRKVNITKWSIQHPGGQRVIGHYAGEDATDAFRAF 75
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 3 PTPRYFTWDEVAQRSGCEERWLVIDRKVNISBFTRRHPGGSRVISHYAGQDATDPFVAF 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 76 HPDLFVGVKFLKPLIGELAPEEPSQDHGKNSKITEDFRALRKTADNMLFKTNHVFLL 135
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 63 HINKGLVKKNYNSLLIGELSPQSPFPTKKNKLTDFRELATVERMGLMKANHVFFLL 122
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 136 LLAHIIALESIAFWTFYFGNGWIPITLITAFVL-ATSOAQAGWLQHDYGHLSYVRKPKWN 194
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 123 YLLHILLDGAALWLTWVFGTSFLPFLCAVLLSAVQQAQAGWLQHDYGHLSYVRKPKWN 182
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 195 HLHVKFVGHILKGSANWNNHRRHFQHAKEPNIFHKDPDVMNLHVFLGEMQPIEYKCKKL 254
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 183 HLHVKFVGHILKGSANWNNHRRHFQHAKEPNIFHKDPDVMNLHVFLGEMQPIEYKCKKL 242
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 255 KYLPNYHQHEYFFLIGPPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFIYIPFY 314
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 243 KYLPNYHQHEYFFLIGPPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFIYIPFY 302
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

QY 315 GILGALLFLNFRFLESHFVWVQNNHIVMEIDQAYRDWFSSQATCNVEQSFNDW 374
 DDb 303 GILGALLFLNFRFLESHFVWVQNNHIVMEIDQAYRDWFSSQATCNVEQSFNDW 362
 QY 375 FSGHLNFQIEHLFPPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKS 434
 DDb 363 FSGHLNFQIEHLFPPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKS 422
 QY 435 KLWLDAYLHK 444
 DDb 423 KLWLDAYLHK 432

RESULT 16

AAW85135
 ID AAW85135 standard; Protein; 746 AA.

XX AC AAW85135;

DT 11-FEB-1999 (first entry)

DE A desaturase enzyme encoded by contig 253538a.

XX Fatty acid; desaturase; polyunsaturated fatty acid;
 XX malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

FF Misc-difference 746

FT /note= "not specified"

PN WO9846765-A1.

XX 22-OCT-1998.

XX 10-APR-1998; 98WO-US07422.

XX 11-APR-1997; 97US-0833610.

XX (ABBO) ABBOTT LAB.

XX (CALJ) CALGENE LLC.

XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;

XX Thurmond J;

XX WPI; 1999-009334/01.

XX N-PSDB; AAW82642.

XX New nucleic acid encoding delta5 and other desaturase enzymes -

XX useful in production of oils of increased arachidonic acid content,

XX used, e.g. for treating cancer, as foods, animal feeds and cosmetics

XX Claim 87; Pages 119-120; 153pp; English.

XX The present sequence represents a human desaturase enzyme. The enzyme
 XX sequence is used in the methods of the invention. The specification
 XX describes methods for desaturating a fatty acid and for producing a
 XX desaturated fatty acid by expressing increased levels of a desaturase.
 XX The enzyme can be used for desaturating fatty acids. The enzyme can be
 XX used to produce polyunsaturated fatty acids, which can be used for
 XX treating malnutrition, in pharmaceutical compositions, in cosmetics or
 XX in animal feed. The polyunsaturated fatty acids can be used for treating
 XX e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,
 XX asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.
 XX They can also be used to inhibit platelet aggregation, cause
 XX vasodilation, lower cholesterol levels, inhibit proliferation of vessel
 XX wall smooth muscle, and fibrous tissue, reduce or prevent
 XX gastro-intestinal bleeding and other side effects caused by non-steroidal

CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual
 CC synarone, treat myalgic encephalomyelitis and chronic fatigue after
 CC viral infections, treat AIDS, multiple sclerosis, acute respiratory
 CC syndrome, hypertension and inflammatory skin disorders.

XX Sequence 746 AA;

Query Match 79.4%; Score 1935; DB 20; Length 746;

Best Local Similarity 81.9%; Pred. No. 1.3e-202;

Matches 352; Conservative 30; Mismatches 44; Indels 4; Gaps 2;

QY 19 PT---FSWEETQXNLRDGLNVDKVNITKWSIOHGGQVIGHYAGEDATDAFRF 75

Db 3 PTPRYFTWDEVAQRSGCEERWLVIDRKVINISEPTRRHGGSRVISHYAGQDATDPVAF 62

QY 76 HPDLEFVGKFLKPLLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEDMNLKTNHVPFL 135

Db 63 HINKGLVKVMNSLLIGELSPQSPFPTKNKELTDSFRELRTATVERMGLMKANHVFFLL 122

QY 136 LLAHIIALESIAETVTFYFGNGWIPITLITAFVL-ATSOQAQWLOHDYGHLSVYRKPKWN 194

Db 123 YLLHILLDDGAAMJLWVFGTSFPLLCVLLSAVQAQAGWLOHDYGHLSVYRKPKWN 182

QY 195 HLVKHFVIGHLKASANWNNHRHFQHHAKPNIFHKDPDVMNLHVFLGEPQIEYGGKKL 254

Db 183 HLVKHFVIGHLKASANWNNHRHFQHHAKPNIFHKDPDVMNLHVFLGEPQIEYGGKKL 242

QY 255 KYLPYNHCHYEYFFLIGPPLIPMYFQYQIIMLVHKNVDLAWAVSYIRFTTIPFY 314

Db 243 KYLPYNHCHYEYFFLIGPPLIPMYFQYQIIMLVHKNVDLAWAVSYIRFTTIPFY 302

QY 315 GILGALLFNFRFLESHFVWVQNNHIVMEIDQAYRDWFSSQATCNVEQSFNDW 374

Db 303 GILGALLFNFRFLESHFVWVQNNHIVMEIDQAYRDWFSSQATCNVEQSFNDW 362

QY 375 FSGHLNFQIEHLFPPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKS 434

Db 363 FSGHLNFQIEHLFPPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKS 422

QY 435 KLWLDAYLHK 444

Db 423 KLWLDAYLHK 432

RESULT 17

AA92618

ID AA92618 standard; Protein; 752 AA.

XX AC AA92618;

XX 10-AUG-2000 (first entry)

XX Human desaturase homologue encoded by DNA contig 2535.

XX delta-6 desaturase; gamma-linolenic acid; biosynthesis;

XX transgenic insect cell; polyunsaturated long chain fatty acid;

XX antiinflammatory; antirheumatic; antiasthmatic; antipsoriatic;

XX osteopathic; cytostatic; antidiabetic; dermatological; gynecological;

XX anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;

XX antiaggregant; vasotropic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 433 /note= "encoded by TAA"

FT Misc-difference 459 /note= "encoded by TAA"

FT Misc-difference 596 /note= "encoded by TGA"

FT Misc-difference 629 /note= "encoded by TGA"

FT Misc-difference 655 /note= "encoded by TGA"

XX Nucleic acid construct able to express fatty acid desaturase in
 PT plants - useful in human or animal nutrition, as cosmetics and
 PT therapeutically, e.g. for restenosis, cancer and diabetes
 XX
 PS Claim 48; Page 169-171; 210pp; English.
 XX
 CC The invention relates to a nucleic acid construct that contains at least
 CC one of the nucleotide sequences (AA00889 to AA00891) encoding
 CC Mortierella alpina delta 6, delta 12 and delta 5 desaturases (AA095504 to
 CC AA095506) respectively, coupled to an expression control sequence
 CC functional in plants. Recombinant plant cells containing at least one DNA
 CC encoding a M. alpina fatty acid desaturase (FAD), can be used for the
 CC production of polyunsaturated fatty acid (PUFA). These recombinant cells
 CC or plants containing them are used to produce oils such as linoleic
 CC acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic
 CC acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils
 CC are used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
 CC dietary supplements or substitutes, for use in humans or animals; (iii)
 CC for treating disorders associated with inadequate consumption or
 CC production of PUFA (or their metabolites such as prostaglandins), e.g.
 CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics,
 CC and (v) as animal feeds. Fragments of the DNA are used as probes to
 CC isolate related coding sequences. Recombinant plants can produce high
 CC yields of PUFA, since new pathways can be created and unwanted ones
 CC suppressed. Plants can be engineered to express oils of particular PUFA
 CC composition, e.g. one similar to that in human milk, and product recovery
 CC is simpler than with e.g. fish. Sequences AA095508-514 represent amino
 CC acid sequences of various contigs of human desaturase genes which are
 CC similar to the M. alpina desaturase sequences.
 XX
 SQ Sequence 753 AA;

Query Match 79.4%; Score 1935; DB 20; Length 753;
 Best Local Similarity 81.9%; Pred. No. 1.3e-202;
 Matches 352; Conservative 30; Mismatches 44; Indels 4; Gaps 2;

QY 19 PT---FSWEIQKLNRTDGLVDRKVNITKSIQHPGQGVIGHYAGEDATDAFRAF 75
 Db 3 PTPRYFTWDEVAQSGCEERWLVDRKVNISFTRHPGGSRVISHYAGQDATDFVAF 62
 QY 76 HPDLFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEEDMNLFTKNHVFLL 135
 Db 63 HINKGLVKYKYNLSLIGELSPQSPFETKTKELTDFRELRTATVERMGLMKANHYVFFLL 122
 QY 136 LLAHIIALETANETVYFNGWMTPTLITAFVL-ATSOAGWLQHDYGHLSYVRPKWN 194
 Db 123 YLLHILLDGAWLTLWVFGTSFPLFLCAVLLSAVQQAQAGLQHDYGHLSYVRPKWN 182
 QY 195 HLVKFVIGHLKGASANNWNRHFPQHEAKPNIHKPDVNVNHLVFLGVEQPIEYGGKKL 254
 Db 183 HLVKFVIGHLKGASANNWNRHFPQHEAKPNIHKPDVNVNHLVFLGVEQPIEYGGKKL 242
 QY 255 KILPYNHCHYEYFFLIGPLLPIMYFOYCIINTMIVHKNWDLAWNSYIRFETITIPFY 314
 Db 243 KILPYNHCHYEYFFLIGPLLPIMYFOYCIINTMIVHKNWDLAWNSYIRFETITIPFY 302
 QY 315 GILGALLFLNIRFLESHWFVWVTQNMHIVMEIDQEAIRDWFSQLTATCNVEQSPENDW 374
 Db 303 GILGALLFLNIRFLESHWFVWVTQNMHIVMEIDQEAIRDWFSQLTATCNVEQSPENDW 362
 QY 375 FSGHNFQIEHLLPTPRNHLKIAPLVKSCLAKHIEQEKELLRALLDIIRSLKSG 434
 Db 363 FSGHNFQIEHLLPTPRNHLKIAPLVKSCLAKHIEQEKELLRALLDIIRSLKSG 422
 QY 435 KWLDDAYLHK 444
 Db 423 KWLDDAYLHK 432

RESULT 19
 AAY84703

ID XX AAY84703 standard; Protein; 753 AA.
 AC AAY84703;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Amino acid sequence of a contig of a human desaturase enzyme.
 XX
 KW Deltas-desaturase; poly-unsaturated long chain fatty acid; PUFA;
 KW arachidonic acid; infant formula; dietary supplement; dietary substitute;
 KW cosmetic; stress; metabolic disorder; gastrointestinal difficulty;
 KW malabsorption; restenosis; angioplasty; inflammation; kidney stone;
 KW rheumatoid arthritis; asthma; psoriasis; osteoporosis; tract stone;
 KW cancer; cachexia; diabetes; eczema; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder;
 KW blood score; platelet aggregation; vasodilatation;
 KW gastro-intestinal bleeding.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 XX Misc-difference 1..752
 FT /note= "Xaa is an unspecified residue encoded by
 FT stop codons"
 FT
 FT Misc-difference 753
 FT /note= "encoded by TG"
 FT
 PN WO200020603-A1.
 XX 13-APR-2000.
 PD
 XX 29-SEP-1999; 99WO-US22692.
 XX
 PR 05-OCT-1998; 98US-0103109.
 XX
 PA (ABCO) ABBOTT LAB.
 XX
 PI Mukerji P, Huang Y, Parker-Barnes JH, Das T;
 XX
 DR WPI: 2000-364599/31.
 N-PSDB; AAA14594.
 XX
 PT Novel transgenic insect cell with modified delta-5-desaturase
 PT production, useful for altering fatty acid biosynthesis -
 XX
 PS Example 9; Page 154-155; 161pp; English.
 XX
 CC AAY84697-Y84703 are encoded by contigs of a human desaturase. The
 CC specification describes a Mortierella alpina deltas-desaturase. The
 CC protein is involved in the biosynthesis of poly-unsaturated long chain
 CC fatty acids (PUFAs). The polynucleotide is to produce PUFAs, especially
 CC arachidonic acid. The oils produced by the invention are used in
 CC pharmaceutical compositions, infant formulas, dietary supplements,
 CC dietary substitutes, and cosmetics. The nutritional compositions can be
 CC used to treat normal individuals temporally exposed to stress, or
 CC individuals having specialized needs due to chronic or acute diseases
 CC (e.g. metabolic disorders such as gastrointestinal difficulties and/or
 CC malabsorption, and other disorders such as restenosis after angioplasty,
 CC symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis,
 CC osteoporosis, kidney stones, tract stones, cancer, cachexia associated
 CC with cancer, diabetes, eczema, endometriosis, premenstrual syndrome,
 CC myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis,
 CC acute respiratory syndrome, hypertension, inflammatory skin disorders,
 CC as well as reduce blood score, inhibit platelet aggregation, cause
 CC vasodilatation, inhibit proliferation of vessel wall smooth muscle and
 CC fibrous tissue, prevent or reduce gastro- intestinal bleeding, and for
 CC Geriatric treatments).
 XX
 SQ Sequence 753 AA;

Query Match 79.4%; Score 1935; DB 21; Length 753;
 Best Local Similarity 81.9%; Pred. No. 1.3e-202;

Matches 352; Conservative 30; Mismatches 44; Indels 4; Gaps 2;
Qy 19 PT---FSWBIQKHNLRTDGLVIDRKVYNITKWSIQHGGQVRVIGHYAGEDATDAFRAP 75
Db 3 PTPRYFTWDEVAQRSGCEERMLVIDRKVYNISFTREHFGSRVISHYAGQATDFPVAP 62
Qy 76 HPDLFVGVKLPKLLIGELAPEPSQDHGKSKITDFRALRTADDMFLKTNHVFLL 135
Db 63 HINKGLVKYKNSLLIGELSPQSPPTKNTKELTDFRELRTATVERMGLMKANHVFFLL 122
Qy 136 LLAHIIALESIAFTVYFGNGWIPITLITAFVL-ATSQAQAGWLOHDYGHLSVYRKPKN 194
Db 123 YLHILLDGAAMLTLWVFTSFLPFLLCVLLSAVQAQAGWLOHDYGHLSVYRKPKN 182
Qy 195 HLHVKFVIGHLKGASANNWHRHFOHAKENIFHKDPDVNMLHVFVLGEWQPIEYKXKL 254
Db 183 HLHVKFVIGHLKGASANNWHRHFOHAKENIFHKDPDVNMLHVFVLGEWQPIEYKXKL 242
Qy 255 KYLPYNHQHEVFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSYIRFFITVIFY 314
Db 243 KYLPYNHQHEVFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSYIRFFITVIFY 302
Qy 315 GILGALLFLNFIREFSHWVVTQNNHIVMEIDQAYRDWFSQLTATCNVEQSFNDW 374
Db 303 GILGALLFLNFIREFSHWVVTQNNHIVMEIDQAYRDWFSQLTATCNVEQSFNDW 362
Qy 375 FSGHLNFQIEHLLFPPTMRNLHKLAPLVKSLCAKHGIEYQEKPLRALLDIIRSLKSG 434
Db 363 FSGHLNFQIEHLLFPPTMRNLHKLAPLVKSLCAKHGIEYQEKPLRALLDIIRSLKSG 422
Qy 435 KLMLDAYLHK 444
Db 423 KLMLDAYLHK 432

RESULT 20
AA93456
ID AA93456 standard; Protein; 322 AA.
AC AA93456;
DT 06-NOV-2001 (first entry)
DE Human polypeptide, SEQ ID NO: 3112.
XX Human; full length cDNA; cDNA synthesis; oligo-capping.
XX Homo sapiens.
PN EPI130094-A2.
XX 05-SEP-2001.
XX 07-JUL-2000; 2000EP-0114089.
XX 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183785.
XX (HELI-) HELIX RES INST.
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524255/58.
DR N-PSDB; AAK94377.
XX 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX Claim 8; SEQ ID NO 3112; 1380pp + sequence listing; English.
XX The invention relates to primers for synthesizing full length cDNA

CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a polypeptide
CC encoded by a full length human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 322 AA;
Query Match 73.4%; Score 1790; DB 22; Length 322;
Best Local Similarity 100.0%; Pred. No. 3e-187;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 123 MNLKTNHVFLLLAHIIALESIAFTVYFGNGWIPITLITAFVLATSQAQAGWLOHDY 182
Db 1 MNLKTNHVFLLLAHIIALESIAFTVYFGNGWIPITLITAFVLATSQAQAGWLOHDY 60
Qy 183 GHLSVYRKPKNHVLHVFVIGHLKGASANNWHRHFOHAKENIFHKDPDVNMLHVFVLG 242
Db 61 GHLSVYRKPKNHVLHVFVIGHLKGASANNWHRHFOHAKENIFHKDPDVNMLHVFVLG 120
Qy 243 EWQPIEYKXKLKYL PYNHQHEVFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSY 302
Db 121 EWQPIEYKXKLKYL PYNHQHEVFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSY 180
Qy 303 YIRFFITVIFYGILGALLFLNFIREFSHWVVTQNNHIVMEIDQAYRDWFSQLT 362
Db 181 YIRFFITVIFYGILGALLFLNFIREFSHWVVTQNNHIVMEIDQAYRDWFSQLT 240
Qy 363 TCNVEQSFNDWFSGLNFQIEHLLFPPTMRNLHKLAPLVKSLCAKHGIEYQEKPLRA 422
Db 241 TCNVEQSFNDWFSGLNFQIEHLLFPPTMRNLHKLAPLVKSLCAKHGIEYQEKPLRA 300
Qy 423 LLDIIRSLKSGKMLDAYLHK 444
Db 301 LLDIIRSLKSGKMLDAYLHK 322
RESULT 21
AA95448
ID AA95448 standard; Protein; 294 AA.
XX AA95448;
XX 10-OCT-2000 (first entry)
XX Human delta-5-desaturase-related contig 2535-encoded protein.
XX Delta-5-desaturase; human; polyunsaturated fatty acid;
XX arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;
XX docosahexaenoic acid; nutrition; feedstuff.
XX Homo sapiens.
XX WO200040705-A2.
XX 13-JUL-2000.
XX 29-DEC-1999; 99WO-US31163.
XX 08-JAN-1999; 99US-0227613.
XX (ABBO) ABBOTT LAB.
XX Mukerji P, Leonard AEY, Huang Y, Parker-Barnes JM;
XX WPI; 2000-465975/40.
DR N-PSDB; AAA49938.

XX New polypeptide useful for preparation of nutritional supplements based
PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids
PT at carbon 5 -
XX
XX Example 1; Fig 18; 127pp; English.
XX
XX The present sequence is that of the polypeptide encoded by the
CC partial open reading frame of contig 2535 (see AAA49938). The
CC translated sequence shows homology to Mortierella alpina
CC delta-5-desaturase and delta-6-desaturase sequences, suggesting a
CC human desaturase-like protein. The contig was utilised in the
CC isolation of cDNA (see AAA49932) encoding human delta-5-desaturase
CC (see AA95445). Delta-5-desaturase catalyzes the conversion of
CC dihomono-gamma-linolenic acid to arachidonic acid and of 20:4n-3 to
CC eicosapentaenoic acid. Recombinant enzyme, expressed in prokaryotic
CC or eukaryotic hosts using the isolated human delta-5-desaturase
CC cDNA, can be used in the production of polyunsaturated fatty acids
CC that may be added to nutritional, veterinary and pharmaceutical
CC compositions.
XX
XX Sequence 294 AA;
SQ
Query Match 67.5%; Score 1646; DB 21; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.6e-171;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 151 VFYFGNGWIPITLITAFVLATSOAGWLOHDYGHLSVYRKPKNNHLVHKFVIGHLKGASA 210
Db 1 VFYFGNGWIPITLITAFVLATSOAGWLOHDYGHLSVYRKPKNNHLVHKFVIGHLKGASA 60
QY 211 NWNHRRHFQHAKEPNI FHKDPDVNMLHVFLVGEWQPIEYGGKKLKYLPYNHQHEYFFLIG 270
Db 61 NWNHRRHFQHAKEPNI FHKDPDVNMLHVFLVGEWQPIEYGGKKLKYLPYNHQHEYFFLIG 120
QY 271 PELLIPMYFOYQIIMTIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFNIRFLE 330
Db 121 PELLIPMYFOYQIIMTIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFNIRFLE 180
QY 331 SHWFWVTQNNHIVMEIDQEAIRDVDFSSQLTATCNVEQSFNDWFSGLHNFQIEHHLFPT 390
Db 181 SHWFWVTQNNHIVMEIDQEAIRDVDFSSQLTATCNVEQSFNDWFSGLHNFQIEHHLFPT 240
QY 391 MPRNHLKIAPLVKSLCAKGIYEYQEKPLRALLDIIRSLKSKGLMDAYLHK 444
Db 241 MPRNHLKIAPLVKSLCAKGIYEYQEKPLRALLDIIRSLKSKGLMDAYLHK 294
RESULT 22
AAW84155
ID AAW84155 standard; Protein; 608 AA.
XX
XX AAW84155;
AC
XX
DT 15-FEB-1999 (first entry)
XX
DE Human desaturase enzyme encoded by contig 2535.
XX
XX Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome; human;
KW myalgic cephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 608
FT
XX
XX W09846763-A1.
XX
XX

PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US07126.
XX
PR 11-APR-1997; 97US-0834655.
XX
PA (ABBO) ABBOTT LAB.
PA (CALJ) CALGENE LLC.
XX
PI Chaudhary S, Huang Y, Knutzon D, Leonard AB, Mukerji P;
PI Thurmond J;
XX
DR WPI: 1998-594582/50.
DR N-PSDB; AAV63642.
XX
PT New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT compositions, nutritional compositions, cosmetics or animal feed
XX
PS Example 12; Pages 123-124; 165pp; English.
XX
CC The present sequence is a human desaturase enzyme. The cDNA sequence was
CC identified based on homology between human cDNA sequences and Mortierella
CC alpina desaturase gene sequences. The specification describes methods for
CC desaturating a fatty acid and for producing a desaturated fatty acid by
CC expressing increased levels of a desaturase. The enzyme can be used for
CC desaturating fatty acids. The enzyme can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma,
CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They
CC can also be used to inhibit platelet aggregation, cause vasodilation,
CC lower cholesterol levels, inhibit proliferation of vessel wall smooth
CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
CC and other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC cephalomyelitis and chronic fatigue after viral infections, treat
CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
XX
SQ Sequence 608 AA;
Query Match 67.5%; Score 1646; DB 19; Length 608;
Best Local Similarity 100.0%; Pred. No. 4.6e-171;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 151 VFYFGNGWIPITLITAFVLATSOAGWLOHDYGHLSVYRKPKNNHLVHKFVIGHLKGASA 210
Db 1 VFYFGNGWIPITLITAFVLATSOAGWLOHDYGHLSVYRKPKNNHLVHKFVIGHLKGASA 60
QY 211 NWNHRRHFQHAKEPNI FHKDPDVNMLHVFLVGEWQPIEYGGKKLKYLPYNHQHEYFFLIG 270
Db 61 NWNHRRHFQHAKEPNI FHKDPDVNMLHVFLVGEWQPIEYGGKKLKYLPYNHQHEYFFLIG 120
QY 271 PELLIPMYFOYQIIMTIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFNIRFLE 330
Db 121 PELLIPMYFOYQIIMTIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFNIRFLE 180
QY 331 SHWFWVTQNNHIVMEIDQEAIRDVDFSSQLTATCNVEQSFNDWFSGLHNFQIEHHLFPT 390
Db 181 SHWFWVTQNNHIVMEIDQEAIRDVDFSSQLTATCNVEQSFNDWFSGLHNFQIEHHLFPT 240
QY 391 MPRNHLKIAPLVKSLCAKGIYEYQEKPLRALLDIIRSLKSKGLMDAYLHK 444
Db 241 MPRNHLKIAPLVKSLCAKGIYEYQEKPLRALLDIIRSLKSKGLMDAYLHK 294
RESULT 23
AAW85134
ID AAW85134 standard; Protein; 608 AA.
XX
XX AAW85134;
AC

XX 11-FEB-1999 (first entry)
 XX A desaturase enzyme encoded by contig 2535.
 XX Fatty acid; desaturase; polyunsaturated fatty acid;
 XX malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 XX cancer; diabetes; eczema; platelet aggregation; vasodilation;
 XX cholesterol level; endometriosis; premenstrual syndrome;
 XX myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 XX acute respiratory syndrome; hypertension; inflammatory skin disorder.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 608
 FT /note= "not specified"
 XX
 XX WO9846765-A1.
 XX
 XX 22-OCT-1998.
 XX
 XX 10-APR-1998; 98WO-US07422.
 XX
 XX 11-APR-1997; 97US-0833610.
 XX (ABBO) ABBOTT LAB.
 XX (CALJ) CALGENE LLC.
 XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;
 XX Thurmond J;
 XX WPI; 1999-009334/01.
 XX N-PSDB; AAV82641.
 XX New nucleic acid encoding delta5 and other desaturase enzymes -
 XX useful in production of oils of increased arachidonic acid content,
 XX used, e.g. for treating cancer, as foods, animal feeds and cosmetics
 XX Claim 87; Pages 117-119; 153pp; English.
 XX
 XX The present sequence represents a human desaturase enzyme. The enzyme
 XX sequence is used in the methods of the invention. The specification
 XX describes methods for desaturating a fatty acid and for producing a
 XX desaturated fatty acid by expressing increased levels of a desaturase.
 XX The enzyme can be used for desaturating fatty acids. The enzyme can be
 XX used to produce polyunsaturated fatty acids, which can be used for
 XX treating malnutrition, in pharmaceutical compositions, in cosmetics or
 XX in animal feed. The polyunsaturated fatty acids can be used for treating
 XX e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,
 XX asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.
 XX They can also be used to inhibit platelet aggregation, cause
 XX vasodilation, lower cholesterol levels, inhibit proliferation of vessel
 XX wall smooth muscle and fibrous tissue, reduce or prevent
 XX gastro-intestinal bleeding and other side effects caused by non-steroidal
 XX anti-inflammatory drugs, prevent or treat endometriosis and premenstrual
 XX syndrome, treat myalgic encephalomyelitis and chronic fatigue after
 XX viral infections, treat AIDS, multiple sclerosis, acute respiratory
 XX syndrome, hypertension and inflammatory skin disorders.
 XX Sequence 608 AA;
 XX
 XX Query Match 67.5%; Score 1646; DB 20; Length 608;
 XX Best Local Similarity 100.0%; Pred. No. 4.6e-171;
 XX Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 151 VFYFGNGWIPLTIAFVLAATSAQAAGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLKGASA 210
 XX
 XX 1 VFYFGNGWIPLTIAFVLAATSAQAAGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLKGASA 60
 XX
 XX 211 NWNHNRHFQHHAKPNIFFKDDVNMHLVFLVGEWQPIEYGGKKLKLPYNHQHIEYFFLIG 270
 XX
 XX 61 NWNHNRHFQHHAKPNIFFKDDVNMHLVFLVGEWQPIEYGGKKLKLPYNHQHIEYFFLIG 120

QY 271 PPLLPMYFOYQIIMTMIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRELE 330
 DB 121 PPLLPMYFOYQIIMTMIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRELE 180
 QY 331 SHWFVVTOMNHVMEIDQAYRDWFSSQLTATCNVEQSFNDWFSGHNFQIEHHLFPT 390
 DB 181 SHWFVVTOMNHVMEIDQAYRDWFSSQLTATCNVEQSFNDWFSGHNFQIEHHLFPT 240
 QY 391 MPRHNLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGKWLDAVLHK 444
 DB 241 MPRHNLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGKWLDAVLHK 294
 RESULT 24
 AAY92617
 ID AAY92617 standard; Protein; 614 AA.
 XX
 XX AC AAY92617;
 XX
 XX DT 10-AUG-2000 (first entry)
 XX DE Human desaturase homologue encoded by partial DNA contig sequence.
 XX
 XX KW delta-6 desaturase; gamma-linolenic acid; biosynthesis;
 KW transgenic insect cell; polyunsaturated long chain fatty acid;
 KW antiinflammatory; antirheumatic; antiasthmatic; antipsoriatic;
 KW osteopathic; cytostatic; antidiabetic; dermatological; gynecological;
 KW anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;
 KW antiaggregant; vasotropic.
 XX
 XX OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 295 /note= "encoded by TAA"
 FT Misc-difference 321 /note= "encoded by TAA"
 FT Misc-difference 458 /note= "encoded by TGA"
 FT Misc-difference 491 /note= "encoded by TGA"
 FT Misc-difference 517 /note= "encoded by TAA"
 FT Misc-difference 535 /note= "encoded by TGA"
 FT Misc-difference 550 /note= "encoded by TGA"
 XX WO2000020602-A2.
 XX 13-APR-2000.
 XX 29-SEP-1999; 99WO-US22686.
 XX 05-OCT-1998; 98US-0103110.
 XX (ABBO) ABBOTT LAB.
 XX Mukerji P, Huang Y, Parker-barnes JM, Das T;
 XX WPI; 2000-328935/28.
 XX N-PSDB; AAA09452.
 XX Novel transgenic insect cells comprising a nucleotide sequences which
 XX encode delta-6-desaturase or delta-12- desaturase, useful for producing
 XX poly-unsaturated long chain fatty acids, e.g. arachidonic acid
 XX Example 13; Page 166-167; 170pp; English.
 XX AAY92612-18 are identified based on homology to Mortierella alpina
 XX delta-5 and delta-6 desaturase genes. The human DNA's were aligned
 XX based on areas of homology to form a contig. Consensus sequences were

RESULT	25	
AAW95513		
ID	AAW95513 standard; Protein; 615 AA.	
XX		
XX	AC	
XX	AAW95513;	
XX		
DT	26-MAR-1999 (first entry)	
DE	Amino acid sequence of human desaturase gene contig 2535.	
XX		
KW	Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;	
KW	polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;	
KW	stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;	
KW	dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;	
KW	rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;	
KW	diabetes; cosmetic; animal feed; human.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 295	/note= "encoded by TGA"
FT	Misc-difference 321	/note= "encoded by TGA"
FT	Misc-difference 458	
FT		

QY 211 NWNHRHFQHKAKNIFHKDPDYNMLHVFVLGEWQPIEYKXKKLKYLPYNHQHEYPFLIG 270
 DB 61 NWNHRHFQHKAKNIFHKDPDYNMLHVFVLGEWQPIEYKXKKLKYLPYNHQHEYPFLIG 120
 QY 271 PPLLIPIWYFOYQIIMTWIHKWVDLAWAVSYIRFFITIPYIGLIGALLFNIRFLE 330
 DB 121 PPLLIPIWYFOYQIIMTWIHKWVDLAWAVSYIRFFITIPYIGLIGALLFNIRFLE 180
 QY 331 SHWFVVTQNMHIYMEIDQAYRDWFSQSLTATCNVEQSFNDWFSCHLNFOIEHHLFPT 390
 DB 181 SHWFVVTQNMHIYMEIDQAYRDWFSQSLTATCNVEQSFNDWFSCHLNFOIEHHLFPT 240
 QY 391 MPRNLHKTAPLVKSLCAKGIYQEKPLRALDLIIRSLKSGKMLDAYLHK 444
 DB 241 MPRNLHKTAPLVKSLCAKGIYQEKPLRALDLIIRSLKSGKMLDAYLHK 294

RESULT 26

AA84702
 ID AAY84702 standard; Protein; 615 AA.

AC AAY84702;

DT 08-AUG-2000 (first entry)

DE Amino acid sequence of a contig of a human desaturase enzyme.

XX Delta5-desaturase; poly-unsaturated long chain fatty acid; PUFA;
 KW arachidonic acid; infant formula; dietary supplement; dietary substitute;
 KW cosmetic; stress; metabolic disorder; gastrointestinal difficulty;
 KW malabsorption; restenosis; angioplasty; inflammation; kidney stone;
 KW rheumatoid arthritis; asthma; psoriasis; osteoporosis; tract stone;
 KW cancer; cachexia; diabetes; eczema; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder;
 KW blood score; platelet aggregation; vasodilatation;
 KW gastro-intestinal bleeding.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..614 /note= "Xaa is an unspecified residue encoded by stop codons"

FT Misc-difference 615 /note= "encoded by TG"

XX WO200020603-A1.

XX 13-APR-2000.

XX 29-SEP-1999; 99WO-US22692.

XX 05-OCT-1998; 98US-0103109.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Huang Y, Parker-Barnes JH, Das T;

XX WPI; 2000-364599/31.

XX N-PSDB; AAA14593.

XX Novel transgenic insect cell with modified delta-5-desaturase
 FT production, useful for altering fatty acid biosynthesis -

XX Example 9; Page 153-154; 161pp; English.

XX AAY84697-Y84703 are encoded by contigs of a human desaturase. The
 CC specification describes a Mortierella alpina delta5-desaturase. The
 CC protein is involved in the biosynthesis of poly-unsaturated long chain
 CC fatty acids (PUFAs). The polynucleotide is to produce PUFAs, especially
 CC arachidonic acid. The oils produced by the invention are used in
 CC pharmaceutical compositions, infant formulas, dietary supplements,

CC dietary substitutes, and cosmetics. The nutritional compositions can be
 CC used to treat normal individuals temporality exposed to stress, or
 CC individuals having specialized needs due to chronic or acute diseases
 CC (e.g. metabolic disorders such as gastrointestinal difficulties and/or
 CC malabsorption, and other disorders such as restenosis after angioplasty,
 CC symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis,
 CC osteoporosis, kidney stones, tract stones, cancer, cachexia associated
 CC with cancer, diabetes, eczema, endometriosis, premenstrual syndrome,
 CC myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis,
 CC acute respiratory syndrome, hypertension, inflammatory skin disorders,
 CC as well as reduce blood score, inhibit platelet aggregation, cause and
 CC vasodilatation, inhibit proliferation of vessel wall smooth muscle and
 CC fibrous tissue, prevent or reduce gastro- intestinal bleeding, and for
 CC geriatric treatments).

XX Sequence 615 AA;

Query Match 67.5%; Score 1646; DB 21; Length 615;
 Best Local Similarity 100.0%; Pred. NO. 4.7e-171; Indels 0; Gaps 0;
 Matches 294; Conservative 0; Mismatches 0;

QY 151 VFYFGNGWIPITLITAFVLATSSQAQAGWLQHDYGLSVYRKPKWNHLVHKFVIGLKGASA 210
 DB 1 VFYFGNGWIPITLITAFVLATSSQAQAGWLQHDYGLSVYRKPKWNHLVHKFVIGLKGASA 60
 QY 211 NWNHRHFQHKAKNIFHKDPDYNMLHVFVLGEWQPIEYKXKKLKYLPYNHQHEYPFLIG 270
 DB 61 NWNHRHFQHKAKNIFHKDPDYNMLHVFVLGEWQPIEYKXKKLKYLPYNHQHEYPFLIG 120
 QY 271 PPLLIPIWYFOYQIIMTWIHKWVDLAWAVSYIRFFITIPYIGLIGALLFNIRFLE 330
 DB 121 PPLLIPIWYFOYQIIMTWIHKWVDLAWAVSYIRFFITIPYIGLIGALLFNIRFLE 180
 QY 331 SHWFVVTQNMHIYMEIDQAYRDWFSQSLTATCNVEQSFNDWFSCHLNFOIEHHLFPT 390
 DB 181 SHWFVVTQNMHIYMEIDQAYRDWFSQSLTATCNVEQSFNDWFSCHLNFOIEHHLFPT 240
 QY 391 MPRNLHKTAPLVKSLCAKGIYQEKPLRALDLIIRSLKSGKMLDAYLHK 444
 DB 241 MPRNLHKTAPLVKSLCAKGIYQEKPLRALDLIIRSLKSGKMLDAYLHK 294

RESULT 27

ABG94699

ID ABG94699 standard; Protein; 356 AA.

AC ABG94699;

XX 02-DEC-2002 (first entry)

DE Human delta5-desaturase #9.

XX Human; delta5-desaturase; polyunsaturated fatty acid; DGLA;

KW dihydro-gamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;
 KW eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;
 KW enzyme.

XX Homo sapiens.

XX US6432684-B1.

XX 13-AUG-2002.

XX 08-JAN-1999; 99US-0227613.

XX 11-APR-1997; 97US-0833610.

XX 10-APR-1998; 98WO-US07422.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Leonard AE, Huang Y, Das T;

XX WPI; 2002-689761/74.

XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing
PT the conversion of dihydro-gamma-linolenic acid to arachidonic acid and
PT in the conversion of 20:4n-3 to eicosapentaenoic acid -
XX
XX
XX Example 1; Figure 18; 88pp; English.
XX
XX The invention relates to an isolated human delta5-desaturase nucleotide
CC sequence (I) which desaturates polyunsaturated fatty acids at
CC carbon 5. The nucleotide sequence (I) may be used in the recombinant
CC production of vectors and host cells for the production of delta5-
CC desaturase. Delta5-desaturase may be utilised in the conversion of
CC dihydro-gamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the
CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA or
CC polyunsaturated fatty acids produced from it may be added to
CC pharmaceutical compositions, nutritional compositions, animal feeds, as
CC well as other products such as cosmetics. ABG94691-ABG94708 represent
CC human delta5-desaturase amino acid sequences of the invention.
XX
SQ Sequence 356 AA;
Query Match 66.8%; Score 1628.5; DB 23; Length 356;
Best Local Similarity 99.7%; Pred. No. 1.8e-169;
Matches 293; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 151 VFYFGNGWIPTLITAFVLATSAQAQGLQHDYGHLSVYRKPKNHVLVHKFVIGHLKGASA 210
DB 1 VFYFGNGWIPTLITAFVLATSAQAQGLQHDYGHLSVYRKPKNHVLVHKFVIGHLKGASA 60
QY 211 NWNHHRHFQHKAPNIHKDPDVMNLHVFLGEMQPIEYGGKKLKYLPYNHGHYEYFLIG 270
DB 61 NWNHHRHFQHKAPNIHKDPDVMNLHVFLGEMQPIEYGGKKLKYLPYNHGHYEYFLIG 120
QY 271 PPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFFITIPFYIGLALLFLNFRFLE 330
DB 121 PPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFFITIPFYIGLALLFLNFRFLE 179
QY 331 SHWFVWVTQNMHIVMEIDQEAIRDWFSQSQTATCNVQSPFNDWFSGLHNFQIEHLFPT 390
DB 180 SHWFVWVTQNMHIVMEIDQEAIRDWFSQSQTATCNVQSPFNDWFSGLHNFQIEHLFPT 239
QY 391 MPRNLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSKMLDAYLHK 444
DB 240 MPRNLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSKMLDAYLHK 293
RESULT 28
ABG96517
ID ABG96517 standard; Protein; 356 AA.
XX
XX ABG96517;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human partial desaturase protein from contig 2535.
XX
KW Human; enzyme; delta5 desaturase; polyunsaturated fatty acid;
KW PUFA; nutritional; animal feed; cosmetic; skin aging; burn; angioplasty;
KW inflammation; rheumatoid arthritis; asthma; psoriasis; osteoporosis;
KW kidney stone; urinary tract stone; cancer; cachexia; diabetes; eczema;
KW AIDS; multiple sclerosis; blood pressure; platelet aggregation;
KW vasodilation; cholesterol; proliferation of fibrous tissue;
KW endometriosis; myalgic encephalomyelitis; human breast milk;
KW dietary supplement; chromosome 11q12.
XX
OS Homo sapiens.
XX
PN US6428990-B1.
XX
PD 06-AUG-2002.
XX
PF 12-NOV-1999; 99US-0439261.
XX

PR 11-APR-1997; 97US-0833610.
PR 10-APR-1998; 98WO-US07422.
PR 08-JAN-1999; 99US-0227613.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;
XX WPI; 2002-730518/79.
XX
XX Producing a polyunsaturated fatty acid (PUFA), useful in dietary
PT supplements and in treating diseases e.g., cancer, comprises expressing
PT human delta 5-desaturase enzyme and exposing enzyme to substrate PUFA
PT to convert to product PUFA -
XX
XX Example 1; Fig 18; 104pp; English.
XX
XX The invention relates to producing (M1) a polyunsaturated fatty acid
CC (PUFA), comprising: (i) isolating a fully defined human Delta5-desaturase
CC gene sequence (I); (ii) constructing a vector comprising (I);
CC (iii) introducing the vector into a host cell for expression of the
CC human Delta5-desaturase enzyme (II); and (iv) exposing (iii) to a
CC substrate PUFA (III) such that it is converted to a product PUFA (IV).
CC The method is useful for producing a polyunsaturated fatty acid
CC such as arachidonic acid (AA), eicosapentaenoic acid (EPA), adrenic
CC acid, (n-3)-docosapentaenoic acid, (n-6)-docosapentaenoic acid and/or
CC docosahexaenoic (DHA) acid. The PUFAs produced by the method, such
CC as arachidonic acid (AA), eicosapentaenoic acid (EPA) and/or
CC docosahexaenoic (DHA) acid, are useful for replicating the PUFA content
CC of human breast milk or to alter the presence of PUFAs normally found
CC in a non-human mammal's milk. PUFAs produced by (M1) may be added to a
CC dietary substitute or supplement, particularly an infant formula, for
CC patients undergoing intravenous feeding or for preventing or treating
CC malnutrition or other conditions or disease states. The PUFAs are
CC useful for producing nutritional compositions e.g., any food or
CC preparation for human consumption including for enteral or parenteral
CC consumption, which when taken into the body serve to nourish or build
CC up tissues or supply energy and/or maintain, restore or support
CC adequate nutritional status or metabolic function. The PUFAs are also
CC useful in animal feed supplements to alter an animal tissue or milk
CC fatty acid composition to one or more desirable for human or animal
CC consumption, in animal feed substitutes, animal vitamins or in animal
CC topical ointments. The PUFAs produced by this method are useful in
CC producing pharmaceutical compositions for treating rough or aging skin,
CC injured or burnt skin, angioplasty; inflammation, rheumatoid arthritis,
CC asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,
CC cachexia associated with cancer, diabetes, eczema, AIDS, multiple
CC sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting
CC platelet aggregation, inducing vasodilation, reducing cholesterol
CC levels, inhibiting proliferation of fibrous tissue, treating
CC endometriosis, and myalgic encephalomyelitis. The gene for delta5
CC desaturase is located on chromosome 11q12. The present sequence
XX is a partial human delta5 desaturase protein.
XX
SQ Sequence 356 AA;
Query Match 66.8%; Score 1628.5; DB 23; Length 356;
Best Local Similarity 99.7%; Pred. No. 1.8e-169;
Matches 293; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 151 VFYFGNGWIPTLITAFVLATSAQAQGLQHDYGHLSVYRKPKNHVLVHKFVIGHLKGASA 210
DB 1 VFYFGNGWIPTLITAFVLATSAQAQGLQHDYGHLSVYRKPKNHVLVHKFVIGHLKGASA 60
QY 211 NWNHHRHFQHKAPNIHKDPDVMNLHVFLGEMQPIEYGGKKLKYLPYNHGHYEYFLIG 270
DB 61 NWNHHRHFQHKAPNIHKDPDVMNLHVFLGEMQPIEYGGKKLKYLPYNHGHYEYFLIG 120
QY 271 PPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFFITIPFYIGLALLFLNFRFLE 330
DB 121 PPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFFITIPFYIGLALLFLNFRFLE 179
QY 331 SHWFVWVTQNMHIVMEIDQEAIRDWFSQSQTATCNVQSPFNDWFSGLHNFQIEHLFPT 390

Db 180 SHFWVVTQNMHIVMEIDQEAIRDFSSQLTATCNVEQSFDFNDFSGHNFQIEHLPPT 239
391 MPRHNLKIAPLVKSICAKHG: EYQEKPLLRALLDIIRSLKSGKMLDAYLHK 444
240 MPRHNLKIAPLVKSICAKHG: EYQEKPLLRALLDIIRSLKSGKMLDAYLHK 293

RESULT 29
AAB58942
ID AAB58942 standard; Protein; 286 AA.
XX
AC AAB58942;
XX
DT 27-MAR-2001 (first entry)
XX
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 650.
XX
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neotropic; neuroprotective; antiviral; anti-allergic; hepatotropic;
KW antidiabetic; anti-inflammatory; antitumor; antitumor; antitumor;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease.
XX
OS Homo sapiens.
XX
PN WO20005173-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05881.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-611515/59.
DR N-PSDB; AAF21845.
XX

New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention,
PT treatment and diagnosis of cancer, immune disorders, cardiovascular
PT disorders and neurological diseases -
XX
PS Claim 11; Page 1091-1092; 1299pp; English.
XX

Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive;
CC neotropic; neuroprotective; antiviral; anti-allergic; hepatotropic;
CC antidiabetic; anti-inflammatory; antitumor; antitumor; antitumor;
CC antibacterial; antifungal; antiparasitic and cardiant activity. The
CC polynucleotide and protein sequences are used in the diagnosis of cancer,
CC particularly breast and ovarian cancer. The nucleic acid sequences,
CC proteins, agonists and antagonists may also be used in the diagnosis,
CC prevention and treatment of immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; cardiovascular disorders such as
CC myocardial ischaemias; wound healing; neurological diseases such as
CC cerebral anoxia and epilepsy; and infectious diseases.
XX
SQ Sequence 286 AA;

Query Match 65.4%; Score 1594; DB 21; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.7e-166;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 159 IPTLITAFVLATSOAQAQWLOHDYGHLSVYRKPKWNHLYVHKFVIGHLKGASANWNRHF 218
Db 1 IPTLITAFVLATSOAQAQWLOHDYGHLSVYRKPKWNHLYVHKFVIGHLKGASANWNRHF 60
QY 219 QHEAKPNIFHKDPDVMNMLHVFVLGEWQPIEYGGKKLKYLPYNHQBHYFFLIGPPLIPMY 278
Db 61 QHEAKPNIFHKDPDVMNMLHVFVLGEWQPIEYGGKKLKYLPYNHQBHYFFLIGPPLIPMY 120
QY 279 FOYQIIMTLMVHKWVDLAWAVSYIRFTIYIPFYIGLALLFLNFIFLFSHFVWVT 338
Db 121 FOYQIIMTLMVHKWVDLAWAVSYIRFTIYIPFYIGLALLFLNFIFLFSHFVWVT 180
QY 339 QNMHIVMEIDQEAIRDFSSQLTATCNVEQSFDFNDFSGHNFQIEHLPPTMPRNLHK 398
Db 181 QNMHIVMEIDQEAIRDFSSQLTATCNVEQSFDFNDFSGHNFQIEHLPPTMPRNLHK 240
QY 399 IAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGKMLDAYLHK 444
Db 241 IAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGKMLDAYLHK 286

RESULT 30
AAY97540
ID AAY97540 standard; Protein; 445 AA.
XX
AC AAY97540;
XX
DT 15-JAN-2001 (first entry)
XX
DE Human fatty acid desaturase 3 protein sequence.
XX
KW Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;
KW liver disease; coronary artery disease; cancer.
XX
OS Homo sapiens.
XX
PN EPI035207-A1.
XX
PD 13-SEP-2000.
XX
PF 09-MAR-1999; 99EP-0104664.
XX
PR 09-MAR-1999; 99EP-0104664.
XX
PA (MULT-) MULTIGENE BIOTECH GMBH.
XX
PI Weber BHF, Marquardt A;
XX
DR WPI; 2000-559875/52.
DR N-PSDB; AAA90954.
XX

Novel cDNA molecules encoding three human fatty acid desaturases,
PT FADS1, FADS2 and FADS3, useful in the treatment of liver disease,
PT coronary artery disease and cancer -
XX
PS Claim 1; Page 44-46; 72pp; English.
XX

This sequence is the human fatty acid desaturase, FADS-3, of the
CC invention. An antibody directed against the 3 FADS molecule of the
CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or
CC therapeutic purposes. The FADS coding sequences are useful in gene
CC therapy. The polypeptide and antibodies are useful in screening for
CC modulating drugs. The polypeptides are also useful for treating liver
CC disease, coronary artery disease and cancer.
CC Note: Two copies of the sequence listing are present within this
CC patent, which contain different sequences. AAA90952 and AAA90955 are
CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are
CC stated as being SEQ ID's 7-22.
XX


```
SQ Sequence 445 AA;
Query Match 64.0%; Score 1560.5; DB 21; Length 445;
Best Local Similarity 62.3%; Pred. No. 6.9e-162; Mismatches 103; Indels 3; Gaps 2;
Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;

QY 1 MGKGGNQG--EGAAAREVSVPTFSWEEIQKHNLRDGLVIDRKVYNITKWSIQHPGQOR 58
DQ 1 MGVGEPGREGPAQGPALPTFCWEQIRAHQPGDKWLVIRRVYDISRAQRHPGGR 60
QY 59 VIGHYAGEDATDAFRAPHQDLNFKVFLPGLIGELAPEPSQDGHGKSKITEDRALRK 118
DQ 61 LIGHGAEDATDAFRAPHQDLNFKVFLPGLIGELAPEPSQDGHGKSKITEDRALRK 120
QY 119 TAEDMNLFTNHFVFLLLAHIALESIAWFTVFYFGNGWIPTLITAFVLATSQAQAGWL 178
DQ 121 AEDMKLFDASPTFFAFLGHILAMEVLAWLLIYLLGPGWPSALAAFIATISQAQSWCL 180
QY 179 QHDYGHLSVYRKPKNHVLVHKFVGHKLGASANNWHRHFQHHAKPNIFHKDPDVMNLHV 238
DQ 181 QHDLGHASIFKKSNNHVAQKFMVQKLGFSAHWNFRHFQHHAKPNIFHKDPDVTVA 240
QY 239 FVLGEWQPIEYKXKLYLPYNHQBHYFFLIGPPLIPMYFOYQIIMTVHKNWDLAW 298
DQ 241 FLIGE-SSVEYKXKRYLPYNQCHLYFFLIGPPLITLVNFEVENLAYMLVCMQWADLLW 299
QY 299 AVSYIRFFITYIPYIGILGALLFNPIRPLESHWVWVTOMNHVMEIDQAYRDWPS 358
DQ 300 AASFYARFFLSYLPFYGVGVLFFVAVRVLESHEWVWVTOMNHVMEIDQAYRDWPS 359
QY 359 QLTATCNVEQSPFNDWFSCHLNQFIEHLLFPTMPRHNLHAKIAPLVKSLCAKHGLSYEVKP 418
DQ 360 QLAATCNVEPSLFTNWFSGHNLQFIEHLLFPTMPRHNLHAKIAPLVKSLCAKHGLSYEVKP 419
QY 419 LLRALDIIIRSLKSGKMLDAYLHK 444
DQ 420 FLTALVDIVRSLSKSGDIWLDAYLHQ 445

RESULT 31
AAY83229
ID AAY83229 standard; Protein; 445 AA.
AC AAY83229;
DE 16-AUG-2000 (first entry)
XX CYB5RP fatty acid desaturase.
KW CYB5RP; fatty acid desaturase; cytochrome b5; macular degeneration;
KW skin disease; diabetes; inflammation; autoimmune disease;
KW cardiovascular disease; viral infection; virus; identification;
KW human.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Domain 1..102
FT /label= Cytochrome b5 domain
FT Region 182..186
FT /label= His box 1
FT Region 219..223
FT /label= His box 2
FT Region 383..387
FT /label= His box 3
XX WO200021557-A1.
XX 20-APR-2000.
XX 05-OCT-1999; 99WO-US23253.
XX 09-OCT-1998; 98US-0103760.
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XX PA (MERI ) MERCK & CO INC.
XX PI Petrukhin K, Caskey CT;
XX DR WPI; 2000-317847/27.
XX DR N-PSDB; AAZ93706.
XX PT Novel cytochrome b5-related protein useful for identifying modulators
XX PT useful for treating retinal dysfunction such as macular degeneration,
XX PT skin diseases, diabetic complications and cardiovascular disorders
XX PS Claim 3; Figure 3; 44pp; English.
XX CC CYB5RP is a fatty acid desaturase and a cytochrome b5-related protein.
XX CC Pharmaceutical compositions comprising an activator or an inhibitor of
XX CC CYB5RP protein are useful for treating macular degeneration. The
XX CC CYB5RP protein is useful for identifying its activators or inhibitors
XX CC which are useful for treating abnormal conditions associated with
XX CC CYB5RP protein activity such as skin disease, diabetic complications,
XX CC inflammatory and autoimmune disorders, cardiovascular disorders and
XX CC complications of viral infection. Large amounts of valuable essential
XX CC fatty acids can be produced by the expression of CYB5RP protein.
XX SQ Sequence 445 AA;
Query Match 64.0%; Score 1560.5; DB 21; Length 445;
Best Local Similarity 62.3%; Pred. No. 6.9e-162; Mismatches 103; Indels 3; Gaps 2;
Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;

QY 1 MGKGGNQG--EGAAAREVSVPTFSWEEIQKHNLRDGLVIDRKVYNITKWSIQHPGQOR 58
DQ 1 MGVGEPGREGPAQGPALPTFCWEQIRAHQPGDKWLVIRRVYDISRAQRHPGGR 60
QY 59 VIGHYAGEDATDAFRAPHQDLNFKVFLPGLIGELAPEPSQDGHGKSKITEDRALRK 118
DQ 61 LIGHGAEDATDAFRAPHQDLNFKVFLPGLIGELAPEPSQDGHGKSKITEDRALRK 120
QY 119 TAEDMNLFTNHFVFLLLAHIALESIAWFTVFYFGNGWIPTLITAFVLATSQAQAGWL 178
DQ 121 AEDMKLFDASPTFFAFLGHILAMEVLAWLLIYLLGPGWPSALAAFIATISQAQSWCL 180
QY 179 QHDYGHLSVYRKPKNHVLVHKFVGHKLGASANNWHRHFQHHAKPNIFHKDPDVMNLHV 238
DQ 181 QHDLGHASIFKKSNNHVAQKFMVQKLGFSAHWNFRHFQHHAKPNIFHKDPDVTVA 240
QY 239 FVLGEWQPIEYKXKLYLPYNHQBHYFFLIGPPLIPMYFOYQIIMTVHKNWDLAW 298
DQ 241 FLIGE-SSVEYKXKRYLPYNQCHLYFFLIGPPLITLVNFEVENLAYMLVCMQWADLLW 299
QY 299 AVSYIRFFITYIPYIGILGALLFNPIRPLESHWVWVTOMNHVMEIDQAYRDWPS 358
DQ 300 AASFYARFFLSYLPFYGVGVLFFVAVRVLESHEWVWVTOMNHVMEIDQAYRDWPS 359
QY 359 QLTATCNVEQSPFNDWFSCHLNQFIEHLLFPTMPRHNLHAKIAPLVKSLCAKHGLSYEVKP 418
DQ 360 QLAATCNVEPSLFTNWFSGHNLQFIEHLLFPTMPRHNLHAKIAPLVKSLCAKHGLSYEVKP 419
QY 419 LLRALDIIIRSLKSGKMLDAYLHK 444
DQ 420 FLTALVDIVRSLSKSGDIWLDAYLHQ 445

RESULT 32
ABU08788
ID ABU08788 standard; Protein; 445 AA.
XX AC ABU08788;
XX DT 09-JUN-2003 (first entry)
XX DE Human delta 6 desaturase D6DH-1.
XX
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Human; enzyme; D6DH-1; delta 6 desaturase-1; fatty acid desaturase; cardiovascular disease; angina pectoris; atheroma embolism; hypertension; atherosclerosis; arteriosclerosis; cardiac ischaemia; hyperlipidaemia; hypercholesterolaemia; hypertriglyceridaemia; gangrene; decubitus ulcer; mesenteric ischaemia; renal artery stenosis; stroke; nephrosclerosis; aging; Alzheimer's disease; angioimmunoblastic lymphadenopathy; anorexia; basal cell carcinoma; cardiac amyloidosis; cerebral amyloidosis; goiter; chronic lymphatic leukaemia; degenerative osteoarthritis; delirium; dementia; depression; dyskinesia; diabetic hyperosmolar nonketotic coma; glaucoma; hypercholesterolaemia; hypothermia; metabolic bone disease; osteoporosis; normal pressure hydrocephalus; diabetes; Reye's syndrome; Parkinson's disease; polymyalgia; rheumatism; prostatic carcinoma; renal amyloidosis; tuberculosis; urinary incontinence; galactosaemia; fatty acid metabolism disorder; Addison's disease; cystic fibrosis; fatty hepatocirrhosis; hyperadrenalemia; hypoadrenalemia; hyperlipidaemia; hyperparathyroidism; hypoparathyroidism; lipid myopathy; obesity; lipodystrophy; phenylketonuria; cancer.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Region 183..187

FT /label= Histidine_box

FT Region 219..223

FT /label= Histidine_box

FT Region 351..354

FT /label= Histidine_box

XX US6492108-B1.

XX 10-DEC-2002.

XX 26-MAR-1998; 98US-0048888.

XX 26-MAR-1998; 98US-0048888.

XX (INCY-) INCYTE GENOMICS INC.

XX Hillman JL, Guegler KJ, Corley NC, Shah P;

XX WPI: 2003-327308/31.

XX N-PSDB; ABX93651.

XX New isolated polynucleotide encoding polypeptide having delta-6 desaturase activity for use in diagnosis, treatment and prevention of cardiovascular diseases, disorders of aging, disorders of fatty acid metabolism, and cancer -

XX Claim 2; Fig 1; 39pp; English.

XX The invention relates to an isolated polynucleotide encoding a polypeptide comprising an amino acid sequence given in the specification. The polypeptide has fatty acid desaturase activity or delta-6 desaturase activity. For use in the diagnosis, treatment and prevention of cardiovascular diseases (e.g. angina pectoris, atheroma embolism, atherosclerosis, arteriosclerosis, cardiac ischaemia, hypertension, hypercholesterolaemia, hyperlipidaemia, hypertriglyceridaemia, gangrene, mesenteric ischaemia, renal artery stenosis, stroke, nephrosclerosis), disorders of aging (e.g. Alzheimer's disease, angioimmunoblastic lymphadenopathy, anorexia, basal cell carcinoma, cardiac or cerebral amyloidosis, chronic lymphatic leukaemia, decubitus ulcers, degenerative osteoarthritis, delirium, dementia, depression, diabetes, dyskinesia, diabetic hyperosmolar nonketotic coma, glaucoma, hypercholesterolaemia, hypothermia, metabolic bone disease including osteoporosis, normal pressure hydrocephalus, Parkinson's disease, Reye's syndrome, polymyalgia, rheumatism, prostatic carcinoma, renal amyloidosis, tuberculosis, urinary incontinence), disorders of fatty acid metabolism (e.g. Addison's disease, cystic fibrosis, fatty hepatocirrhosis, galactosaemia, goiter, hyperadrenalemia, hypoadrenalemia, obesity, hyperparathyroidism, hypoparathyroidism, hyperlipidaemia, lipid myopathies, lipodystrophies, phenylketonuria) and cancer. The present sequence represents the amino acid sequence of human delta 6 desaturase-1, D6DH-1.

SQ Sequence 445 AA;

Query Match 64.0%; Score 1560.5; DB 24; Length 445;

Best Local Similarity 62.3%; Pred. No. 6.9e-162;

Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;

QY 1 MGKGNQ--EQAAREVSVPTFSWEEIOKHNLRDTSGLVIDRKVYNITKSIQHPGQR 58

DB 1 MGVGPGPREGPAQPGAPLPTFCWEQIRAHDPQDGKWLVIERRVVDISRAQRHPGGR 60

QY 59 VIGHYAGEDATDAFRAFDHDLFVGKFLAPLIGELAPEEPQDGHGKSKITDEPRALK 118

DB 61 LIHGHAEDATDAFRAFDHDLFVGKFLAPLIGELAPEEPQDGLNQLVEDFRLHQ 120

QY 119 TRDMNLKTNHVFVLLLAHIALESIAWTFVFGNGWIPTLITAFVLAISQAQGL 178

DB 121 AEDMKLFDASTPTFFAFLGHLILAMEVLAWLLIYLLPGWVPSALAAFLAISQAQSWCL 180

QY 179 QHDYGHLSVYRKNNHLYHKFVIGHLKASANNWNRHFOHAKPNIFHKDPDNNMLHV 238

DB 181 QHDLGHASIFKSWNNHVAQKFMGOLKGFSAHWNFRFOHAKPNIFHKDPDVTVA 240

QY 239 FVLGEWQPIEYGGKLLKYLPHYNHQBHEFFELIGPPLLIPMYQYQIIMTVHKNWVDLAW 298

DB 241 FLIGE--SSVEYGGKGRYLPYMQOHLVFFELIGPPLLTVNFEVENLAYMLVCWQWADLLW 299

QY 299 ANSVYIRFITYTPFYGILGALLFNFRFLSHWFVWTONNHVMEIDQAYDQWSS 358

DB 300 AASFYARFFLSYLPFYGVGVLLFFVAVRVLESHFVWITQNNHIPKEIGHKHKRDWSS 359

QY 359 QLTATCNVQSPFNDFSGHLNFIQIEHLFFTPMRHNLHKAFLVKSLCAKHGIEYQEK 418

DB 360 QLAATCNVPSLFTNWFSGHLNFIQIEHLFFTPMRHNSRVAPLVKSLCAKHGIEYVKP 419

QY 419 LRLALDIIRSLKSGKMLDAYLHK 444

DB 420 FLTALVDIVRSLSKSGDIWLDAYLHQ 445

RESULT 33

AAM25786

ID AAM25786 standard; Protein; 490 AA.

XX AC AAM25786;

XX DT 16-OCT-2001 (first entry)

XX DE Human protein sequence SEQ ID NO:1301.

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; viricide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnery; antilucer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder; neurobiological disorder.

XX Homo sapiens.

OS WO200153455-A2.

XX PN 26-JUL-2001.

XX PD 22-DEC-2000; 2000WO-US35017.

XX PF

XX

PR 23-DEC-1999; 99US-0471275.
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-457603/49.
 DR N-PSDB; AAH99727.
 XX Isolated human polynucleotides encoding polypeptides, useful for the
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
 PT Claim 20; Page 270; 1217pp; English.
 XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
 CC AAM25963. The proteins can have activities based on the tissues and
 CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;
 CC central nervous system; viricide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antianaemic; antilegionella; haemostatic; vulnerary;
 CC antiulcer; osteoprotective; dermatological; antiallergic; antiasthmatic;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.
 XX SQ Sequence 490 AA;

Query Match 64.0%; Score 1560.5; DB 22; Length 490;
 Best Local Similarity 62.3%; Pred. No. 8e-152;
 Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;
 QY 1 MGKGNQ--EAGAEREVSVPTFWEIEQKHNLTDSGLVIDRKVNTKWSIQHPGQR 58
 DB 46 MGVGPBPREGPAQPGAPLPTFCWEQIRAHQDQDKWLVIERRVYDISRWAPHPGGR 105
 QY 59 VIGHYAGEDATDAFRAHFDLEFVGKFLPLTIGELAPEEPSODHGKNGKITEDFRALRK 118
 DB 106 LIGHGAGEDATDAFRAHFDLEFVGKFLPLTIGELAPEEPSODGFLNQLVEDFRAHQ 165
 QY 119 TAEDMNLFKTNHVFLLALLAHIALESIAWFTVYFGNGWIPFLITAFVLATSOAQAGWL 178
 DB 166 AAEEDMLKFDASPTFFAFLGHILAMEVLWLLIYLLPGWVPSALAAFTLAISOQSWCL 225
 QY 179 OHYDGLSVYRKPNWHLVHKFVIGHLKGSANWNNHRHFOHAKNIFHKDPDVNMLHV 238
 DB 226 QHDLGHASIFKSGWNNHVAQKLVNGKQKGSFANWNNFRFOHAKNIFHKDPDVTVAPV 285
 QY 239 FVLGEMQFIYKGGKLYLPYNHQHEYFFLIGPLIPMYFQYQIIMTVHKNWVDLAW 298
 DB 286 FLLGE-SSVEYGGKKRYLPYNQCHLYFFLIGPLLTNVNFEVLAAYMLVCNQWADLLW 344
 QY 299 AVSYIIRFFTYTPFYGILGALLFLNFIRESHFWVWVTONNHIWMEIDQAYRDWSS 358
 DB 345 AASYARFFYSYLPFYGVGVLLFFVAVRVLESHFWVWVTONNHIWMEIDQAYRDWSS 404
 QY 359 QLTATCNVEQSFNDWFSGLNFQIEHLLFPTMPRHNLHKAFLVKSCLKAGHIEYQK 418
 DB 405 QLANTCNVPSLFTNWFSGHLNFQIEHLLFPRFRHNSYSAFLVKSCLKAGHLSYEVKP 464
 QY 419 LLRALDIIRSLKSKGLWLDAYLHK 444

DB 465 FLTALVDIVRSKSGDILWLDAYLHQ 490
 RESULT 34
 ABG10281
 ID ABG10281 standard; Protein; 446 AA.
 XX AC ABG10281;
 XX DT 13-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #10272.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX FI Drmanac RT, Liu C, Tang YT;
 XX DR WPI; 2001-639362/73.
 XX DR N-PSDB; AAS74468.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 20; SEQ ID No 40640; 103pp; English.
 The invention relates to isolated polynucleotide (I) and
 polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG0377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: the sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 446 AA;
 Query Match 62.6%; Score 1527; DB 22; Length 446;
 Best Local Similarity 61.7%; Pred. No. 3.3e-158;
 Matches 276; Conservative 61; Mismatches 106; Indels 4; Gaps 3;
 QY 1 MGKGNQ--EAGAEREVSVPTFWEIEQKHNLTDSGLVIDRKVNTKWSIQHPGQR 58
 DB 1 MGVGPBPREGPAQPGAPLPTFCWEQIRAHQDQDKWLVIERRVYDISRWAPHPGGR 60

PR 26-OCT-2000; 2000US-243009P.
XX (XENO-) XENON GENETICS INC.
XX Winther MD, Knickle LC, Haardt M, Allen SJ, Ponton A;
PI De Antueno RJ, Jenkins DK, Nwaka SO;
XX
XX
XX WPI; 2002-454647/48.
XX
XX Novel control region of delta-5-desaturase gene useful as a target for
PT screening compounds useful in the treatment of diseases involving
PT abnormal lipid metabolism including diabetic neuropathy
XX
XX
XX Disclosure; Fig 4; 93pp; English.
XX
XX The invention relates to human delta-5-desaturase (hDSD) gene control
CC region used as a target for screening drugs useful in treatment of
CC diseases involving abnormal lipid metabolism including diabetic
CC neuropathy, arterial hypertension, hypercholesterolaemia, atherosclerotic
CC heart disease, chronic inflammatory disorders, autoimmune disorders, such
CC as rheumatoid arthritis, diminished lymphocyte proliferation,
CC T-cell-mediated cytotoxicity, natural killer cell activity,
CC macrophage-mediated cytotoxicity, monocyte and neutrophil chemotaxis,
CC major histocompatibility class II expression and antigen presentation,
CC production of pro-inflammatory cytokines (interleukins 1 and 6, tumour
CC necrosis factor), and adhesion molecule expression, eczema, psoriasis,
CC acute respiratory distress syndrome (ARDS), articular cartilage
CC degradation (ACD) and cancer. Host cell containing the control
CC region of DSD gene is useful for screening for a modulator capable
CC of regulating the expression of a mammalian DSD gene, especially for
CC identifying modulators that modulate lipid metabolism or diabetic
CC neuropathy. The screening method is an assay for identifying modulators
CC that modulate the n-3 lipid metabolic pathway, conversion of
CC 18:3n3-22:6n3, or n-9 lipid metabolic pathway, conversion of
CC 16:0-22:4n9 or n-6 lipid metabolic pathway, conversion of 18:2n6-22:5n6.
CC The human DSD control region provides a powerful tool for dissecting the
CC role of DSD gene expression and inducing modifications, which eliminate
CC or control alterations associated with metabolic disorders. The
CC present sequence is C-terminal tagged human delta-5-desaturase
CC (hDSD) enzyme.
XX
XX SQ Sequence 473 AA;
Query Match 62.2%; Score 1516; DB 23; Length 473;
Best Local Similarity 62.0%; Pred. No. 5.7e-157;
Matches 272; Conservative 62; Mismatches 99; Indels 6; Gaps 3;
QY 11 AAEVSVPT---PSWEEIQKHNLRDTSGLVIDRKVYNITKWSIQHPPGQGVIGHYAGED 67
DB 7 AAETAAAGPTFRYFTWDEVAQRSCERWLVDRKVTNISEFTFRHPGGRVISHVAGQD 66
QY 68 ATDAFRAPDLEFVGKFLKPLLIGELAPEEPQDHGKSKITEDFRALKTAEDNVLFK 127
DB 67 ATDFVFAFHINKGLVKVYMSLLIGELSPQSPSEPTKNEKLTDFRELTAATVERMGLMK 126
QY 128 TNHVPFLLLLAHIALSIAHFTVYFGNGHPIPLITAFVLATSOAAGWLQHDYGLSLV 187
DB 127 ANHVFFLLYLLHLLDGAALTLTWFTGTSPLPELLCAVLLSAVQAQGLQDFGLSLV 186
QY 188 YRKPKWNHVKFVIGHLKAGASANNWNRHFPQHAKENIFHKQPDVNNMLH--VFVLGEWQ 245
DB 187 FSTSKWNHLLHFVIGHLKAGAPASNNWNRHFPQHAKENIFHKQPDVNNMLH--VFVLGEWQ 245
QY 246 PIEVGKKLKYLPYNHQQEYFFLGPPLLIPIYQYQIIMTIVKQWVLAQVSVYIR 305
DB 246 SVELGQKKKYPYNNHQQEYFFLGPPLLIPIYQYQIIMTIVKQWVLAQVSVYIR 305
QY 306 PFITVPIYGLGALLFLNFIRESHFVWVMTQNNHIVMEIDQAYEDWFFSSOLTATCN 365
DB 306 PFLTVPLGLGKAFGLGLEFVIFRLESNFWVMTQNNHIVMEIDQAYEDWFFSSOLTATCN 365
QY 366 VEQSPFNDFWFSGLHNFQIEHLLFPTMPRNHLHKTAPLVKSLCAKGEIYQEKPLLRALLD 425

DB 366 VHKSAFNDFWFSGLHNFQIEHLLFPTMPRNHLHKTAPLVKSLCAKGEIYQEKPLLRALLD 425
QY 426 IIRSLKKSGLMLDAYLHK 444
DB 426 IIRSLKKSGLMLDAYLHK 444
RESULT 37
ABU08789
ID ABU08789 standard; Protein; 444 AA.
XX
XX AC ABU08789;
XX
XX DT 09-JUN-2003 (first entry)
XX Human delta 6 desaturase D6DH-2.
DE
XX
XX Human; enzyme; D6DH-2; delta 6 desaturase-2; fatty acid desaturase;
KW cardiovascular disease; angina pectoris; atheroma embolism; hypertension;
KW atherosclerosis; arteriosclerosis; cardiac ischaemia; hyperlipidaemia;
KW hypercholesterolaemia; hypertriglyceridaemia; gangrene; decubitus ulcer;
KW mesenteric ischaemia; renal artery stenosis; stroke; nephrosclerosis;
KW aging; Alzheimer's disease; angioimmunoblastic lymphadenopathy; anorexia;
KW basal cell carcinoma; cardiac amyloidosis; cerebral amyloidosis; Goiter;
KW chronic lymphatic leukaemia; degenerative osteoarthritis; delirium;
KW dementia; hypercholesterolaemia; hypothermia; metabolic bone disease;
KW glaucoma; depression; dyskinesia; diabetic hyperosmolar nonketotic coma;
KW osteoporosis; normal pressure hydrocephalus; diabetes; Reye's syndrome;
KW Parkinson's disease; polymyalgia; rheumatism; prostatic carcinoma;
KW renal amyloidosis; tuberculosis; urinary incontinence; galactosaemia;
KW fatty acid metabolism disorder; Addison's disease; cystic fibrosis;
KW fatty hepatocirrhosis; hyperadrenism; hypoadrenism; hyperlipaemia;
KW hyperparathyroidism; hypoparathyroidism; lipid myopathy; obesity;
KW lipodystrophy; phenylketonuria; cancer.
XX Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT Region 179..183
FT /label= Histidine_box
FT Region 217..221
FT /label= Histidine_box
FT Region 343..347
FT /label= Histidine_box
XX US6492108-B1.
XX 10-DEC-2002.
XX 26-MAR-1998; 98US-0048888.
XX 26-MAR-1998; 98US-0048888.
XX (INCY-) INCYTE GENOMICS INC.
XX Hillman JL, Guegler KJ, Corley NC, Shah P;
XX WPI; 2003-327308/31.
XX N-PSDB; ABX93652.
XX New isolated polynucleotide encoding polypeptide having delta-6
PT desaturase activity for use in diagnosis, treatment and prevention of
PT cardiovascular diseases, disorders of aging, disorders of fatty acid
PT metabolism, and cancer -
XX
XX Claim 3; Fig 2; 39pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide comprising an amino acid sequence given in the specification.
CC The polypeptide has fatty acid desaturase activity or delta-6 desaturase
CC activity. For use in the diagnosis, treatment and prevention of
CC cardiovascular diseases (e.g. angina pectoris, atheroma embolism,

CC atherosclerosis, arteriosclerosis, cardiac ischaemia, hypertension,
 CC hypercholesterolaemia, hyperlipidaemia, hypertriglyceridaemia, gangrene,
 CC mesenteric ischaemia, renal artery stenosis, stroke, nephrosclerosis,
 CC disorders of aging (e.g. Alzheimer's disease, angiodysplastic
 CC lymphadenopathy, anorexia, basal cell carcinoma, cardiac or cerebral
 CC amyloidosis, chronic lymphatic leukaemia, decubitus ulcers, degenerative
 CC osteoarthritis, delirium, dementia, depression, diabetes, dyskinesia,
 CC diabetic hyperosmolar nonketotic coma, glaucoma, hypercholesterolaemia,
 CC hypothermia, metabolic bone disease including osteoporosis, normal
 CC pressure hydrocephalus, Parkinson's disease, Reye's syndrome,
 CC polymyalgia, rheumatism, prostatic carcinoma, renal amyloidosis,
 CC tuberculosis, urinary incontinence, disorders of fatty acid metabolism
 CC (e.g. Addison's disease, cystic fibrosis, fatty hepatocirrhosis,
 CC galactosaemia, goiter, hyperadrenalemia, hypoadrenalemia, obesity,
 CC hyperparathyroidism, hypoparathyroidism, hyperlipaemia, lipid myopathies,
 CC lipodystrophies, phenylketonuria) and cancer. The present sequence
 CC represents the amino acid sequence of human delta 6 desaturase-2, D6D-2.
 XX
 SQ Sequence 444 AA;
 Query Match 62.1%; Score 1515; DB 24; Length 444;
 Best Local Similarity 62.0%; Pred. No. 6.7e-157;
 Matches 272; Conservative 62; Mismatches 99; Indels 6; Gaps 3;
 QY 11 AAREVSVPT---FSWEEIOKHLRTDGLVIDRKVNIITKWSIQHPGQGVIGHYAGED 67
 DB 7 AAEIAAQGPTRYTWDEAGRSCEERWLVIDRKVNISEFTRRHGGSRVISHYAGQD 66
 QY 68 ATDAFRAHPDLEFVGKPLKPLIGELAPEPSQDHGKNSKITEDFRLAKRTAEDMNLFK 127
 DB 67 ATDPFVAFHINKGLVKYMNLSLIGELSPQSPPTKNEKLTDFEELRATVERMGLMK 126
 QY 128 TNHVFLLLAHIIALESIAFTVFYFGNGWIPTLITAFVLATSOAAGWLQHDYGLSV 187
 DB 127 ANHVFLLYLHLILLEGAAWLTWVFGTSLFPLLCVALLSAVOAAGWLQHDYGLSV 186
 QY 188 YRKPKNHLVHKFVIGHLKGASANNWNRHFQHHAKPNI FHKDPDVMNLH--VFVLGEWQ 245
 DB 187 FSTSKWNHLHFFVIGHLKGAPASWWSHMHFQHHAKPNCFRKDPDINN-HPFFSALGKIL 245
 QY 246 PIEYKGGKLYLPYNHGHYEFLLGPPLIIPMYFOYQIIMTVHKNWDLANAVSYIR 305
 DB 246 SVELGKQKKYMPYNHGHYEFLLGPPLIIPMYFOYQIIMTVHKNWDLANAVSYIR 305
 QY 306 FFITYIPYIGLGLALLFNIRFLESNFWVVTQNNHIVMEIDQEAAYRDWFSQLTATCN 365
 DB 306 FFLLTVPLGLKAFGLFFIVRFLSNFWVVTQNNHIVMEIDQEAAYRDWFSQLTATCN 365
 QY 366 VEQSFNDWFSGLHNFQIEHHLFPTMPRHNLKIAPIVKSICAKHGIEYQEKPLLRALLD 425
 DB 366 VHKSANFNDWFSGLHNFQIEHHLFPTMPRHNLKIAPIVKSICAKHGIEYQEKPLLSAFAD 425
 QY 426 IIRSLKSGKWLWDAYLHK 444
 DB 426 IHSIKESQQLWLDAYLHQ 444
 RESULT 38
 AAM93314
 ID AAM93314 standard; Protein; 501 AA.
 XX
 AC AAM93314;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide, SEQ ID NO: 2827.
 XX
 KW Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX
 OS Homo sapiens.
 XX
 FN EP1130094-A2.
 XX

PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114089.
 XX
 PR 08-JUL-1999; 99JP-0194486.
 PR 11-JAN-2000; 2000JP-0118774.
 PR 02-MAY-2000; 2000JP-0183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR MPI; 2001-524355/58.
 DR N-P8DB; AAX94234.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX
 PS Claim 8; SEQ ID NO 2827; 1380pp + sequence listing; English.
 XX
 CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 CC molecules have been determined. Primers for synthesising the full length
 CC cDNA are useful for cloning the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is a polypeptide
 CC encoded by a full length human cDNA of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 XX
 SQ Sequence 501 AA;
 Query Match 62.1%; Score 1515; DB 22; Length 501;
 Best Local Similarity 62.0%; Pred. No. 8e-157;
 Matches 272; Conservative 62; Mismatches 99; Indels 6; Gaps 3;
 QY 11 AAREVSVPT---FSWEEIOKHLRTDGLVIDRKVNIITKWSIQHPGQGVIGHYAGED 67
 DB 64 AAEIAAQGPTRYTWDEAGRSCEERWLVIDRKVNISEFTRRHGGSRVISHYAGQD 123
 QY 68 ATDAFRAHPDLEFVGKPLKPLIGELAPEPSQDHGKNSKITEDFRLAKRTAEDMNLFK 127
 DB 124 ATDPFVAFHINKGLVKYMNLSLIGELSPQSPPTKNEKLTDFEELRATVERMGLMK 183
 QY 128 TNHVFLLLAHIIALESIAFTVFYFGNGWIPTLITAFVLATSOAAGWLQHDYGLSV 187
 DB 184 ANHVFLLYLHLILLEGAAWLTWVFGTSLFPLLCVALLSAVOAAGWLQHDYGLSV 243
 QY 188 YRKPKNHLVHKFVIGHLKGASANNWNRHFQHHAKPNI FHKDPDVMNLH--VFVLGEWQ 245
 DB 244 FSTSKWNHLHFFVIGHLKGAPASWWSHMHFQHHAKPNCFRKDPDINN-HPFFSALGKIL 302
 QY 246 PIEYKGGKLYLPYNHGHYEFLLGPPLIIPMYFOYQIIMTVHKNWDLANAVSYIR 305
 DB 303 SVELGKQKKYMPYNHGHYEFLLGPPLIIPMYFOYQIIMTVHKNWDLANAVSYIR 362
 QY 306 FFITYIPYIGLGLALLFNIRFLESNFWVVTQNNHIVMEIDQEAAYRDWFSQLTATCN 365
 DB 363 FFLLTVPLGLKAFGLFFIVRFLSNFWVVTQNNHIVMEIDQEAAYRDWFSQLTATCN 422
 QY 366 VEQSFNDWFSGLHNFQIEHHLFPTMPRHNLKIAPIVKSICAKHGIEYQEKPLLRALLD 425
 DB 423 VHKSANFNDWFSGLHNFQIEHHLFPTMPRHNLKIAPIVKSICAKHGIEYQEKPLLSAFAD 482
 QY 426 IIRSLKSGKWLWDAYLHK 444
 DB 483 IHSIKESQQLWLDAYLHQ 501

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1646	67.5	444	1	FADS BRARE	Q9dex7	brachydanio
2	210	8.6	359	1	LLCD SYNY3	Q08871	synechocyst
3	173	7.1	133	1	CYBS BOVIN	P00171	bos taurus
4	172	7.1	133	1	CYBS PIG	P00172	sus scrofa
5	169.5	7.0	133	1	CYBS RABIT	P00169	oryctolagus
6	162	6.6	133	1	CYBS HORSE	P00170	equus caball
7	160	6.6	133	1	CYBS RAT	P00173	rattus norv
8	159.5	6.5	447	1	FD3C SESIN	P48620	sesamum ind
9	159	6.5	133	1	CYBS HUMAN	P00167	homo sapien
10	158	6.5	573	1	CYBS HANAN	P09437	hansenuia a
11	157	6.4	133	1	CYBS MOUSE	P56395	mus musculus
12	155.5	6.4	351	1	DE3A SPIPL	O54794	spirulina p
13	153.5	6.3	881	1	NIAL PHAVU	P39865	phaseolus v
14	151.5	6.2	87	1	CYBS ALOSE	P00168	alouatta se
15	149	6.1	131	1	CYBS RHIST	Q09hrv1	rhizopus st
16	148.5	6.1	146	1	CYMS RAT	P04166	rattus norv
17	148.5	6.1	383	1	FD3E BRANA	P48624	brassica na
18	147.5	6.1	139	1	CYBS NEUCR	Q9P510	neurospora
19	147.5	6.1	460	1	FD3C RICCO	P48619	ricinus com
20	146.5	6.0	146	1	CYMS HUMAN	O43169	homo sapien
21	146	6.0	447	1	FD3C SPIOL	P48629	spinacia ol
22	145.5	6.0	379	1	FD3E TOBAC	P48626	nicotiana t
23	144.5	5.9	138	1	CYBS CHICK	P00174	gallus gall
24	143.5	5.9	400	1	FD12 MORIS	P59668	mortierella
25	142.5	5.8	400	1	FD12 MORAP	Q9Y8h5	mortierella
26	141	5.8	134	1	CY52 ARATH	O48845	arabidopsis
27	141	5.8	384	1	SC57 YEAST	Q03529	saccharomyc
28	139.5	5.7	917	1	NIA2 ARATH	P11035	arabidopsis
29	137.5	5.6	386	1	FD3E ARATH	P48623	arabidopsis
30	137.5	5.6	918	1	NIA4 CUCMA	P17569	cucurbita m
31	137	5.6	448	1	FD6C ARATH	P46312	arabidopsis
32	136.5	5.6	124	1	CY51 SCHPO	O94391	schizosacch
33	135	5.5	435	1	FD3D ARATH	P48622	arabidopsis

```

Best Local Similarity 64.6%; Pred. No. 3.6e-129;
Matches 287; Conservative 63; Mismatches 94; Indels 0; Gaps 0;
QY 1 MGKGNGQGEAAREVSVPTSWETIQKHLRTDSGLVIDRKNVITKWSIQHGGQORVI 60
Db 1 MGKGNGQGEAAREVSVPTSWETIQKHLRTDSGLVIDRKNVITKWSIQHGGQORVI 60
QY 61 GHYAGEDATAPRAHPDLEFVGKLPKLLIGELAPESPQDHGKNSKITDFPALAKTA 120
Db 61 GHYAGEDATAPRAHPDLEFVGKLPKLLIGELAPESPQDHGKNSKITDFPALAKTA 120
QY 121 EDNMFKNHVPFLLLAHIIAIESIAWFTVYFNGMIPTLITAFVLATSOAAGMLQH 180
Db 121 EDNMFKNHVPFLLLAHIIAIESIAWFTVYFNGMIPTLITAFVLATSOAAGMLQH 180
QY 181 DYGHLSVTRKPKNHLVHKFVGHKGSANWNRHHRFHQHAKEPIFKDPDVMNLHV 240
Db 181 DYGHLSVTRKPKNHLVHKFVGHKGSANWNRHHRFHQHAKEPIFKDPDVMNLHV 240
QY 241 LGEMOPIEYKGGKLVLPYNHGHYFFLIGPPLIPMYFOYQIIMTIVHKNWYDLAW 300
Db 241 LGEMOPIEYKGGKLVLPYNHGHYFFLIGPPLIPMYFOYQIIMTIVHKNWYDLAW 300
QY 301 SYIIRFFTYIPYIGLALLFLNIRFLESFVWVTQNMHIVMEIDQAYRDFWFSQ 360
Db 301 SYIIRFFTYIPYIGLALLFLNIRFLESFVWVTQNMHIVMEIDQAYRDFWFSQ 360
QY 361 TATCNVEQSFDFWFSGLNFOIEHLLPPTMPRHNLHIAPIVKSCLAKHGIEYQEKPL 420
Db 361 TATCNVEQSFDFWFSGLNFOIEHLLPPTMPRHNLHIAPIVKSCLAKHGIEYQEKPL 420
QY 421 RALLDIIRSLKXSGKLWLDAYLHK 444
Db 421 RALLDIIRSLKXSGKLWLDAYLHK 444

RESULT 2
LLCD_SINY3 STANDARD; PRT; 359 AA.
AC Q08871;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Linoleoyl-CoA desaturase (EC 1.14.19.3) (Delta(6)-desaturase).
DE DES6 OR SL0262.
GN Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN SEQUENCE FROM N.A.
RP MEDLINE=9326363; PubMed=8389613;
RA Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;
RT "Isolation of a delta 6-desaturase gene from the cyanobacterium
RT Synechocystis sp. strain PCC 6803 by gain-of-function expression in
RT Anabaena sp. strain PCC 7120."
RL Plant Mol. Biol. 22:293-300(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita M., Sasaki S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -I- CATALYTIC ACTIVITY: Linoleoyl-CoA + AH(2) + O(2) = gamma-
CC linolenyl-CoA + A + 2 H(2)O.
CC -I- COFACTOR: IRON.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC -----
CC EMBL; L11421; AAA27286.1; --
CC EMBL; D90914; BAA18502.1; --
CC InterPro; IPR005804; FA_desat_fam.
CC Pfam; PF00487; FA_desaturase; 1.
CC ProDom; PD001081; FA_desat_fam; 1.
CC Oxidoreductase; Iron; Complete proteome.
CC SEQUENCE 359 AA; 41425 MW; 33FB165AEB98C05F CRC64;

Query Match 8.6%; Score 210; DB 1; Length 359;
Best Local Similarity 23.5%; Pred. No. 4.3e-10;
Matches 85; Conservative 53; Mismatches 135; Indels 88; Gaps 18;
QY 127 KTNHVPFLLLAHIIAIESIAWFTVYFNGMIPTLITAFVLATSOAAGMLQHDY 182
Db 35 RDNPSMYLKTLLIVLWLPF--ANAFVLFAVIFPVLGCMVLAIALAFAFNVG--HDA 90
QY 183 GHLSVTRKPKNHN---LVHKFVGHKGSANWNRHHRFHQHAKEPIFKDPDVMNLHV 238
Db 91 NNNAYSGNPHNRVLGMYTFV-----GLSSFLMRYRHHYLTHTYTNILGHDFEI--- 140
QY 239 FVLGEQPTIEYKGGKLVLPYN-----HOHEYFFLIGPPLIPMY-FOYQIIMTIVHKN 292
Db 141 -----HGDGAVRMSPEQEHVGIYRFOFYIWLGLYLFIPFYWFLYDVVLNKGKY 190
QY 293 -----WDLAWAVSYIIRFFI-----TPIPYIGLALL 321
Db 191 HDHKIPFPQFLELASLLGKLLMLGYVGLFGLALGFSIPEVLIGASVTYMT-YGIWVCTI 249
QY 322 FLNFIREFSHWFWVTQNMHIVMEIDQAYRDFWFSQLTATCN-VEQSFFNDFSGHL 379
Db 250 FM-LAHVLESTELTPDGESG---ALDDE-----WAICQIETTANPATNPFVN-WFCGL 300
QY 380 NFOIEHLLPPTMPRHNLHIAPIVKSCLAKHGIEYQEKPLRALLDIIRSLKXSGKLWLD 439
Db 301 NHQVTHLFPNICHHPOLENIKDVQCQFGEYKVPYTFKAAI-----ASNYRWLE 353
QY 440 A 440
Db 354 A 354

RESULT 3
CYB5_BOVIN STANDARD; PRT; 133 AA.
AC P00171; Q27947; Q28837;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytochrome b5.
GN CYB5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128451; PubMed=2915932;
RA Cristiano R.J., Steggle A.W.;
RT "The complete nucleotide sequence of bovine liver cytochrome b5
RT mRNA."
RL Nucleic Acids Res. 17:799-799(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94010928; PubMed=8406485;

```

RA Cristiano R.J., Giordano S.J., Steggle A.W.;
RT "the isolation and characterization of the bovine cytochrome b5 gene,
RL and a transcribed pseudogene.";
RN Genomics 17:348-354 (1993).
RX (3)
RP SEQUENCE OF 1-97.
RT TISSUE=ERYTHROCYTE;
RX MEDLINE=85299161; PubMed=4030743;
RA Abe K., Kimura S., Kikawa R., Ahan F.K., Sugita Y.;
RT "Amino acid sequences of cytochrome b5 from human, porcine, and
RT bovine erythrocytes and comparison with liver microsomal cytochrome
RT b5.";
RL J. Biochem. 97:1659-1668 (1985).
RN (4)
RP SEQUENCE OF 1-10 AND 130-133.
RX MEDLINE=74080219; PubMed=4810060;
RA Ozols J.;
RT "Cytochrome b5 from microsomal membranes of equine, bovine, and
RT porcine livers. Isolation and properties of preparations containing
RT the membranous segment.";
RL Biochemistry 13:426-434 (1974).
RN (5)
RP SEQUENCE OF 5-96.
RX MEDLINE=70067001; PubMed=5391285;
RA Ozols J., Strittmatter P.;
RT "Correction of the amino acid sequence of calf liver microsomal
RT cytochrome b5.";
RL J. Biol. Chem. 244:6617-6618 (1969).
RN (6)
RP SEQUENCE OF 5-95.
RX MEDLINE=70289989; PubMed=527324;
RA Tsugita A., Kobayashi M., Tani S., Kyo S., Rashid M.A., Yoshida Y.,
RA Kajihara T., Hagiwara B.;
RT "Comparative study of the primary structures of cytochrome b5 from
RT four species.";
RL Proc. Natl. Acad. Sci. U.S.A. 67:442-447 (1970).
RN (7)
RP SEQUENCE OF 91-133.
RX MEDLINE=78218214; PubMed=670203;
RA Fleming P.J., Dailey H.A., Corcoran D., Strittmatter P.;
RT "The primary structure of the nonpolar segment of bovine cytochrome
RT b5.";
RL J. Biol. Chem. 253:5369-5372 (1978).
RN (8)
RP SEQUENCE OF 1-10.
RX MEDLINE=89323209; PubMed=2752049;
RA Ozols J.;
RT "Structure of cytochrome b5 and its topology in the microsomal
RT membrane.";
RL Biochim. Biophys. Acta 997:121-130 (1989).
RN (9)
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF OXIDIZED FORM.
RA Mathews F.S., Argos P., Levine M.;
RT "The structure of cytochrome b-5 at 2.0-A resolution.";
RL Cold Spring Harb. Symp. Quant. Biol. 37:387-395 (1971).
RN (10)
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF REDUCED FORM.
RA Argos P., Mathews F.S.;
RT "The structure of ferrocyclochrome b5 at 2.8-A resolution.";
RL J. Biol. Chem. 250:747-751 (1975).
RN (11)
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RA Durley R.C.E., Mathews F.S.;
RT "Refinement and structural analysis of bovine cytochrome b5 at 1.5-A
RT resolution.";
RL Acta Crystallogr. D 52:65-76 (1996).
RN (12)
RP X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 7-88, AND MUTAGENESIS.
RX MEDLINE=20303064; PubMed=10842340;
RA Wu J., Gan J.-H., Xia Z.-X., Wang Y.-H., Wang W.-H.,
RA Xue L.-L., Xie Y., Huang Z.-X.;
RT "Crystal structure of recombinant trypsin-solubilized fragment of

RT cytochrome b5 and the structural comparison with Val6His mutant.";
RL Proteins 40:249-257 (2000).
RN (13)
RP STRUCTURE BY NMR.
RX MEDLINE=96200988; PubMed=8613986;
RA Muskett F.W., Kelly G.P., Whitford D.;
RT "The solution structure of bovine ferricytochrome b5 determined using
RT heteronuclear NMR methods.";
RL J. Mol. Biol. 258:172-189 (1996).
RN (14)
RP STRUCTURE BY NMR OF 7-88, AND MUTAGENESIS.
RX MEDLINE=21145463; PubMed=11248680;
RA Wu Y., Qian C., Lu J., Li E., Wang W., Lu J., Xie Y.,
RA Wang J., Zhu D., Huang Z., Tang W.;
RT "Solution structure of cytochrome b5 mutant (E44/48/56A/D60A) and its
RT interaction with cytochrome c.";
RL Eur. J. Biochem. 268:1620-1630 (2001).
RN (15)
RP STRUCTURE BY NMR OF 7-88, AND MUTAGENESIS.
RX MEDLINE=21571982; PubMed=11714912;
RA Qian C., Yao Y., Ye K., Wang J., Tang W., Wang Y., Wang W., Lu J.,
RA Xie Y., Huang Z.;
RT "Effects of charged amino-acid mutation on the solution structure of
RT cytochrome b5 and binding between cytochrome b5 and cytochrome c.";
RL Protein Sci. 10:2451-2459 (2001).
CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES.
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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DR EMBL; X13617; CAA13949.1; -
DR EMBL; M63328; AAC14455.1; ALT SEQ.
DR EMBL; M63326; AAC14455.1; JOINED.
DR EMBL; M63327; AAC14455.1; JOINED.
DR EMBL; L22966; -; NOT_ANNOTATED_CDS.
DR PIR; A47215; CEBOS.
DR PDB; 1CYO; 15-MAR-00.
DR PDB; 1HKO; 25-MAR-03.
DR PDB; 1FO3; 23-MAY-01.
DR PDB; 1FO4; 23-MAY-01.
DR PDB; 1SHB; 15-NOV-00.
DR PDB; 1ES1; 15-NOV-00.
DR PDB; 115U; 31-DEC-02.
DR PDB; 1LQX; 04-SEP-02.
DR PDB; 1LR6; 04-SEP-02.
DR PDB; 1M20; 11-SEP-02.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation;
KW 3D-structure.
FT INIT MET 0 0
FT MOD_RES 1 1
FT DOMAIN 1 90
FT DOMAIN 91 133
FT METAL 43 43
FT METAL 67 67
FT METAL 67 67
FT CONFLICT 1 4
FT CONFLICT 15 17
FT CONFLICT 61 61
FT CONFLICT 97 97
FT S -> SES (IN REF. 2).
FT S -> SES (IN REF. 2).
FT ACETYLATION
FT HEME-BINDING.
FT MEMBRANE-BINDING.
FT IRON (HEME AXIAL LIGAND).
FT IRON (HEME AXIAL LIGAND).
FT ARES -> ZS22BA (IN REF. 5).
FT BIC -> QIE (IN REF. 5).
FT N -> D (IN REF. 5 AND 6).
FT S -> SES (IN REF. 2).

PT CONFLICT 133 133 N -> D (IN REF. 4).

PT STRAND 10 11

PT HELIX 13 16

PT TURN 17 18

PT STRAND 20 21

PT STRAND 22 23

PT STRAND 24 29

PT TURN 30 31

PT STRAND 32 35

PT TURN 37 42

PT TURN 44 45

PT TURN 48 53

PT HELIX 54 55

PT STRAND 57 57

PT STRAND 59 64

PT TURN 65 66

PT HELIX 69 75

PT TURN 76 78

PT STRAND 79 83

PT HELIX 85 90

SQ SEQUENCE 133 AA; 15198 MW; E27B600B61E0BC43 CRC64;

Query Match 7.1%; Score 173; DB 1; Length 133;

Best Local Similarity 32.0%; Pred. No. 1.6e-07;

Matches 47; Conservative 26; Mismatches 48; Indels 26; Gaps 4;

QY 11 AAREVSVPTSEWIEIOKHNLRDTSGLVIDRKVNITKWSIOHPGGORVIGHAGEDATD 70

DB 1 ABEESKAVKYTLEBIEIOKHNKSTWLTLYHYKVDLTKFUEHPGGBEVLRQAGGATE 60

QY 71 AFRAFHPDLEFVG-----KELKPLLIGELAPEPSQDHGKNSKITDFRALRKRTARDMN 124

DB 61 NF-----EDVGHSTDAELSKTFIIGELHPDD-----RSKITPSSIIITIDSNP 106

QY 125 LFKTN-----HVFPLLALHIALES 145

DB 107 SWTWNWLPALSALEFVALIYHLYTSEN 133

RESULT 4

CYB5_PIG STANDARD; PRT; 133 AA.

AC P00172; O18813;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome b5.

GN CYB5.

OS Sus. scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE=Blood, and Liver;

RX MEDLINE=98042520; PubMed=9367886;

RA Vandermark P.K.; Steggles A.W.;

RT "The isolation and characterization of the soluble and membrane-bound

RT porcine cytochrome b5 cDNAs."

RL Biochem. Biophys. Res. Commun. 240:80-83 (1997).

RN [2]

RN SEQUENCE.

RC TISSUE=Erythrocyte, and Liver;

RX MEDLINE=85289161; PubMed=4030743;

RA Abe K., Kimura S., Kizawa R., Anan F.K., Sugita Y.;

RT "Amino acid sequences of cytochrome b5 from human, porcine, and

RT bovine erythrocytes and comparison with liver microsomal cytochrome

RT b5."

RL J. Biochem. 97:1659-1668 (1985).

RN [3]

RP SEQUENCE OF 1-6.

RX MEDLINE=74060219; PubMed=4810060;

RA Ozols J.;

"Cytochrome b5 from microsomal membranes of equine, bovine, and porcine livers. Isolation and properties of preparations containing the membranous segment.";

Biochemistry 13:426-434 (1974).

[4]

RP SEQUENCE OF 7-88.

RX MEDLINE=71134790; PubMed=4993957;

RA Nobrega F.G., Ozols J.;

RT "Amino acid sequences of tryptic peptides of cytochromes b5 from

RT microsomes of human, monkey, porcine, and chicken liver.";

RL J. Biol. Chem. 246:1706-1717 (1971).

RN [5]

RP SEQUENCE OF 89-133, AND REVISIONS TO 14; 15 AND 61.

RX MEDLINE=78012290; PubMed=289425;

RA Ozols J., Gerard C.;

RT "Primary structure of the membranous segment of cytochrome b5."

RL Proc. Natl. Acad. Sci. U.S.A. 74:3725-3729 (1977).

RN [6]

RP SEQUENCE OF 1-10.

RX MEDLINE=89323209; PubMed=2752049;

RA Ozols J.;

RT "Structure of cytochrome b5 and its topology in the microsomal

RL Biochim. Biophys. Acta 997:121-130 (1989).

CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH

CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND

CC OXYGENASES.

CC -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE (LIVER FORM). BOUND TO

CC THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM. OR CYTOPLASMIC

CC (ERYTHROCYTE FORM).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1; Synonyms=Liver, Membrane-bound;

CC IsoId=P00172-1; Sequence=Displayed;

CC Name=2; Synonyms=Erythrocyte, Cytoplasmic;

CC IsoId=P00172-2; Sequence=VSP 001242, VSP 001243;

CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; AF016388; AAC48779.1; -.

DR EMBL; AF016389; AAC48780.1; -.

DR PIR; JC5782; CBPGS.

DR PIR; JC5783; JC5783.

DR HSP; P00171; LCYO.

DR InterPro; IPR001199; Cyt_B5.

DR Pfam; PF00173; heme_1; 1.

DR ProDom; PD000612; Cyt_B5; 1.

DR PROSITE; PS00191; CYTOCHROME B5_1; 1.

DR PROSITE; PS0255; CYTOCHROME B5_2; 1.

KW Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation;

KW Alternative splicing.

FT INIT_MET 0 0

FT MOD_RES 1 1 ACETYLATION (PARTIAL).

FT DOMAIN 1 90 HEME-BINDING.

FT DOMAIN 91 133 MEMBRANE-BINDING.

FT METAL 43 43 IRON (HEME AXIAL LIGAND).

FT METAL 67 67 IRON (HEME AXIAL LIGAND).

FT VARSPIC 97 97 T -> S (in isoform 2).

FT VARSPIC 98 133 /FTID=VSP 001242.

FT VARSPIC 98 133 Missing (in isoform 2).

FT VARSPIC 98 133 /FTID=VSP 001243.

FT CONFLICT 61 61 N -> D (IN REF. 4).

SQ SEQUENCE 133 AA; 15179 MW; 986FE1150BF30C4C CRC64;

Query Match 7.1%; Score 172; DB 1; Length 133;

Best Local Similarity 31.3%; Pred. No. 1.9e-07;

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Matches 47; Conservative 28; Mismatches 47; Indels 28; Gaps 4;
QY 11 AAEVSVPTFSEWIEIOKHNRDTSGLVIDRVKNITKWSIOHGGQGVIGHYAGEDATD 70
DB 1 AEQSDKAVKYVTLSEIKHNNKSTWLIHKKVYDLTKFLEHPGGEVLEQAGGDATE 60
QY 71 AFRAHPDLEFVG-----KFKPLLIGELAPEPSQDHGKNSKITEDFRALRKTAEQDN 124
DB 61 NF-----EDVGHSTDAELSKTIIGELHPDD-----RSKIAPSEVLIITVSNS 106
QY 125 LFKTNHVFLLLAHIIALESIAWTFVYF 154
DB 107 SWNTNW-----IPASIALVWSLMYHF 128

RESULT 5
CYB5_RABIT
ID CYB5_RABIT STANDARD; PRT; 133 AA.
AC P00169; Q28726;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytochrome b5.
GN CYB5.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID:9986;
RN [1]_TaxID:9986;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=89128816; PubMed=322232;
RA Darius N., Fisher C.W., Steggle A.W.;
RT "The nucleotide sequence of rabbit liver cytochrome b5 mRNA.";
RN Protein Seq. Data Anal. 1:351-353(1988).
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX STRAIN=New Zealand white.
RA Takamatsu H., Kozutsumi Y., Suzuki A., Kawasaki T.;
RT "Molecular cloning of rabbit cytochrome b5 genes: evidence for the
RT occurrence of two separate genes encoding the soluble and microsomal
RT forms.";
RN Biochem. Biophys. Res. Commun. 185:845-851(1992).
RP SEQUENCE OF 8-45 AND 49-90.
RX MEDLINE=69108767; PubMed=5709273;
RA Tsugita A., Kobayashi M., Kajihara T., Hagihara B.;
RT "Primary structure of rabbit liver cytochrome b5.";
RN J. Biochem. 64:727-730(1968).
RP SEQUENCE OF 6-7 AND 46-48.
RX MEDLINE=70289899; PubMed=5272324;
RA Tsugita A., Kobayashi M., Tani S., Kyo S., Rashid M.A., Yoshida Y.,
RA Kajihara T., Hagihara B.;
RT "Comparative study of the primary structures of cytochrome b5 from
RT four species.";
RN Proc. Natl. Acad. Sci. U.S.A. 67:442-447(1970).
RP SEQUENCE OF 4-97.
RX MEDLINE=71001482; PubMed=5506260;
RA Ozols J.;
RT "Amino acid sequence of rabbit liver microsomal cytochrome b5.";
RN J. Biol. Chem. 245:4863-4874(1970).
RP SEQUENCE OF 91-133.
RX MEDLINE=80049603; PubMed=500581;
RA Kondo K., Tajima S., Sato R., Narita K.;
RT "Primary structure of the membrane-binding segment of rabbit
RT cytochrome b5.";
RN J. Biochem. 86:1119-1128(1979).
RP SEQUENCE OF 98-133.
RX MEDLINE=80115672; PubMed=7354043;
```

```
RA Takagaki Y., Gerber G.E., Nibei K., Khorana H.G.;
RT "Amino acid sequence of the membranous segment of rabbit liver
RT cytochrome b5. Methodology for separation of hydrophobic peptides.";
RN J. Biol. Chem. 255:1536-1541(1980).
RP SEQUENCE OF 1-10.
RX MEDLINE=89323209; PubMed=2752049;
RA Ozols J.;
RT "Structure of cytochrome b5 and its topology in the microsomal
RT membrane.";
RN Biochim. Biophys. Acta 997:121-130(1989).
RP STRUCTURE BY NMR OF 6-99.
RX MEDLINE=20117684; PubMed=10651812;
RA Banci L., Bertini I., Rosato A., Scacchieri S.;
RT "Solution structure of oxidized microsomal rabbit cytochrome b5
RT factors determining the heterogeneous binding of the heme.";
RN Eur. J. Biochem. 267:755-766(2000).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES.
CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.
CC -1- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Liver, Membrane-bound;
CC IsoId=P00169-1; Sequence=Displayed;
CC Name=2; Synonyms=Erythrocyte, Cytoplasmic;
CC IsoId=P00169-2; Sequence=VSP 001244, VSP 001245;
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC EMBL; M24844; AAB03878.1; -.
CC EMBL; D10901; BAA01712.1; -.
CC PIR; JN0316; JN0316.
CC PIR; S03373; CBRB5.
CC PDB; 1DO9; 20-MAR-00.
CC InterPro: IPR001199; Cyt_B5.
CC Pfam; PF00173; heme_1_1_1.
CC ProDom; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS0255; CYTOCHROME_B5_2; 1.
CC Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation;
CC Alternative splicing; 3D-structure.
CC INIT MET 0 0
CC MOD_RES 1 1 ACETYLATION.
CC DOMAIN 1 90 HEME-BINDING.
CC DOMAIN 91 133 MEMBRANE-BINDING.
CC METAL 43 43 IRON (HEME AXIAL LIGAND).
CC METAL 67 67 IRON (HEME AXIAL LIGAND).
CC VARSPPLIC 97 97 T -> P (in isoform 2).
CC VARSPPLIC 98 133 Missing (in isoform 2).
CC VARSPPLIC 98 133 /FTID:VSP_001244.
CC CONFLICT 61 61 N -> D (IN REF. 3 AND 5).
CC CONFLICT 103 103 D -> N (IN REF. 6).
CC SEQUENCE 133 AA; 15218 MW; 2E48AEC20BC39720 CRC64;
Query Match 7.0%; Score 169.5; DB 1; Length 133;
Best Local Similarity 33.1%; Pred. No. 3.1e-07;
Matches 46; Conservative 27; Mismatches 45; Indels 21; Gaps 4;
QY 11 AAEVSVPTFSEWIEIOKHNRDTSGLVIDRVKNITKWSIOHGGQGVIGHYAGEDATD 70
DB 1 AAQSDKAVKYVTLSEIKHNNKSTWLIHKKVYDLTKFLEHPGGEVLEQAGGDATE 60
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QY 71 AFRAHPDLFVVG-----KFLKPLLIGELAPEPSQDHGKNSKITEDFRALRKTAEDWN 124
 Db 61 NF-----EDVGHSDARELSKTFIIGELHPDD-----RSKSKPMETLITITVDSNS 106
 QY 125 LFKTNHVFLLLAHIAL 143
 Db 107 SWTNVW-IPAISALIVAL 124

RESULT 6

CYB5_HORSE STANDARD; PRT; 133 AA.
 AC P00170;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 GN CYB5.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE OF 1-98.
 RX MEDLINE=7028943; PubMed=977596;
 RA Ozols J., Gerard C., Nobrega F.G.;
 RT "Proteolytic cleavage of horse liver cytochrome b5. Primary structure
 of the heme-containing moiety.";
 RL J. Biol. Chem. 251:6767-6774 (1976).
 RN [2]
 RP SEQUENCE OF 89-133.
 RX MEDLINE=78045981; PubMed=562879;
 RA Ozols J., Gerard C.;
 RT "Covalent structure of the membranous segment of horse cytochrome b5.
 Chemical cleavage of the native hemoprotein.";
 RL J. Biol. Chem. 252:8549-8553 (1977).
 RN [3]
 RP SEQUENCE OF 1-10.
 RX MEDLINE=89323209; PubMed=2752049;
 RA Ozols J.;
 RT "Structure of cytochrome b5 and its topology in the microsomal
 membrane.";
 RL Biochim. Biophys. Acta 997:121-130 (1989).
 CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 OXYGENASES.
 CC -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR HSP; P00171; ICYO.
 DR InterPro; IPR001199; Cyt_B5.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5; 1.
 DR PROSITE; PS00255; CYTOCHROME_B5; 2; 1.
 KW Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation.
 FT MOD_RES 1 1
 FT DOMAIN 1 90
 FT HEME-BINDING.
 FT DOMAIN 91 133
 FT IRON (HEME AXIAL LIGAND).
 FT METAL 43 43
 FT METAL 57 57
 FT METAL 67 67
 FT CONFLICT 1 5
 FT AEOQSD--ZEDAS (IN REF. 1).
 SQ SEQUENCE 133 AA; 15140 MW; 85E50818D8CF4247 CRC64;

Query Match 6.6%; Score 162; DB 1; Length 133;
 Best Local Similarity 27.3%; Pred. No. 1.3e-06;
 Matches 45; Conservative 28; Mismatches 44; Indels 48; Gaps 5;
 QY 11 AAEVSVPFVFWELIQHNLTDSGLVIDRKVYNITKWSIQHPGQGVIGHYAGEDATD 70
 Db 1 AEQSKAVKYITLEIKKHNSKSTWLILHHKVYDLTKFLEDHPGGEVLEQAGGDATE 60

QY 71 AFRAHPDLFVVG-----KFLKPLLIGELAPEPSQDHGKNSKITEDFRALRKTAEDWN 124
 Db 61 NF-----EDIGHSTDAEELSFTIIGELHPDD-----RSKIAPVETLITITVD--- 103
 QY 125 LFKTNHVFLLLAHIALIALESIAWFTVYFGNGWIPTLITAFVLA 169
 Db 104 -----SNSSWWT-----NWVIPAISAVVA 123

RESULT 7

CYB5_RAT STANDARD; PRT; 133 AA.
 AC P00173; O35768;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cytochrome b5.
 GN CYB5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93011015; PubMed=1396500;
 RA Mitoma J.-Y., Ito A.;
 RT "The carboxy-terminal 10 amino acid residues of cytochrome b5 are
 necessary for its targeting to the endoplasmic reticulum.";
 RL EMBO J. 11:4197-4203 (1992).
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=97396150; PubMed=9245704;
 RA Yoo M.;
 RT "Identification of two homologous cytochrome b5s in rat brain.";
 RL Biochem. Biophys. Res. Commun. 236:641-642 (1997).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE=82232110; PubMed=7093287;
 RA Ozols J., Heinemann F.S.;
 RT "Chemical structure of rat liver cytochrome b5. Isolation of peptides
 by high-pressure liquid chromatography.";
 RL Biochim. Biophys. Acta 704:163-173 (1982).
 RN [4]
 RP SEQUENCE OF 1-10.
 RX MEDLINE=89323209; PubMed=2752049;
 RA Ozols J.;
 RT "Structure of cytochrome b5 and its topology in the microsomal
 membrane.";
 RL Biochim. Biophys. Acta 997:121-130 (1989).
 RN [5]
 RP SEQUENCE OF 6-88.
 RX MEDLINE=83182449; PubMed=6840088;
 RA Lederer F., Ghir R., Guillard B., Cortial S., Ito A.;
 RT "Two homologous cytochromes b5 in a single cell.";
 RL Eur. J. Biochem. 132:95-102 (1983).
 RN [6]
 RP STRUCTURE BY NMR OF 1-98.
 RX MEDLINE=96234953; PubMed=8639599;
 RA Falzone C.J., Mayer M.R., Whitman E.L., Moore C.D., Lecomte J.T.J.;
 RT "Design challenges for hemoproteins: the solution structure of
 apocytochrome b5.";
 RL Biochemistry 35:6519-6526 (1996).
 RN [7]
 RP STRUCTURE BY NMR OF 5-98.
 RX MEDLINE=98028409; PubMed=9363779;
 RA Banci L., Bertini I., Ferroni F., Rosato A.;
 RT "Solution structure of reduced microsomal rat cytochrome b5.";
 RL Eur. J. Biochem. 249:270-279 (1997).
 RN [8]
 RP STRUCTURE BY NMR OF 5-98.
 RX MEDLINE=98067675; PubMed=9425037;
 RA Arnesano F., Banci L., Bertini I., Fellì I.C.;

RT "The solution structure of oxidized rat microsomal cytochrome b5."; Biochemistry 37:173-184 (1998).

RN [9].

RP STRUCTURE BY NMR OF 5-98.

RX MEDLINE=9828557; PubMed=9622481;

RA Dangi B., Sarma S., Van C., Banville D.L., Guiles R.D.;

RA "The origin of differences in the physical properties of the equilibrium forms of cytochrome b5 revealed through high-resolution NMR structures and backbone dynamic analyses.";

RT Biochemistry 37:8289-8302 (1998).

RN [10].

RP STRUCTURE BY NMR OF 1-98.

RX MEDLINE=21191748; PubMed=11294656;

RA Falzone C.J., Wang Y., Vu B.C., Scott N.L., Bhattacharya S.,

RA Lecante J.T.J.;

RT "Structural and dynamic perturbations induced by heme binding in cytochrome b5.";

RL Biochemistry 40:4879-4891 (2001).

CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES. IT IS ALSO INVOLVED IN SEVERAL STEPS OF THE STEROL BIOSYNTHESIS PATHWAY, PARTICULARLY IN THE C-5 DOUBLE BOND INTRODUCTION DURING THE C-5 DESATURATION.

CC -!- SUBCELLULAR LOCATION: MICROSOmal MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Long;

CC IsoId=P00173-1; Sequence=Displayed;

CC Name=Short;

CC IsoId=P00173-2; Sequence=VSP_001246, VSP_001247;

CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

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CC -----

DR EMBL; D13205; BAA02492.1; -

DR EMBL; AF007107; AAB67609.1; -

DR EMBL; AF007108; AAB67610.1; -

DR PIR; JC5596; JCS596.

DR PIR; S28404; CBRT5.

DR PDB; 1LET; 21-APR-97.

DR PDB; 1IEU; 21-APR-97.

DR PDB; 1AQA; 17-SEP-97.

DR PDB; 1AW3; 04-FEB-98.

DR PDB; 1AXX; 04-MAR-98.

DR PDB; 2AXX; 04-MAR-98.

DR PDB; 1BSA; 17-JUN-98.

DR PDB; 1BSB; 17-JUN-98.

DR PDB; 1BPX; 12-AUG-98.

DR PDB; 1BLV; 29-JUL-98.

DR PDB; 1187; 16-MAY-01.

DR PDB; 118C; 16-MAY-01.

DR PDB; 11B7; 04-APR-01.

DR PDB; 1JEX; 11-JUL-01.

DR PDB; 1MNY; 13-NOV-02.

DR InterPro; IPR001199; Cyt_B5.

DR Pfam; PF00173; heme_1; 1.

DR ProDom; PD006612; Cyt_B5; 1.

DR PROSITE; PS00191; CYTOCHROME B5_1; 1.

DR PROSITE; PS0255; CYTOCHROME B5_2; 1.

KW Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation;

KW Alternative splicing; 3D-structure.

FT INIT MET 0

FT MOD_RES 1 1 ACETYLATION.

FT DOMAIN 1 90 HEME-BINDING.

FT DOMAIN 91 133 MEMBRANE-BINDING.

FT METAL 43 43 IRON (HEME AXIAL LIGAND).

FT METAL 67 67 IRON (HEME AXIAL LIGAND).

FT VARSPLIC 96 99 ETLL -> HSAL (in isoform Short).

FT VARSPLIC 100 133 Missing (in isoform Short).

FT CONFLICT 17 17 /FTId=VSP_001246.

FT STRAND 11 11 Missing (in isoform Short).

FT HELIX 13 18 /FTId=VSP_001247.

FT TURN 19 20 Q -> E (IN REF. 5).

FT TURN 20 23

FT TURN 22 23

FT STRAND 26 29

FT TURN 30 31

FT STRAND 32 35

FT TURN 37 38

FT HELIX 39 42

FT TURN 44 45

FT HELIX 47 53

FT TURN 54 55

FT STRAND 57 57

FT HELIX 59 65

FT TURN 69 70

FT HELIX 71 78

FT STRAND 79 83

FT HELIX 85 90

SQ SEQUENCE 133 AA; 15224 MW; AE568036F3B105B4 CRC64;

Query Match 6.6%; Score 160; DB 1; Length 133;

Best Local Similarity 27.9%; Pred.No. 1.9e-06;

Matches 46; Conservative 26; Mismatches 45; Indels 48; Gaps 5;

QY 11 AAREVSVPTFSWEIIOKHLRTDSGLVIDRKVYNITKWSIOHPGQGVICHVAGEDATD 70

DB 1 AEQSDKDVYLTLEIIOKHKDSKTWILHKKVYDLTKFLEHPGGEVLREQAGDATE 60

QY 71 AFRAFHDPLELVG-----KFLKPLIGELAPEEPSQDHGKNSKITDFRALRTADMN 124

DB 61 NF-----EDVGHSKDARELSKTYIIGELHPDD-----RSKIAPSETLTIVT-- 103

QY 125 LFKTNHVFPELLLAHIALLESIAWFTVYFGNGWIPTLITAFVLA 169

DB 104 -----SNSSWWT-----NWVIFAISALVVA 123

RESULT 8

FD3C SESIN STANDARD; PRT; 447 AA.

AC P49620;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).

GN FAD7.

OS Sesamum indicum (Oriental sesame) (Gingelly).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; lamiales; Lamiales; Pedaliaceae; Sesamum.

OX NCBI_TaxID=4182;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. 4294; TISSUE=Cotyledon;

RA Shoji K.;

RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.

CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.

CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).

CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/ OR BE INVOLVED IN METAL ION BINDING.

CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U25817; AAA70334.1; --
CC InterPro; IPR005804; FA_Gesat fam.
CC Pfam; PF00487; FA_desaturase; 1.
CC ProDom; PD01081; FA_desat fam; 2.
CC Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Transit peptide.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 447 OMEGA-3 FATTY ACID DESATURASE.
FT DOMAIN 167 171 HISTIDINE BOX-1.
FT DOMAIN 203 207 HISTIDINE BOX-2.
FT DOMAIN 370 374 HISTIDINE BOX-3.
SQ SEQUENCE 447 AA; 51116 MW; 4576250DDSDAGB1 CRC64;

Query Match 6.5%; Score 159.5; DB 1; Length 447;
Best Local Similarity 20.6%; Pred. No. 8.6e-06;
Matches 94; Conservative 70; Mismatches 164; Indels 129; Gaps 23;

QY 32 RTD-----SGLVIDRKVNITKSIQHDPGQGVICHYAGEDATDAFRAHPDLEFVGKFLK 87
DB 39 RTDLGSSCLSGILRKWALVSAPLRVLQVEEENKSGERVINGEEDFGAPP 98
QY 88 PLLIGELAPEPSODHGNKSTIDFALAKTAEDNNLFKTNHVFLLLAHIALESTIA 147
DB 99 PFKLSIDREATP-----KHCVKDPWRSVMGVVRD-----VAVVFGLAAVA 139
QY 148 WFTVYFENGWIPLTITAFVLATSCAQAGWLQHDYGHLSVVRKPKMNLVHKFVIGHLKG 207
DB 140 ----AYF--NNWVWPLVFAQSTFWALFVLGHDCGHSFNPDKLNS-----VVGHLH 199
QY 208 ASA-----NNWNRHFQHAKNIPHKDPDVMNMLHVFVLGKQNP-----IEYKKKXK 255
DB 190 SSILVPVHGWRISHRTH--QNHGIVENDES-----WHPLSEKIYKNLDTATKKLR 238
QY 256 Y-LPNHGHQHEFFLIGPRLIIPMF-----OYQIMTMIIVHK 291
DB 239 FTLPF-----PLALPVLVMSRSPQKQSHFHPDSDLFVFNKQDVITSTVCWT 287
QY 292 NNVDLAWAVSVYIRFFIYIPYGI--LGALLFLNFIREFLESH-----WFWVVTQMH 342
DB 288 AMIALLVGLSFVIG-PVQLLKLYGIPYLGVMWLDLVLYLHHGHGDKLPWY----- 338
QY 343 IWEIDQAYRDW--FSSQLTATCNVEQSFNDWFSGLNFQIEHLLFPTMPRHNLKIA 400
DB 339 -----RGKWSVYLRGLT-TLDRDYGWINN-IHHDIGTHVIHLLFPQIPHYHLIEAT 388
QY 401 PLVKSICAKHGTEYQE-----KPLRALLDIIRSLKK 432
DB 389 EAAKPVLGKY-----YREPKSAPLPHLLGLDLSLR 422

RESULT 9

CYB5_HUMAN
ID CYB5_HUMAN STANDARD; PRT; 133 AA.
AC P00167;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5.
GN CYB5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

CC TISSUE=Liver;
CC MEDLINE=89025904; PubMed=3178851;
CC Yoo M., Steggle A.W.;
CC "The complete nucleotide sequence of human liver cytochrome b5 mRNA.";
CC Biochem. Biophys. Res. Commun. 156:576-580(1988).
CC [2]
CC SEQUENCE FROM N.A.
CC Li X.R., Giordano S.J., Yoo M., Steggle A.W.;
CC Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC [3]
CC SEQUENCE OF 1-97 FROM N.A.
CC TISSUE=Erythrocyte;
CC MEDLINE=91298976; PubMed=1712589;
CC Giordano S.J., Steggle A.W.;
CC "The human liver and reticulocyte cytochrome b5 mRNAs are products
CC from a single gene.";
CC Biochem. Biophys. Res. Commun. 178:38-44(1991).
CC [4]
CC SEQUENCE OF 1-97.
CC TISSUE=Erythrocyte;
CC MEDLINE=85289161; PubMed=4030743;
CC Abe K., Kimura S., Kizawa R., Anan F.K., Sugita Y.;
CC "Amino acid sequences of cytochrome b5 from human, porcine, and
CC bovine erythrocytes and comparison with liver microsomal cytochrome
CC b5.";
CC J. Biol. Chem. 246:1706-1717(1971).
CC [5]
CC SEQUENCE OF 1-90.
CC MEDLINE=71134790; PubMed=4993957;
CC Nobrega F.G., Ozols J.;
CC "Amino acid sequences of tryptic peptides of cytochromes b5 from
CC microsomes of human, monkey, porcine, and chicken liver.";
CC J. Biol. Chem. 246:1706-1717(1971).
CC [6]
CC SEQUENCE OF 1-90.
CC MEDLINE=72154531; PubMed=5062820;
CC Ozols J.;
CC "Cytochrome b5 from a normal human liver. Isolation and the partial
CC amino acid sequence.";
CC J. Biol. Chem. 247:2242-2245(1972).
CC [7]
CC SEQUENCE OF 1-90.
CC MEDLINE=74074962; PubMed=4770377;
CC Rashid M.A., Hagihara B., Kobayashi M., Tani S., Tsugita A.;
CC "Structural studies of cytochrome b5. 3. Sequential studies on human
CC liver cytochrome b5.";
CC J. Biochem. 74:985-1002(1973).
CC [8]
CC SEQUENCE OF 1-35 AND 83-133.
CC MEDLINE=89323209; PubMed=2752049;
CC Ozols J.;
CC "Structure of cytochrome b5 and its topology in the microsomal
CC membrane.";
CC Biochim. Biophys. Acta 997:121-130(1989).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES.
CC -1- SUBCELLULAR LOCATION: MICROSOmal MEMBRANE (LIVER FORM). BOUND TO
CC THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM. OR CYTOPLASMIC
CC (ERYTHROCYTE FORM).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Liver, Membrane-bound;
CC IsoId=P00167-1; Sequence=Displayed;
CC Name=2; Synonyms=Erythrocyte, Cytoplasmic;
CC IsoId=P00167-2; Sequence=VSP 001240, VSP 001241;
CC -1- DISEASE: DEFECTS IN CYB5 ARE THE CAUSE OF TYPE IV HEREDITARY
CC METHEMOGLOBINEMIA.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M22865; AAA35729.1; --
 CC EMBL; L39945; AAA63169.1; ALT SEQ.
 CC EMBL; L39792; AAA63169.1; JOINED.
 CC EMBL; L39941; AAA63169.1; JOINED.
 CC EMBL; L39944; AAA63169.1; JOINED.
 CC EMBL; L39943; AAA63169.1; JOINED.
 CC EMBL; L39944; AAA63169.1; JOINED.
 CC EMBL; M60174; AAA52165.1; --
 CC PIR; A28936; CBHUS.
 CC PIR; JN0075; CBHUS.
 CC KSP; P00171; 1BHB.
 CC GSP; HGNC:2570; CYB5.
 CC MIM; 250790; --
 CC GO:0004129; F:cytochrome c oxidase activity; TAS.
 CC InterPro; IPR001199; Cyt B5.
 CC Pfam; PF00173; heme_1; 1.
 CC PRINTS; PR00363; CYTOCHROME B5.
 CC PRODOM; PD000612; Cyt B5; 1.
 CC PROSITE; PS00191; CYTOCHROME B5_1; 1.
 CC PROSITE; PS0255; CYTOCHROME B5_2; 1.
 CC Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation;
 CC Alternative splicing.
 CC INIT MET 0
 CC MOD RES 1 1
 CC DOMAIN 1 90
 CC HEME-BINDING.
 CC MEMBRANE-BINDING.
 CC IRON (HEME AXIAL LIGAND).
 CC IRON (HEME AXIAL LIGAND).
 CC T -> P (in isoform 2).
 CC /FtId=VSP_001240.
 CC Missing (in isoform 2).
 CC /FtId=VSP_001241.
 CC MISSING (IN REF. 5).
 CC Q -> E (IN REF. 8).
 CC EBIQ -> QBIQ (IN REF. 5, 6 AND 7).
 CC MISSING (IN REF. 7).
 CC N -> D (IN REF. 5, 6 AND 7).
 CC RPK -> KPR (IN REF. 4, 5, 6 AND 7).
 CC A -> V (IN REF. 8).
 CC CONFLICT 121 121
 CC SEQUENCE 133 AA; 15199 MW; 2FAD2AE87B5C992E CRC64;
 CC
 CC Query Match 6.5%; Score 159; DB 1; Length 133;
 CC Best Local Similarity 30.8%; Pred. No. 2.3e-06;
 CC Matches 44; Conservative 27; Mismatches 44; Indels 28; Gaps 4;
 CC
 CC 11 AAREVSVPTFSWEIIOKHLRTDGLVIDRKVYNTKSIQHPGGORVIGHVAGEDATD 70
 CC 1 AEQDEAVKYTLEIIQKHHSKSTWILHKKYDITKFLPEHPGGVEVLREQAGGDATE 60
 CC 71 AFRAHPDLPFVG-----KFLKELLIGELAPEPSQDHGKNSKITEDFALRKTAEDMN 124
 CC 61 NF-----EDVGHSTDAEMSKTFIIGELHPDD-----RPLKPKPTLTITDSSS 106
 CC 125 LFKTNHYVFFLLLAHLALLESIA 147
 CC 107 SWTNWV-----IPASAVA 121
 CC
 CC RESULT 10
 CC CYB2 HANAN
 CC ID CYB2 HANAN STANDARD; PRT; 573 AA.
 CC AC P09437;
 CC DT 01-MAR-1999 (Rel. 10, Created)
 CC DT 01-JAN-1990 (Rel. 13, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Cytochrome B2, mitochondrial precursor (EC 1.1.2.3) (L-lactate
 CC dehydrogenase [cytochrome]) (L-lactate ferricytochrome C
 CC oxidoreductase) (L-LCR).

GN CYB2.
 OS Hansenula anomala (Yeast) (Candida pelliculosa).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4927;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90045973; PubMed=2813072;
 RA Rielor Y., Tegoni M., Gervais M.;
 RT "Nucleotide sequence of the Hansenula anomala gene encoding
 RT flavocytochrome b2 (b₂-lactate:cytochrome c oxidoreductase).";
 RL Nucleic Acids Res. 17:8381-8391(1989).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9008451; PubMed=2688640;
 RA Black M.T., Gunn F.J., Chapman S.K., Reid G.A.;
 RT "Structural basis for the kinetic differences between
 RT flavocytochromes b2 from the yeasts Hansenula anomala and
 RT Saccharomyces cerevisiae.";
 RL Biochem. J. 263:973-976(1989).
 RN (3)
 RP SEQUENCE OF 80-163.
 RX MEDLINE=88082787; PubMed=3319613;
 RA Haumont P.-Y., Thomas M.-A., Labeyrie F., Lederer F.;
 RT "Amino-acid sequence of the cytochrome-b₅-like heme-binding domain
 RT from Hansenula anomala flavocytochrome b₂.";
 RL Eur. J. Biochem. 169:539-546(1987).
 CC -!- CATALYTIC ACTIVITY: (S)-lactate + 2 ferricytochrome c = pyruvate +
 CC 2 ferricytochrome c.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial intermembrane space.
 CC -!- MISCELLANEOUS: THIS ENZYME BINDS FMN AND PROTOHEME IX PROSTHETIC
 CC GROUPS.
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
 CC B5 FAMILY.
 CC -!- SIMILARITY: TO SPINACH GLYOXALATE OXIDASE (33% IDENTITY), TO
 CC P. PUTIDA S-MANDELATE DEHYDROGENASE, AND TO M.SMEGWATIS LACTATE
 CC 2-MONOOXYGENASE.
 CC
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 CC -----
 CC EMBL; X16051; CAA34183.1; --
 CC PIR; S06600; S06600.
 CC HSSP; P00175; ILCO.
 CC InterPro; IPR001199; Cyt B5.
 CC InterPro; IPR003009; FMN_enzyme.
 CC InterPro; IPR000262; FMN_hydxyc_dh.
 CC Pfam; PF01070; FMN_dh; 1.
 CC Pfam; PF00173; heme_1; 1.
 CC PRINTS; PR00363; CYTOCHROME B5.
 CC PRODOM; PD000612; Cyt B5; 1.
 CC PROSITE; PS00191; CYTOCHROME B5_1; 1.
 CC PROSITE; PS0255; CYTOCHROME B5_2; 1.
 CC PROSITE; PS00557; FMN HYDROXY ACID DH; 1.
 CC Electron transport; Respiratory chain; Oxidoreductase; Flavoprotein;
 CC FMN; Heme; Mitochondrion; Transit peptide.
 CC TRANSIT 1 73
 CC CHAIN 74 573
 CC CYTOCHROME B2.
 CC DOMAIN 80 163
 CC METAL 115 115
 CC METAL 138 138
 CC ACT_SITE 432 432
 CC ACT_SITE 435 435
 CC ACT_SITE 573 AA; 64202 MW; 83EEF645C580BC8E CRC64;
 CC SEQUENCE 573 AA; 64202 MW; 83EEF645C580BC8E CRC64;
 CC
 CC Query Match 6.5%; Score 158; DB 1; Length 573;
 CC

```

Best Local Similarity 23.7%; Pred. No. 1.5e-05;
Matches 52; Conservative 40; Mismatches 73; Indels 54; Gaps 8;

QY 13 EREVSVFTFSWBIQ-----KXNLTDSGLVIDRKVNITKWSIQHFGQGVIGHYAG 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 DKFISADVPHWKDTELTPETVSVQHNKXDDLWVVLNGQVYDLTDFLNFHPGQKIIIRYAG 127

QY 66 EDATDAFRAHPDLEFVGKFLKP-----LLIGELAPEPSQDHGKNSKI----- 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 KDAIKIVFVPHPP-DTTEKIPPEKHGLPIVGPEQEELSDEBDRLERIERKPLSQ 186

QY 110 ---TEDFRALK-----TAEDMNLFKTNH-----VFILLLAHIITALSSIAW 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 MINLHDPETIARQLPPPALAVYCSAADDEVTLRNHNAYHRIFFNPKI--LIDVQDVI 244

QY 149 FTVVYFGNGMPTLITAFVLATSQAQGLQHDYGHLSV 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 STEFFGKTSAPFYISATALK-----LHPGEVAI 276

RESULT 11
CYB5_MOUSE
ID _CYB5_MOUSE STANDARD; PRT; 133 AA.
AC P56395;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5.
GN CYB5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
RA Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
RA Schellenberg K., Steptoe M., Tan P., Underwood K., Moore B.,
RA Theising B., Wylie T., Lennon G., Soares B., Wilson R., Waterston R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases
CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES. IT IS ALSO INVOLVED IN SEVERAL STEPS OF THE STEROL
CC BIOSYNTHESIS PATHWAY, PARTICULARLY IN THE C-5 DOUBLE BOND
CC INTRODUCTION DURING THE C-5 DESATURATION.
CC -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC -----
CC EMBL; AA107504; -; NOT ANNOTATED CDS.
CC DR EMBL; W62851; -; NOT ANNOTATED CDS.
CC DR EMBL; AA104561; -; NOT ANNOTATED CDS.
CC DR EMBL; AA107511; -; NOT ANNOTATED CDS.
CC DR EMBL; AA086847; -; NOT ANNOTATED CDS.
CC DR EMBL; AA105541; -; NOT ANNOTATED CDS.
CC DR HSSP; P00173; 1AQA.
CC DR MGD; MGI:1926952; Cyb5.
CC DR SWISS-2DPAGE; P56395; MOUSE.
CC DR InterPro; IPR001199; Cyt B5.
CC DR Pfam; PF00173; heme_b1;
CC DR PRINTS; PR00363; CYTOCHROMES.
CC DR ProDom; PD000612; Cyt B5; 1.
CC DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
CC DR PROSITE; PS0255; CYTOCHROME B5_2; 1.
CC DR Electron transport; Transmembrane; Heme; Iron; Microsome.

FT INIT MET 0 0 BY SIMILARITY.
FT DOMAIN 1 90 HEME-BINDING (BY SIMILARITY).
FT DOMAIN 91 133 MEMBRANE-BINDING (BY SIMILARITY).
FT METAL 43 43 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 67 67 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 133 AA; 15110 MW; 58540A370B38CEAE CRC64;

Query Match 6.4%; Score 157; DB 1; Length 133;
Best Local Similarity 33.1%; Pred. No. 3.4e-06;
Matches 42; Conservative 22; Mismatches 43; Indels 20; Gaps 3;

QY 11 AAREVSVPTFSWEIOKHNLRITDSGLVIDRKVNITKWSIQHFGQGVIGHYAGEDATD 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 AGQSDKVYVTLBEIQHKDSKTWILHHKYDLTKFLEHFGGEBVLREQAGDATE 60

QY 71 AFRAPHPDLEFVG-----KFLKPLLIGELAPEPSQDHGKNSKITDFFRALRKTAE 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 NP-----EDVGHSTDAEELSKTYIIGELHPDD-----RSKIAKPSDTLITTVES 106

QY 125 LFKTNHV 131
   : : : : :
Db 107 SWWTNWV 113

RESULT 12
DESA_SPIPL
ID _DESA_SPIPL STANDARD; PRT; 351 AA.
AC Q54794;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fatty acid desaturase (EC 1.14.19.-) (Delta 12 desaturase).
GN DESA.
OS Spirulina platensis.
OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
OX NCBI_TaxID=1156;
RN [1]
RP SEQUENCE FROM N.A.
RA Murata N., Deshniun P., Tasaka Y.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CAN INTRODUCE A SECOND CIS DOUBLE BOND AT THE DELTA 12
CC POSITION OF FATTY ACID BOUND TO MEMBRANES GLYCEROLIPIDS. THIS
CC ENZYME IS INVOLVED IN CHILLING TOLERANCE BECAUSE THE PHASE
CC TRANSITION TEMPERATURE OF LIPIDS OF CELLULAR MEMBRANES DEPENDS ON
CC THE DEGREE OF UNSATURATION OF FATTY ACIDS OF THE MEMBRANE LIPIDS.
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC -----
CC EMBL; X86736; CAA60415.1; -
CC DR PIR; S54259; S54259; -
CC DR InterPro; IPR005804; FA_desat_fam.
CC DR InterPro; IPR005803; FA_desaturase.
CC DR Pfam; PF00487; FA_desaturase; 1.
CC DR ProDom; PD001081; FA_desat_fam; 2.
CC DR PROSITE; PS00574; FATTY ACID DESATUR 2; FALSE NEG.
CC DR Oxidoreductase; Fatty acid biosynthesis; Membrane.
CC DR DOMAIN 89 93 HISTIDINE BOX-1.
CC DR DOMAIN 125 129 HISTIDINE BOX-2.
CC DR FT DOMAIN 286 290 HISTIDINE BOX-3.
CC DR SEQUENCE 351 AA; 40928 MW; 125A9F1E07E5EE97 CRC64;

Query Match 6.4%; Score 155.5; DB 1; Length 351;
Best Local Similarity 24.0%; Pred. No. 1.4e-05;
Matches 74; Conservative 35; Mismatches 122; Indels 77; Gaps 16;

QY 147 ANFTVF-----YFGNGWIPLITAFVLA-----TSQAQAGW--LQHDYGHLSVYRPKWN 194

```



```
FT CONFLICT 57 57 T -> A (IN REF. 2).
FT CONFLICT 64 64 A -> V (IN REF. 2).
FT CONFLICT 68 68 M -> V (IN REF. 2).
FT CONFLICT 78 78 L -> F (IN REF. 2).
FT CONFLICT 84 84 V -> A (IN REF. 2).
FT CONFLICT 113 114 SV -> TA (IN REF. 2).
FT CONFLICT 162 162 P -> S (IN REF. 2).
FT CONFLICT 181 181 I -> L (IN REF. 2).
FT CONFLICT 195 195 F -> Y (IN REF. 2).
FT CONFLICT 232 232 D -> G (IN REF. 2).
FT CONFLICT 264 264 E -> D (IN REF. 2).
FT CONFLICT 320 321 RA -> KS (IN REF. 2).
FT CONFLICT 383 383 AA; 43936 MW; DAD7C3AGFA12866A CRC64;
SQ SEQUENCE 383 AA; 43936 MW; DAD7C3AGFA12866A CRC64;

Query Match 6.1%; Score 148.5; DB 1; Length 383;
Best Local Similarity 22.5%; Pred. No. 5.9e-05;
Matches 92; Conservative 62; Mismatches 149; Indels 105; Gaps 25;

QY 65 GEDATDAFRAPHPDLEFVGKFLKPLLLIGELAPEPSQDHGKNSKITEDPRLAKRTAEDMN 124
DB 13 GDSGARKEEGDPSAQ-----PPFKIGDTRAAIP-----KHCWKSPLRMS-----54
QY 125 LFKTNHVFLLLAHIALESIAWF--TVFVGNGWTPTLITA-FVLATSOAGWLOHD 181
DB 55 -YVTRDIFAVAALA-MAAVYFDSWFLWPLVVAQG---TLFWAIFVLG-----HD 99
QY 182 YGHLVYRKPKWN---HLVHKFVIGHLKGSANWNRHFRHQAENIHKDPDVMNLH 237
DB 100 CGHGSFSDIPLLNSVGHILSHFLVPHG-----WISHRTH--QNHGHVENDES---149
QY 238 VFVLGEMQPIEGKKKLYLPNQHVEYFFLIGPLIPMYFOQIIMTVHVN-----292
DB 150 -----WVPLP--EKLYKNLPHSTRMLRYTVPLPMLAYPIYLMYRSPKSGSHENPYSSL 201
QY 293 -----WDLAVASVYIRFF---ITYIPFYGLGALLFLNFIRLESHWF 334
DB 202 PAPSERKUIASTTCW-SIMLATVILSFLVDPTVLKVGCV-----PYLIFVMWLD-----253
QY 335 VVWVQNHVIMBIDOEAYR--DW--FSSQLTATCNVEQSPFNDFNSGHLNFQIEHHLFPT 390
DB 254 -----VTVLHHGHDKLPYRGKWSYLRGLT-TIDRDYGIENN-IHHDIGTHVHHLFPQ 309
QY 391 MPRHNLKTAIPLVSKLAKH-GIEYQEKPLLRAL-LDIIRSLKSGK 435
DB 310 IPHYHL-----VDATRAAKHVLGRYRBPKTSKAIPHILVESLVASIK 352

RESULT 18
CYB5_NEUCR STANDARD; PRT; 139 AA.
AC Q9P5L0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable cytochrome b5.
GN B23121.190.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A / FGSC 987;
RX PubMed=12655011;
RA Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
RA Hohnes J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
RA Schulte U.;
RT "What's in the genome of a filamentous fungus? Analysis of the
RT Neurospora genome sequence."
RL Nucleic Acids Res. 31:1944-1954(2003).
CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenases (By similarity).
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
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CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL356172; CAB91687.2; -
CC InterPro; IPR001199; Cyt B5.
CC Pfam; PF00173; heme 1; 1.
CC PRINTS; PR00363; CYTOCHROME B5.
CC ProDom; PR000612; Cyt B5; 1.
CC PROSITE; PS00191; CYTOCHROME B5_1; 1.
CC PROSITE; PS02555; CYTOCHROME B5_2; 1.
CC Electron transport; Transmembrane; Heme; Iron; Microsome.
KW DOMAIN 1 78 HEME-BINDING.
FT TRANSMEM 105 125 POTENTIAL.
FT METAL 37 37 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 61 61 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 139 AA; 14613 MW; 404BF3BA1DF5D575 CRC64;

Query Match 6.1%; Score 147.5; DB 1; Length 139;
Best Local Similarity 40.0%; Pred. No. 2.2e-05;
Matches 32; Conservative 19; Mismatches 16; Indels 13; Gaps 2;

QY 21 FSWBRIQHNLTDSGLVTRKVNITKWS:QHPGQQRVIGHYAGEDATDAFRAPHPDLE 80
DB 5 FTYQVVAENTKDIYVHDKVYDITKVEDEHFGSEVLLDVAGQDSTEAF-----E 57
QY 81 FVG-----KFLKPLLLIGEL 94
DB 58 DVGHSDEAREALEPLLVGTL 77

RESULT 19
FD3C_RICCO STANDARD; PRT; 460 AA.
ID FD3C_RICCO
AC P48619;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
GN FAD7A-1.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Baker 296; TISSUE=Seed;
RC MEDLINE=94302177; PubMed=8029360;
RA van de Loo F.J., Somerville C.R.;
RT "Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis.";
RL Plant Physiol. 105:443-444(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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DR EMBL; L25897; AAA73511.1; -;
 DR PIR; T10063; T10063.
 DR InterPro; IPR005804; FA desat fam.
 DR Pfam; PF00487; FA desaturase; 1.
 DR ProDom; PD001081; FA desat fam; 2.
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KW Transit peptide.
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN 177 460 OMEGA-3 FATTY ACID DESATURASE.
 FT DOMAIN 177 181 HISTIDINE BOX-1.
 FT DOMAIN 213 217 HISTIDINE BOX-2.
 FT DOMAIN 380 384 HISTIDINE BOX-3.
 SQ SEQUENCE 460 AA; 52561 MW; 836592904EF3C7B0 CRC64;

Query Match 6.1%; Score 147.5; DB 1; Length 460;
 Best Local Similarity 22.5%; Pred. No. 8.9e-05;
 Matches 101; Conservative 59; Mismatches 176; Indels 113; Gaps 23;

QY 40 DRKVN-----ITKWSIQHPGQGV-----IGHVAGED--ATDAFRAFPDLEFVGK 84
 DB 41 DSKSYNLCSFKYSSNSKSNKALNVAVPNVSTVSGEDDREREENGIVNVDSKGGE 100
 QY 85 FL-----KPLIGELAPEEBSQHGKSKITEDFRALKRTAEDMNLKTNHVPFLLLLAH 139
 DB 101 FFDAGAPPTFLADIRAAIP-----KHCWYKNPWSNSVYLRDVV-----VFGLAAVA- 149
 QY 140 IIALESIAWTVFVFGNGWPTLITAFVLATSAQAQWLOHDYGHLSVYRKPKNHLVHK 199
 DB 150 -----AYP-----NNWVAPLYWFCQGTWFWALFVLGDCGSGFSNNPKLNS--- 192
 QY 200 FVIGHLKGAGA-----NWNHRRHQHAKNPIFKHPDPVNMHLVFLGEGQPIYGYKKLK 255
 DB 193 -VVGHLHSSILVPHYHGWRISHRTH--QNHGVENDES-----NHPL--SEKIFK 238
 QY 256 YLPVNHQHEVFFLIGPPLIPMYF-----QYQIMTIVKHNVNDLAWAVSYIR 305
 DB 239 SLDNVTKLRLSPLFFMLAYPFYLSRSPGKSGSHFDPDGLFVPERKDI----- 289
 QY 306 FFITYIPFYGILGALL-FLNF-----IRFLESH-----WFWVTQMNHIVMEIDQEA 351
 DB 290 --ITSTACTWAMAALLVYLFNSMGVPQMLKLYGIPYMFVWMLDFVTVLHHGHEDKLPW 347
 QY 352 YRDWFSSQL---TATCNVEQSFNDWFSGLNFCQIEHLEPTWPRNLHKIALPLVKSICA 408
 DB 348 YRGKAWSYLRGGTLTDRDYGWINN-IHHDIGTHVHHLPFPQIPHVLVEATEAARPMVG 406
 QY 409 KHGIEYQEK-----PL-LRALDIDIRSLKK 432
 DB 407 KY---YREPCKSGFLPLHLLGLSVRSME 432

RESULT 20
 ID CYN5_HUMAN STANDARD; PRT; 146 AA.
 AC O43169;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5 outer mitochondrial membrane isoform precursor.
 GN CYB5M OR OMB5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Ishibashi K.;

"Cytochrome b5 and aquaporins share the last transmembrane amino acids sequence".
 RT Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

CC FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH

CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND

CC OXYGENASES (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Mitochondrial outer membrane (By

CC similarity).

CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

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CC EMBL; AB009282; BAA23735.1; -;

DR HSSP; P04166; 1B5M.

DR InterPro; IPR001199; Cyt_B5.

DR Pfam; PF00173; heme_1; 1.

DR PRINTS; PR00363; CYTOCHROMEBS.

DR ProDom; PD000612; Cyt_B5; 1.

DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.

DR PROSITE; PS02055; CYTOCHROME_B5_2; 1.

KW Electron transport; Mitochondrion; Outer membrane; Transmembrane;

KW Heme; Iron.

FT PROPEP 1 11 BY SIMILARITY.

FT CHAIN 12 146 CYTOCHROME B5 OUTER MITOCHONDRIAL

FT DOMAIN 12 103 HEME-BINDING.

FT TRANSMEM 119 136 POTENTIAL.

FT METAL 55 55 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

FT METAL 79 79 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

SQ SEQUENCE 146 AA; 16332 MW; 2FF7DEA97124E19 CRC64;

Query Match 6.0%; Score 146.5; DB 1; Length 146;

Best Local Similarity 35.4%; Pred. No. 2.8e-05;

Matches 40; Conservative 20; Mismatches 34; Indels 19; Gaps 4;

QY 5 GNOCEGAAREVSVPTFSWEIQLKHLRTDGLVIDRKVYNITKWSIQHPGQGVIGHYA 64

DB 8 GSDGKG-QEVTSTVYKLEEVAKRNSKELMLVHGVRVDVTRFLEHFGGEVLEQA 66

QY 65 GEDATDAFRAFPDLEFVG-----KFLKPLIG-----ELAPEPSQDHGKN 106

DB 67 GVDASEP-----EDVGHSSDAREMLKQYVIGDIHPSDLKPSSGSKDPSON 112

RESULT 21

ID FD6C_SPTOL STANDARD; PRT; 447 AA.

AC P48629;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).

GN FAD6.

OS Spinacia oleracea (Spinach).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.

OX NCBI_TaxID=3582;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 66-78.

RC STRAIN=cv. Subito; TISSUE=Leaf;

RC MEDLINE=95036044; PubMed=7948918;

RA Schmidt H.; Dresselhaus T.; Buck F.; Heinz E.;

RT "Purification and PCR-based cDNA cloning of a plastidial n-6

RT desaturase."

CC Plant Mol. Biol. 26:631-642(1994).

-!- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES

THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.

-!- PATHWAY: Polyunsaturated fatty acid biosynthesis.

-!- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).

-!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/ OR BE INVOLVED IN METAL ION BINDING.

-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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EMBL; X78311; CAA55121.1; -.

PIR; S53309; S53309.

InterPro; IPR005804; FA desat. fam.

Pfam; PF00487; FA desaturase; 1.

ProDom; PD001081; FA desat. fam; 2.

Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane; Transit peptide.

TRANSIT 1 65 CHLOROPLAST.

CHAIN 66 447 OMEGA-6 FATTY ACID DESATURASE.

DOMAIN 171 175 HISTIDINE BOX-1.

DOMAIN 207 211 HISTIDINE BOX-2.

DOMAIN 367 371 HISTIDINE BOX-3.

SEQUENCE 447 AA; 51306 MW; 2BA7C87FF953508 CRC64;

Query Match 6.0%; Score 146; DB 1; Length 447;
Best Local Similarity 20.4%; Pred. No. 0.00011;
Matches 79; Conservative 60; Mismatches 142; Indels 106; Gaps 19;

QY 91 IGEAPEPSQDHGKNSKITEDEFRALRKTAEADNMNLFKTNHVFLLLAHIALESTIA--- 147
DB 97 IGEPLDDVT-----MRDIITSLPKQVPEINDTKAWGTVLISVTSVALGIFMIAKAP 148

QY 148 WFTVFYFGNGHIPILITAFVLATSOAAGWLQHDYGHLSVYRKPKNHLVHKFVIGHLKG 207
DB 149 WY-LPLAWAWGTGTAITFFV-----IGHDCAHKSPK-----NKLVED-IVGLTAP 193

QY 208 ASANW-----WNRHIFQHAKENIPIHKD-----PDVNMHLVFYLG---EWQP 246
DB 194 MPLIYVPEWPKDQHHKTNMLEEDTAWLPIMKEDIESPGLRKALIYAYGPLRTWMS 253

QY 247 IEYGGKKLYLPYNNQHEY-----FPLIGPPLIPMYFOYQIINTMIVHKWV 294
DB 254 IAHMLKVHFNKDFRQSEVKRATISLAAYFAFMVIGWPL-----IYKGTI 299

QY 295 DLAWAVSYVIRFTIYIPFYGILGALLFNIRFLESHWVVMVTQNMHIVMEIDQEAIRD 354
DB 300 -GVW-----IKWL--MPWLG-----HFWMTFTIVHTAHPIPKSKKE 337

QY 355 W--FSSQATCNVQSFNFDFWFSQHLNFAQEHHLFPTMPRNLHKLAPLVKSLCAKHGI 412
DB 338 WNAQAQLSGTVCHDCYPRWIEILCHDISVHIPHTISPKIPSYNLRAN---QSLENWG- 393

QY 413 EYQKEP-----LRLALDLIRSLKSG 434
DB 394 EYLNPKSNWRLMRTIMTTCYIDKDG 420

RESULT 22
ID_3E_TOBAC
ED3E_TOBAC STANDARD; PRT; 379 AA.
AC P48626;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-).

GN Nicotiana tabacum (Common tobacco).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.

OX NCBI_TaxID=4097;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. SRI; TISSUE=Leaf;

RC MEDLINE=95011632; PubMed=7926817;

RA Hamada T., Kodama H., Nishimura M., Iba K.;

RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.";

RL Gene 147:293-294 (1994).

CC -!- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.

CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER PHOSPHOLIPIDS.

CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.

CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum.

CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/ OR BE INVOLVED IN METAL ION BINDING.

CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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EMBL; J26509; BAA05515.1; -.

PIR; J26555; J26555.

InterPro; IPR005804; FA desat. fam.

Pfam; PF00487; FA desaturase; 1.

ProDom; PD001081; FA desat. fam; 2.

Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum; Transmembrane.

FT TRANSMEM 52 72 POTENTIAL.

FT TRANSMEM 213 233 POTENTIAL.

FT TRANSMEM 236 256 POTENTIAL.

FT DOMAIN 97 101 HISTIDINE BOX-1.

FT DOMAIN 133 137 HISTIDINE BOX-2.

FT DOMAIN 300 304 HISTIDINE BOX-3.

SQ SEQUENCE 379 AA; 44149 MW; 87221A21AB0251B2 CRC64;

Query Match 6.0%; Score 145.5; DB 1; Length 379;
Best Local Similarity 21.3%; Pred. No. 0.0001;
Matches 86; Conservative 56; Mismatches 143; Indels 119; Gaps 23;

QY 78 DLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDEFRALRKTAEADNMNLFKTNHVFLLLL 137
DB 19 EREFDPSAPPPFLAEIRNVIP-----KHCWKYKDLRSLSYVVRDV-----IFVAILI 66

QY 138 AHIIALESIAFTVFYFGNGWIPTLITA-FVLATSOAAGWLQHDYGHLSVYRKPKWN-- 194
DB 67 GRAIHLDLSMLFPLYWAIQG---TTFWAIPLVIG-----HDCGHGSPDSQLNNV 113

QY 195 --HLVHKFVIGHLKGASANNWNRHIFQHAKENIPIHKDPPVNMHLVFLVGEWQP----- 246
DB 114 VGHILHSAILVPYHG-----WRISHKTHRQHNQVETDE-----SWVPMPEKLY 157

QY 247 --IEYGGKKLY-LPYNHQHEYFFLIGPPLIPMYF----- 279
DB 158 NKVYSTKFLRYKIPF-----FLIAPMYLMKESPGKSGSHFNPSYDLFQPHR 206

QY 280 QYQIIMTMIVHKWVDLAWAVSYVIRFTIYIPFYGILGA--LLFLNFRFLSHWFWVWV 337
DB 207 KYVVTSTLC---WTWMA-ALLYLCTAFGSLQMFYIGAPYLIFV-----MWLDFV 253

QY 338 TQNMHIVMEIDQEAIR--DW--FSSQATCNVQSFNFDFWFSQHLNFAQEHHLFPTMPR 393


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Db 254 TYLHGEYKPKLPYRGKWSYLRGLT-TVDRDYGLFNN-IHHDIGTHVIHHLFPQIPH 311
QY 394 HNLKIAPIVLKSLCAKHGEYOEK-----PL-LRALLDIIRSLKK 432
Db 312 YHLREATKAAPVLGKY---YREPKSGPIPHLVKDLTSKQ 352

RESULT 23
CYBS_CHICK STANDARD; PRT; 138 AA.
ID P00174;
AC CYB5_CHICK STANDARD; PRT; 138 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Atherinomorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=90314412; PubMed=2369133;
RA Zhang H., Somerville C.;
RT "Soluble and membrane-bound forms of cytochrome b5 are the products
of a single gene in chicken."
RL Arch. Biochem. Biophys. 280:412-415(1990).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=88280278; PubMed=3395128;
RA Zhang H., Somerville C.;
RT "The primary structure of chicken liver cytochrome b5 deduced from
the DNA sequence of a cDNA clone."
RL Arch. Biochem. Biophys. 264:343-347(1988).
RN [3]
RN SEQUENCE OF 14-97.
RP MEDLINE=71134790; PubMed=4993957;
RA Nobrega F.G., Ozols J.;
RT "Amino acid sequences of tryptic peptides of cytochromes b5 from
microsomes of human, monkey, porcine, and chicken liver."
RL J. Biol. Chem. 246:1706-1717(1971).
RN [4]
RN SEQUENCE OF 4-16 AND 89-138.
RP MEDLINE=89323209; PubMed=2752049;
RA Ozols J.;
RT "Structure of cytochrome b5 and its topology in the microsomal
membrane."
RL Biochim. Biophys. Acta 957:121-130(1989).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
OXYGENASES.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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CC -----
CC EMBL; M32293; AAA48740.1; -.
CC DR EMBL; M18539; AAA48733.1; -.
CC DR PIR; A28811; CECH5.
CC DR HSP; P00171; LEHB.
CC DR InterPro; IPR001199; Cyt B5.
CC DR Pfam; PF00173; heme_1; 1_1.
CC DR ProDom; PD000612; Cyt B5; 1.
CC DR PROSITE; PS00151; CYTOCHROME_B5_1; 1.
CC DR PROSITE; PS00255; CYTOCHROME_B5_2; 1.

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KW Electron transport; Transmembrane; Heme; Iron; Microsome.
FT DOMAIN 1 96 HEME-BINDING.
FT DOMAIN 97 138 MEMBRANE-BINDING.
FT METAL 49 73 IRON (HEME AXIAL LIGAND).
FT METAL 73 73 IRON (HEME AXIAL LIGAND).
FT CONFLICT 12 12 W -> E (IN REF. 4).
FT CONFLICT 27 29 NSQ -> ZSB (IN REF. 3).
FT CONFLICT 67 67 N -> D (IN REF. 3).
FT CONFLICT 124 124 A -> T (IN REF. 4).
FT CONFLICT 138 138 E -> EE (IN REF. 4).
SQ SEQUENCE 138 AA; 15545 MW; 168F0B87251557A8 CRC64;

Query Match 5.98; Score 144.5; DB 1; Length 138;
Best Local Similarity 26.2%; Pred. No. 3.8e-05;
Matches 45; Conservative 26; Mismatches 50; Indels 51; Gaps 6;

QY 4 GGNCGEAGAEVSVPTFSWEEIQKHLRTDGLVIDRKVYNTKWSIQHPGQQRVIGHY 63
Db 3 GSSEAGCEAWRG---RYRLLEEVQKHNSSQSTWIVHRIYDITKFLDEHPGGEVLREQ 59
QY 64 AGEDATDAFRAHPDLEFVG-----KFLKPLLIGLAEPEPSQDHGKSKITDFRALR 117
Db 60 AGGDATNF-----EDVGHSTDAALSETFIIGELHP-----DDPKLQ 98
QY 118 KTAEDMNLFTNHFVFFLLAHIALESIAWFTVFYFGNGWIPTLITAFVLA 169
Db 99 KPAE-----TLITTVQSNSSW-----SNWVIPAIAAIVA 129

RESULT 24
FD12 MORIS STANDARD; PRT; 400 AA.
ID AC P59668;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Delta-12 fatty acid desaturase (EC 1.14.99.-).
OS Mortierella isabellina (Umbelopsis isabellina).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
OC Mucorales incertae sedis; Umbelopsis.
OX NCBI_TaxID=91625;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=M6-22;
RA Liu L., Li M., Xing L., Hu G.;
RT "Delta 12 fatty acid desaturase mRNA of Mortierella isabellina."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)
to linoleic acid (delta9, delta12-18:2) (By similarity).
CC -1- PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- DOMAIN: The histidine box domains may contain the active site
and/or be involved in metal ion binding.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF417245; AAU13301.1; -.
CC DR GO; GO:0016431; F:oxidoreductase; IDA.
CC DR GO; GO:0006633; P:fatty acid biosynthesis; IDA.
CC DR InterPro; IPR005804; FA desat fam.
CC DR Pfam; PF00487; FA desaturase; 1.
CC DR ProDom; PD001081; FA desat fam; 1.
CC DR Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.
FT TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
FT TRANSMEM 245 265 POTENTIAL.

```

FT TRANSMEM 277 297 POTENTIAL.
 FT DOMAIN 112 116 HISTIDINE BOX-1.
 FT DOMAIN 148 152 HISTIDINE BOX-2.
 FT DOMAIN 339 343 HISTIDINE BOX-3.
 SQ SEQUENCE 400 AA; 46016 MW; F5512D3F8210DBD2 CRC64;
 Query Match 5.9%; Score 143.5; DB 1; Length 400;
 Best Local Similarity 22.0%; Pred. No. 0.00016;
 Matches 69; Conservative 42; Mismatches 95; Indels 107; Gaps 17;
 Qy 177 W-LQHDYGHLSVVRKPKWNLV-----HKFVGHKLGASANWNRHHRFOHAK 223
 Db 108 WLAHECGHQSFTSKTLNNTVGMILHSMMLVPHYSHSK-----HHKATGHMTK 160
 Qy 224 PNIF-----HKDPDVMNLHVFLGEMOPIEYKKKLY 256
 Db 161 DQVFPKTRQVGLPPKESAAAQVEDMSVHLDEAPITLVF-----WVIOFLGWPAY 216
 Qy 257 LPYN-----HQHEFFLIGPPLIPMYFOYQIIMT-----MIVKKNWVD 295
 Db 217 LIMNASQDYGRWTSHEFTY-----SPIFEPRNF-FDIIISDLGLVLAALGALYASMQLS 270
 Qy 296 LAMAVSYIRFFITYIPFYGILGALLFLNFIREFLSHFWVVTOMNHVMEIDQAYRD- 354
 Db 271 LLTVTKYI-----LPVNF-----WLVLTFLQHTDPKLPH--YREG 308
 Qy 355 -WFSQLTATCNVEQS---PFNDWFSGHLNFQIEHHLFPTMPRHNLHKIAPLVKSLCAKH 410
 Db 309 AW-NFQRGALCTVDRSFGKFLDHFGHIVTHVAHLFSQMPFYHAEATYHLKLLGEY 367
 Qy 411 GIEYQEKPLRAL 423
 Db 368 YV-YDPSPIVAV 379

RESULT 25

FD12 MORAP STANDARD; PRT; 400 AA.
 AC Q918H5, Q96TH3, Q9UVV4, PRT;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE Delta-12 fatty acid desaturase (EC 1.14.99.-).
 OS Mortierella alpina.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
 OC Mortierellaceae; Mortierella.
 OX NCBI_taxid=64516;
 RN [1]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RC STRAIN=IS-4;
 RX MEDLINE=99234062; PubMed=10215899;
 RA Sakuradani E., Kobayashi M., Ashikari T., Shimizu S.;
 RT "Identification of delta12-fatty acid desaturase from arachidonic
 acid-producing Mortierella fungus by heterologous expression in the
 RT yeast Saccharomyces cerevisiae and the fungus Aspergillus oryzae.";
 RL Eur. J. Biochem. 261:812-820(1999).
 RN [2]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RC STRAIN=ATCC 32221;
 RX MEDLINE=99406036; PubMed=10478922;
 RA Huang Y.-S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,
 RA Chan G.M., Kirchner S.J., Mukerji P., Knutzen D.S.;
 RT "Cloning of delta12- and delta6-desaturases from Mortierella alpina
 RT and recombinant production of gamma-linolenic acid in Saccharomyces
 RT cerevisiae.";
 RL Lipids 34:649-659(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 16266;
 RA Liu L., Li M., Xing L., Hu G.;
 RT "Delta 12 fatty acid desaturase gene of Mortierella alpina.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)

to linoleic acid (delta9, delta12-18:2).
 -!- PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- DOMAIN: The histidine box domains may contain the active site
 CC and/or be involved in metal ion binding.
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC
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EMBL; AB020033; BAA81754.1; -
 DR EMBL; AF110509; AAF08684.1; -
 DR EMBL; AF417244; AAL13300.1; -
 DR GO; GO:001649; F:oxidoreductase; IDA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IDA.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.
 FT TRANSMEM 91 111 POTENTIAL.
 FT TRANSMEM 199 219 POTENTIAL.
 FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 277 297 POTENTIAL.
 FT DOMAIN 112 116 HISTIDINE BOX-1.
 FT DOMAIN 148 152 HISTIDINE BOX-2.
 FT DOMAIN 339 343 HISTIDINE BOX-3.
 FT CONFLICT 17 19 STS -> TTT (IN REF. 3).
 FT CONFLICT 21 23 APT -> PN (IN REF. 2).
 FT CONFLICT 95 95 A -> V (IN REF. 2).
 FT CONFLICT 107 107 I -> V (IN REF. 3).
 FT CONFLICT 179 179 N -> S (IN REF. 1).
 FT CONFLICT 180 182 AAA -> VAV (IN REF. 1).
 FT CONFLICT 261 261 A -> T (IN REF. 1).
 FT CONFLICT 280 280 V -> I (IN REF. 3).
 FT CONFLICT 358 358 Y -> H (IN REF. 1).
 FT CONFLICT 392 392 H -> Q (IN REF. 2).
 SQ SEQUENCE 400 AA; 46001 MW; 40B2FCLC1E01F93F CRC64;

Query Match 5.8%; Score 142.5; DB 1; Length 400;
 Best Local Similarity 21.7%; Pred. No. 0.0002;
 Matches 68; Conservative 43; Mismatches 95; Indels 107; Gaps 17;

Qy 177 W-LQHDYGHLSVVRKPKWNLV-----HKFVGHKLGASANWNRHHRFOHAK 223
 Db 108 WLAHECGHQSFTSKTLNNTVGMILHSMMLVPHYSHSK-----HHKATGHMTK 160
 Qy 224 PNIF-----HKDPDVMNLHVFLGEMOPIEYKKKLY 256
 Db 161 DQVFPKTRQVGLPPKESAAAQVEDMSVHLDEAPITLVF-----WVIOFLGWPAY 216
 Qy 257 LPYN-----HQHEFFLIGPPLIPMYFOYQIIMT-----MIVKKNWVD 295
 Db 217 LIMNASQDYGRWTSHEFTY-----SPIFEPRNF-FDIIISDLGLVLAALGALYASMQLS 270
 Qy 296 LAMAVSYIRFFITYIPFYGILGALLFLNFIREFLSHFWVVTOMNHVMEIDQAYRD- 354
 Db 271 LLTVTKYI-----LPVNF-----WLVLTFLQHTDPKLPH--YREG 308
 Qy 355 -WFSQLTATCNVEQS---PFNDWFSGHLNFQIEHHLFPTMPRHNLHKIAPLVKSLCAKH 410
 Db 309 AW-NFQRGALCTVDRSFGKFLDHFGHIVTHVAHLFSQMPFYHAEATYHLKLLGEY 367
 Qy 411 GIEYQEKPLRAL 423
 Db 368 YV-YDPSPIVAV 379

RESULT 26

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CY52 ARATH          STANDARD;          PRT;    134 AA.
ID  CV52_ARATH
AC  Q48875;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Probable cytochrome b5 isoform 2.
GN  AT2G32720 OR F24L7.14.
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eubids II; Brassicales; Brassicaceae; Arabidopsids.
OX  NCBI_TaxID=3702;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=cv. Columbia;
RX  MEDLINE=20083487; PubMed=10617197;
RA  Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA  Fujii C.Y., Mason T.M., Bowman K.A., Lee J.J., Rensing C.M., Koo H.L.,
RA  Buell C.R., Ketchum K.A., Lee J.J., Rensing C.M., Koo H.L.,
RA  Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Unayam L.,
RA  Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA  Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA  Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA  Venter J.C.,
RT  "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT  thaliana."
RL  Nature 402:761-768 (1999).
CC  -!- FUNCTION: Membrane bound hemoprotein which function as an electron
CC  carrier for several microsome bound oxygenases (By similarity).
CC  -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC  CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC  -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC
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CC  or send an email to license@isb-sib.ch).
CC
CC  EMBL; AC003974; AAC04491.1;
DR  PIR; T00796; T00796.
DR  HSSP; P04166; 1B5M.
DR  InterPro; IPR001199; Cyt_B5.
DR  Pfam; PF00173; heme_1; 1.
DR  PRINTS; PR00363; CYTOCHROMEBS.
DR  ProDom; PD000612; Cyt_B5; 1.
DR  PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR  PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW  Electron transport; Transmembrane; Heme; Iron; Microsome;
KW  Multigene family.
FT  TRANSMEM 107 127 POTENTIAL.
FT  METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT  METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ  SEQUENCE 134 AA; 15016 MW; B405F5430F5716C1 CRC64;
Query Match 5.8%; Score 141; DB 1; Length 134;
Best Local Similarity 33.08; Pred. No. 7.2e-05;
Matches 35; Conservative 15; Mismatches 34; Indels 22; Gaps 3;
Qy 21 FSWEEIQKHLRTDSGLVIRKVNITKWSIQHPGQGVTHYAGEDATDAFRAHPDLE 80
Dy 8 FTLSVESEHQNDCHWVINGKYNVTKFLDEHPGDDVLLSSTGDKDADT-----DFE 60
Qy 81 FVG-----KFLKLLIGELAP-----EESQDHGKNSKITE 111
Dy 61 DVGHSESAREMNEQYVGEIDFTTIPKKVYTPPKQPHYNQDKTSE 106
RESULT 27
SCS7_YEAST

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SCS7_YEAST          STANDARD;          PRT;    384 AA.
ID  Q03529;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Inositolphosphorylceramide-B C-26 hydroxylase (EC 1.-.-.-) (IPC-B
DE  hydroxylase).
GN  SCS7 OR FAH1 OR YMR272C OR YMR156.14C.
OS  Saccharomyces cerevisiae (Baker's yeast).
OC  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC  Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX  NCBI_TaxID=4932;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=S288C / AB972;
RX  PubMed=9169872;
RA  Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA  Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA  Jags K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA  Rice P., Skelton J., Walsh S., Whitehead S., Barréll B.G.,
RT  "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT  XIII."
RL  Nature 387:90-93 (1997).
RN  [2]
RP  CHARACTERIZATION.
RX  MEDLINE=98220296; PubMed=9559540;
RA  Dunn T.M., Haak D., Monaghan E., Bealer T.J.;
RT  "Synthesis of monohydroxylated inositolphosphorylceramide (IPC-C) in
RT  Saccharomyces cerevisiae requires SCS7p, a protein with both a
RT  cytochrome b5-like domain and a hydroxylase/desaturase domain."
RL  Yeast 14:311-321 (1998).
RN  [3]
RP  CHARACTERIZATION.
RX  MEDLINE=98019193; PubMed=9353282;
RA  Mitchell A.G., Martin C.E.;
RT  "Fah1p, a Saccharomyces cerevisiae cytochrome b5 fusion protein, and
RT  its Arabidopsis thaliana homolog that lacks the cytochrome b5 domain
RT  both function in the alpha-hydroxylation of sphingolipid-associated
RT  very long chain fatty acids."
RL  J. Biol. Chem. 272:28281-28288 (1997).
CC  -!- FUNCTION: INVOLVED IN THE ALPHA-HYDROXYLATION OF SPHINGOLIPID-
CC  ASSOCIATED VERY LONG CHAIN FATTY ACIDS. HYDROXYLATES THE C26-FATTY
CC  ACID OF INOSITOLPHOSPHORYLCERAMIDE-B (IPC-B) TO FORM IPC-C.
CC  -!- COFACTOR: IRON (BY SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC  -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC  AND/OR BE INVOLVED IN METAL ION BINDING.
CC  -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC
CC  EMBL; Z49260; CAA89255.1;
DR  PIR; S54484; S54484.
DR  HSSP; P04166; 1EUE.
DR  SGD; S0004885; SCS7.
DR  GO; GO:0005783; C:cytoplasmic reticulum; IMP.
DR  GO; GO:0016491; F:oxidoreductase activity; IMP.
DR  InterPro; IPR001199; Cyt_B5.
DR  Pfam; PF04116; FA hydroxylase; 1.
DR  Pfam; PF00173; heme_1; 1.
DR  PRINTS; PR00363; CYTOCHROMEBS.
DR  ProDom; PD000612; Cyt_B5; 1.
DR  PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR  PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW  Oxidoreductase; Fatty acid biosynthesis; Iron; Electron transport;
KW  Transmembrane; Endoplasmic reticulum; Heme.

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FT DOMAIN 1 90 HEME-BINDING.
FT TRANSNM 197 217 POTENTIAL.
FT TRANSNM 223 243 POTENTIAL.
FT TRANSNM 298 318 POTENTIAL.
FT TRANSNM 353 373 POTENTIAL.
FT METAL 45 45 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 70 70 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 384 AA; 44881 MW; DF4BA5P2E0EA2218 CRC64;

Query Match 5.8%; Score 141; DB 1; Length 384;
Best Local Similarity 21.2%; Pred. No. 0.00025;
Matches 88; Conservative 59; Mismatches 139; Indels 130; Gaps 18;

QY 21 FSWEEIQKHLRTDGLVI--DRKYHNTKWSIQHPGQGVIGHYAGEDATDAFR--AFHP 77
DB 12 FSKTVQEHNTANDCWYQNRKLYDVTFLSHFGDSEILDYACKDITEIMKDSVHE 71
QY 78 DLBFVGKFLK-PLILGELAPEE-----PSQDHGKNSKLTEDFPAUKT----- 119
DB 72 HSDSAVEILDEVLGYLATDEEAARLLTNKNHKVEQLSADGTEFDSTTFVKELPAEEK 131
QY 120 ---AEDNMLPKTHVRFLL---LLAHITIALESIAWTFVF-----YFGNGWI 159
DB 132 LSIATDVSNYKXKHFLLDNRPLMLQLLRSDPKDFVDOIHPRHYGKSAPLFGNPLE 191
QY 160 PTLITAFVLATSAQAQGLQHDYGHLSVYRKPKNHLVHKFVIGHLKGASANNWHRHFQ 219
DB 192 PLTKTAWWV---VPVAWLPVAVYHMGVALK-NNNQLFACFLF----- 229
QY 220 HHAEPNIFHKDPDYNMLHVFVLGHWQPIEYKXKL-----KYLPNYH--QHEVFFFLIGPP 272
DB 230 -----CVGVFV---WTLEIGHRLFHFDDWLPENIAFATHFLHGCH 271
QY 273 LLIPMFQYQIIMTVHKWDLAWAVSYIRFFIYIPFYILGALL----- 321
DB 272 HYLEFM-DKRYLVMPPTL-----FVILCAPFYKLVFALLPLYWAYAGFAG 314
QY 322 -FLAFIRPLESHWV-----WYQNHVMEIDQAYR-----DWFSQLTAT 363
DB 315 GLFGVVCYDECHFFLHHSKLPFMRKLUKXHLHHYKNYQLGFGVTSFWFDEVGT 370

RESULT 28
NIA2 ARATH
ID NIA2 ARATH STANDARD; PRT; 917 AA.
AC P1035;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR2).
GN NIA2 OR CHL3 OR AT1G37130 OR F28122.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=89276888; PubMed=3393528;
RA Crawford N.M., Smith M., Bellissimo D., Davis R.W.;
RT "Sequence and nitrate regulation of the Arabidopsis thaliana mRNA
RT encoding nitrate reductase, a metalloflavoprotein with three
RT functional domains."
RL Proc. Natl. Acad. Sci. U.S.A. 85:5006-5010(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
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RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.B., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzalli A.,
RA Milticher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the Plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
RP [3]
RP SEQUENCE OF 522-917 FROM N.A.
RX MEDLINE=89091069; PubMed=2905260;
RA Cheng C., Dewdney J., Nam H., den Boer B.G.W., Goodman H.M.;
RT "A new locus (NIA 1) in Arabidopsis thaliana encoding nitrate
RT reductase."
RL EMBO J. 7:3309-3314(1988).
RP [4]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=93005711; PubMed=1840922;
RA Wilkinson J.Q., Crawford N.M.;
RT "Identification of the Arabidopsis CHL3 gene as the nitrate reductase
RT of Arabidopsis thaliana with mutations in both nitrate reductase
RT structural genes NIA1 and NIA2."
RL Mol. Genet. 239:289-297(1993).
RP [5]
RP HERBICIDE RESISTANCE.
RX MEDLINE=93287999; PubMed=8510658;
RA Wilkinson J.Q., Crawford N.M.;
RT "Identification and characterization of a chlorate-resistant mutant
RT of Arabidopsis thaliana with mutations in both nitrate reductase
RT structural genes NIA1 and NIA2."
RL Mol. Genet. 239:289-297(1993).
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: ROOT, LEAF, AND SHOOT.
CC -!- MISCELLANEOUS: WHEN MUTATED CONFERS RESISTANCE TO THE HERBICIDE
CC CHLORATE.
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J03240; AAA32830.1; -
CC EMBL; AC007505; RAF19225.1; -
CC EMBL; X13435; CAA31787.1;
CC EMBL; S45385; -; NOT_ANNOTATED_CDS.
CC PIR; A31821; RDMUNH.
CC HSSP; P17571; 2CND.
CC InterPro; IPR001199; Cyt B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR000572; Euk_Mb-oxred.
CC InterPro; IPR001709; FPN_Cyt_redctse.
CC InterPro; IPR005066; Mo-co_dimer.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).
```

[2] SEQUENCE FROM N.A.
 RP STRAIN=cn. Columbia; TISSUE=Hypocotyl;
 RC Watahiki M.C., Yamamoto K.T.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 [3] SEQUENCE FROM N.A.
 RP STRAIN=cn. Columbia;
 RC MEDLINE=94345020; PubMed=8066143;
 RX Nishihuchi T., Nishimura M., Aronold V., Iba K.;
 RA "Genomic nucleotide sequence of a gene encoding a microsomal omega-3
 RT fatty acid desaturase from Arabidopsis thaliana";
 RL Plant Physiol. 105:767-768 (1994).
 [4] SEQUENCE FROM N.A.
 RP STRAIN=cn. Columbia;
 RC MEDLINE=20083487; PubMed=10617197;
 RX Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Rensing C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhagen G.P., Preuss D.,
 RA Nickman W.C., White O., Eissen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana";
 RL Nature 402:761-768 (1999).
 [5] SEQUENCE FROM N.A.
 RP STRAIN=cn. Columbia;
 RC STRAIN=cn. Columbia;
 RX Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RA "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGEC)";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MICROSMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CHROMOPHORE B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARELY
 CC DETECTABLE IN ROOT TISSUE.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L22931; AAA61778.1; -;
 DR EMBL; D17579; BAA04505.1; -;
 DR EMBL; D26508; BAA05514.1; -;
 DR EMBL; AC004680; RAC31854.1; -;
 DR EMBL; AY063966; AAL36322.1; -;
 DR EMBL; AY096462; AAM20102.1; -;
 DR FIR; JQ2335; JQ2335.
 DR InterPro; IPR005804; FA desat fam.
 DR Pfam; PF00487; FA desaturase; 1.
 DR ProDom; PD001081; FA desat fam; 2.
 KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 KW Transmembrane
 FT TRANSMEM 63 83 POTENTIAL.
 FT TRANSMEM 220 240 POTENTIAL.
 FT TRANSMEM 242 262 POTENTIAL.
 FT DOMAIN 101 105 HISTIDINE BOX-1.
 FT

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FT DOMAIN      137 141 HISTIDINE BOX-2.
FT DOMAIN      304 308 HISTIDINE BOX-3.
SQ SEQUENCE    386 AA; 44076 MW; 6A7EA2A692B85164 CRC64;

Query Match      5.6%; Score 137.5; DB 1; Length 386;
Best Local Similarity 22.2%; Pred. No. 0.00049;
Matches 88; Conservative 55; Mismatches 131; Indels 123; Gaps 24;

QY 88 PLLIGELAPEBPSQDGHGKSKITDPRALKTAEDMNLKTNHVFLLLAHIIAIESIA 147
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 33 PFKIGDIRAIP : : : : : : : : : : : : : : : : : : : : : : : : : : :
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 148 -----NF--TVVFNGWIPFLTA--FLVATSOAQAGWLQHDYGLSVYRKPKWN-- 194
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 IAAVYDSWFLWLYAAQG--TLFWAFLVLG-----HDGHSFSDIPLNSV 117
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 195 --HLVHKFVIGHLKGSANWNRHFRQHAKPNIFKDPDVMNLVFLVGEVQPIEYK 252
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 VGHILHSFILVPYHG-----WRISHRTH--QNHGHVENDES-----WVPLP--ER 159
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 253 KLKVLPHNHQHEVFFLIGLPELLIPMYEQY-----OIIIMTIVH 290
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 VYKLPSTRLMRYITVPLPMLVPLVLCYRSPKESHPNYSFLAPSERKLIATST- 218
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 KMWVDLAWAVSYIRPFIYIPYIGILGALLFLN-----FIRLESHWFWVVTQNNH 345
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 -----CWSI-----MFVSLIALSFVFGPLAVLKVGVPIIFV--WMLDAVTY 265
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 346 EIDQAYR--DW--FSSQLATCNVQSFENDFSGHLNFQIEHLLFPTMPRHNLK 401
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 266 DEKLPTWRGKESVLRGLT--TIDRDYGIENN--IHDIQHVHILHLLFPQIPHY 318
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 402 LVKSLCAKH--GHEYQEKPLRAL--LDIIRSLKXSGK 435
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 319 VDATKAHVLRGYRREPDKSGAIPHLVESLVASIK 355

RESULT 30
NIA_CUCMA STANDARD; PRT; 918 AA.
AC P17569;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_taxid=3661;
RN [1]
SEQUENCE FROM N.A.
RA Crawford N.M., Campbell W.H., Davis R.;
RP "Nitrate reductase from squash: cDNA cloning and nitrate regulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8073-8076(1986).
RN [2]
SEQUENCE FROM N.A.
RC TISSUE=Seedling;
RX MEDLINE=92084635; PubMed=1748631;
RA Hyde G.E., Crawford N.M., Campbell W.H.;
RT "The sequence of squash NADH:nitrate reductase and its relationship
to the sequences of other flavoprotein oxidoreductases. A family of
flavoprotein pyridine nucleotide cytochrome reductases.";
RL J. Biol. Chem. 266:23542-23547(1991).
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
GROUP IS CALLED CYTOCHROME B-557.
CC -!- SUBUNIT: Homodimer.
CC -!- INDUCTION: By nitrate.
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE

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CC N-TERMINAL DOMAIN
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL; M33154; AAA33114.1; .
CC PIR; A41667; A41667.
CC HSSP; P17571; 2CND.
CC InterPro; IPR001199; Cyt_B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR000572; Euk_MD_oxred.
CC InterPro; IPR001709; FPN_Cyt_reductse.
CC InterPro; IPR005066; Mo-co_dimer.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).
CC Pfam; PF00970; FAD_binding_6; 1.
CC Pfam; PF00173; heme_1; 1.
CC Pfam; PF03404; Mo-co_dimer; 1.
CC Pfam; PF00175; NAD_binding_1; 1.
CC Pfam; PF00174; oxidored_molyb; 1.
CC PRINTS; PR00406; CYTB5SDRTASE.
CC PRINTS; PR00363; CYTOCHROMEBS.
CC PRINTS; PR00407; EUMOPTERIN.
CC PRODOM; PR000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS02555; CYTOCHROME_B5_2; 1.
CC PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
CC Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation.
FT METAL 195 195 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 249 249 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 434 434 INTERCHAIN (POTENTIAL).
FT METAL 578 578 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 601 601 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 918 AA; 103383 MW; A2CAFDDADEAIB2D1 CRC64;

Query Match      5.6%; Score 137.5; DB 1; Length 918;
Best Local Similarity 31.0%; Pred. No. 0.0013;
Matches 39; Conservative 15; Mismatches 47; Indels 25; Gaps 3;

QY 5 GNQGGAAERE-----VSVP-----TFSWEIOKHNLTDGLVIDR 41
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 507 GNQSGWMDRHRHLEISTESNQLTKKSVTFPMNTASNTYTLSEVKHNSPQSAAWIIHG 566
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 42 KYVNIITKSIQHGGORVIGHVAGDATDAFRAHPDLEFVGKFLKPLLIGELAPEPSQ 101
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 567 HYDCTRLKHPGGSDILLNAGTDCTEEDAIHSDK--AKKMLDYRIGELITTVAS 624
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 102 DHGKNS 107
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 625 DSSNS 630

RESULT 31
FD6C_ARATH STANDARD; PRT; 448 AA.
ID FD6C_ARATH
AC P46312; Q9M094;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
GN FADS6 OR FADC OR A14G30950 OR F6118.140.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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136 LIAHIALESTIA 147
||:|:|:
104 LIALIVLPAIA 115

RESULT 33
FD3D ARATH STANDARD; PRT; 435 AA.
P48622;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DE Temperature-sensitive omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
DE PFAD8 OR AT5G05580 OR MOP10.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia; TISSUE=Aerial parts;
RC MEDLINE=95148742; PubMed=7846164;
RX Gibson S., Arondel V., Iba K., Somerville C.R.;
RA "Cloning of a temperature-regulated gene encoding a chloroplast
RT omega-3 desaturase from Arabidopsis thaliana.";
RL Plant Physiol. 106:1615-1621(1994).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia; TISSUE=Hypocotyl;
RC Watanaki M.C., Yamamoto K.T.;
RX Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC MEDLINE=97471969; PubMed=9330910;
RX Sato S., Kotani H., Nakamura Y., Kaneko T., Asanizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RL features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones.";
RL DNA Res. 4:215-230(1997).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERRODOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- INDUCTION: BY LOW TEMPERATURE.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC -----
CC EMBL; L27158; AAA65621.1; -
DR EMBL; U08216; AAB60302.1; -
DR EMBL; D17578; BAA04504.1; -
DR EMBL; AB005241; BAB11547.1; -
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00457; FA_desaturase; 1
DR ProDom; PD001081; FA_desat_fam; 2
DR OxiReductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW TransIt peptide.
KW

RA Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fuster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulo G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.B.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Scapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA Scapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RA "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review".
RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RL -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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CC -----
CC EMBL; AB003840; AAF59233.3; -
CC HSSP; P00171; 1WDB.
CC FlyBase; FBgn0031189; Cyt-B5.
CC InterPro; IPR001199; Cyt B5.
CC Pfam; PF00173; heme_1; 1.
CC PRINTS; PR00363; CYTOCHROME B5.
CC PRODOM; P000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME B5_1; 1.
CC PROSITE; PS0255; CYTOCHROME B5_2; 1.
CC Electron transport; Transmembrane; Heme; Iron; Microsome.
KW Transmem 111 131 POTENTIAL.
FT METAL 41 41 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 65 65 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 134 AA; 15206 MW; 11D1FB03EFAB40DC CRC64;
Query Match 5.5%; Score 133.5; DB 1; Length 134;
Best Local Similarity 36.5%; Pred. No. 0.0003; Indels 13; Gaps 2;
Matches 31; Conservative 14; Mismatches 27;
QY 20 TFSWEIEQKHNRRTDSGLVIDKVNITKWSIQHFGQGVVGHYAGEDATAFRAHPDL 79
DB 8 TTFRAEVAKENTKDTWLLJHNNIVDTAFLEHFGGEVLIEQAGKDATENF----- 60
QY 80 EFVG-----KFLKPLLIIGELAPER 98
DB 61 EDVGHNSNDARDMMKKYKIGELVESE 85
RESULT 36
FD3E PHAAU STANDARD; PRT; 380 AA.
ID _FD3E PHAAU
AC P32291; (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-)
DE (Indole-3-acetic acid induced protein ARG1).
GN ARG1.
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3916;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypocotyl;
RA Yamamoto K.T., Mori H., Inaseki H.;
RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
RL elongating hypocotyls of mung bean (Vigna radiata).";
CC -!- FUNCTION: MICROSMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC -!- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC -----
CC EMBL; D14410; BAA03306.1; -
CC PIR; T10898; T10898.
CC InterPro; IPR005804; FA desat fam.
CC Pfam; PF00487; FA desaturase; 1.
CC PRODOM; P0001681; FA desat fam; 2.
CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 59 78 POTENTIAL.
FT TRANSMEM 208 231 POTENTIAL.
FT TRANSMEM 238 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX-1.
FT DOMAIN 133 137 HISTIDINE BOX-2.
FT DOMAIN 300 304 HISTIDINE BOX-3.
FT SEQUENCE 380 AA; 43996 MW; 1C005117A8DAE16B CRC64;
SQ SEQUENCE 134 AA; 15206 MW; 11D1FB03EFAB40DC CRC64;

CC	EMBL; L29214; AAAS0157.1; -
DR	PIR; T08136; T08136.
DR	InterPro; IPR005804; FA_desat_fam.
DR	Pfam; PF00487; FA_desaturase; 1.
DR	ProDom; PD001081; FA_desat_fam; 2.
DR	Oxidoreductase; Fatty acid Biosynthesis; Chloroplast; Membrane;
KW	Transit peptide.
FT	TRANSIT 1 64 CHLOROPLAST (BY SIMILARITY).
FT	CHAIN 65 443 OMEGA-6 FATTY ACID DESATURASE.
FT	DOMAIN 166 170 HISTIDINE BOX-1.
FT	DOMAIN 202 206 HISTIDINE BOX-2.
FT	DOMAIN 362 366 HISTIDINE BOX-3.
SQ	SEQUENCE 443 AA; 50755 MW; 27544B33AF2781D8 CRC64;
	Query Match 5.4%; Score 131.5; DB 1; Length 443;
	Best Local Similarity 21.5%; Pred. No. 0.0018;
	Matches 70; Conservative 52; Mismatches 131; Indels 73; Gaps 17;
QY	101 QDHGKSKSTEDPRLRKTA---EDNLFK-----TNHVFFLLLA---HIALESIA 147
DB	94 QDLPDNVTLKDINDTLPKEVFEIDDKAWKSVLISVTYSALGFLNTAKAPWYLPL--A 150
QY	148 WFTVFYFGNGWIPTLTATFAVLATSQAQGLQHDYGHLSVYRKPKNHLVKFVIGHLKG 207
DB	151 W-----AWTGAVTGFVV-----IGHCAKSPFK---NKLVED-IVGTlaf 188
QY	208 ASANW----WNHRHFQHHAKPNIFHKDPDVNMMLHVFLGEWOPI---EYKKKLKYLfYN 260
DB	189 LPVLYPEYWRFRKHDRHAKTNMLVHDT-----AWQVPPEEFDFSSPVL----- 232
QY	261 HQHEYFFLIQP--PLL-----IPMYFYQIIMTVIHKNWDLAWAVSYIRFFITYIPF 313
DB	233 -RKAIFGYGPREPWLISAHVNWHENLRKFRSEVNRVKISLACFAFMVGWPLIIYK 291
QY	314 YGILGALLFNFRFLESH-WFWVTQMHIWMVEIQEAEDW--PSSOLTAFCNVQSOF 370
DB	292 VGVLGWVKW-LMPWLGYHFMSTFTTWVHTAPHIFKPADAENAAQAQLNGTVHCDDPS 350
QY	371 FNDWFSGHLNFQIEHHLFFTMRPHNL 396
DB	351 WIELCHDINVHIPHISPRIPSYNL 376
RESULT 38	
NIAL BRANA	STANDARD; PRT; 911 AA.
ID	NIAL BRANA STANDARD; PRT; 911 AA.
AC	P39867;
DT	01-FEB-1995 (Rel. 31, Created)
DT	01-FEB-1995 (Rel. 31, Last sequence update)
DE	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Nitrate reductase [NADH], clone PBNER1405 (EC 1.7.1.1) (NR).
GN	NIAL.
CS	Brassica napus (Rape).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Brassica.
NCBI_Taxid=3708;	
RX	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=cv. Lisandra;
RK	MEDLINE=36222419; PubMed=8685274;
RA	Fukuoka H., Ogawa T., Minami H., Yano H., Ohkawa Y.;
RT	"Developmental stage-specific and nitrate-independent regulation of
RT	nitrate reductase gene expression in rapeseed.";
RL	Plant Physiol. 111:39-47(1996).
CC	-1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC	step of nitrate assimilation in plants, fungi and bacteria.
CC	-1- CATALYTIC ACTIVITY: Nitrite + NAD(+)+ H(2)O = nitrate + NADH.
CC	-1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
CC	-1- AND ONE MOLYBDENUM ATOM.
CC	-1- SUBUNIT: Homodimer (By similarity).
CC	-1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE

CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D38219; BAA07394.1; --
DR PIR: T08105; T08105.
DR HSP: P17571; 4CND.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR001834; Cyt_B5_reductase.
DR InterPro: IPR000572; Euk_Mb_oxred.
DR InterPro: IPR001709; FPN_Cyt_redctase.
DR InterPro: IPR005066; Mo-Co_dimer.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR InterPro: IPR001221; Phe_hydroxylase.
DR Pfam: PF00970; FAD_binding_6; 1.
DR Pfam: PF00173; heme_1; 1.
DR Pfam: PF03404; Mo-co_dimer; 1.
DR Pfam: PF00175; NAD_binding_1; 1.
DR Pfam: PF00174; oxidored_molyb; 1.
DR PRINTS: PR00406; CYTB5REDTASE.
DR PRINTS: PR00363; CYTOCHROMEBS.
DR PRINTS: PR00407; EUMOPTERIN.
DR PRINTS: PR00371; FPNCR.
DR PRINTS: PR00410; PHEHYDRLXASE.
DR ProDom: PD000612; Cyt_B5; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS00255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00559; MOLVEDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family.
FT METAL 191 191 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 245 245 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 430 430 INTERCHAIN (POTENTIAL).
FT METAL 574 574 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 597 597 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 911 AA; 102252 MW; BBA4E19635E03D8C CRC64;
Query Match 5.4%; Score 131.5; DB 1; Length 911;
Best Local Similarity 27.6%; Pred. No. 0.0042;
Matches 42; Conservative 20; Mismatches 61; Indels 29; Gaps 5;
QY 5 GNQGG--AAREV-----SVPT-----PSWEEIOKHLRTDSGLVIDR 41
DB 503 GNSGGWMAKERQIEKSESHPILKSVSTFFWNTASKYMSGEVRKHSABSAWIIHG 562
QY 42 KVNITKWSIQHPGQGVIGHAGEDATDAFRAFPDLEFVGKFLKPLIGELA-----PE 97
DB 563 HIYDCTFLKDHFGGSSILINAGTCTESFEAIHSDK--AKLLEDYRIGELITTYGDS 620
QY 98 EPSQDHGKSKITEDFPAALAKTAEADNLFKTN 129
DB 621 SPNVSVHGGSVMSLLAPIRQLAPTQNLWN 652
RESULT 39
CYSS_TOBAC
ID -CYSS_TOBAC STANDARD; PRT; 135 AA.
AC P49099;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5, seed isoform.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=40997;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Samsun; TISSUE=Seed;
RA MEDLINE=9609039; PubMed=7580860;
RA Napier J.A., Smith M.A., Stobart A.K., Shewry P.R.;
RT "Isolation of a cDNA encoding a cytochrome b5 specifically expressed
RT in developing tobacco seeds.";
RL Planta 197;200:202(1995).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
CC LIPIDS.
CC -1- SUBCELLULAR LOCATION: MICROSMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING SEEDS.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X80008; CAA56318.1; --
DR PIR: S49200; S49200.
DR HSP: P00171; 1CYO.
DR InterPro: IPR001199; Cyt_B5.
DR Pfam: PF00173; heme_1; 1.
DR ProDom: PD000612; Cyt_B5; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS00255; CYTOCHROME_B5_2; 1.
KW Electron transport; transmembrane; Heme; Iron; Microsome;
KW Multigene family.
FT TRANSMEM 107 127 POTENTIAL.
FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 135 AA; 14869 MW; A36CCA081A72ECBC CRC64;
Query Match 5.4%; Score 131; DB 1; Length 135;
Best Local Similarity 35.0%; Pred. No. 0.00049;
Matches 35; Conservative 11; Mismatches 44; Indels 10; Gaps 2;
QY 21 FSWEEIOKHLRTDSGLVIDRKYVNIKWSIQHPGQGVIGHAGEDATDAF----- 72
DB 8 FTAEVSNHNNAKDCWLIISKVYVTKFLEDHPGGVLLSATGKATDDFDIGHSSS 67
QY 73 -RAFPDLEFVGKFLKPLIGELAPEPSQDHGKNSKITE 111
DB 68 ARAM-LDEYVYVDIDSSITPTKVKYTPPKQPHYNQDKTTE 106
RESULT 40
NIA_CICIN
ID NIA_CICIN STANDARD; PRT; 920 AA.
AC P43101;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
OS NIA.
OS Cichorium intybus (Chicory).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Campanulids; Asterales; Asteraceae; Cichorioideae;
OC Cichorieae; Cichorium.

```

OX NCBI_TaxID=13427;
RN [1]_SEQUENCE FROM N.A.
RP STRAIN=cv. Wicloof; TISSUE=Leaf, and Root;
RC MEDLINE=97141273; PubMed=8987617;
RA Palms B., Goupil P., de Almeida Engler J., Van der Straeten D.,
RX Van Montagu M., Rambour S.;
RT "Evidence for the nitrate-dependent spatial regulation of the nitrate
RT reductase gene in chicory roots.";
RL Planta 200;20-27(1996).
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- TISSUE SPECIFICITY: In cortical cells of roots grown at low
CC nitrate concentrations, in vascular tissues of roots at high
CC nitrate concentrations and in root apex under both conditions.
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X84103; CAA58909.1; -.
CC EMBL; X84102; CAA58908.1; -.
CC PIR; S52301; S52301.
CC HSP; P17571; 2CND.
CC InterPro; IPR001199; Cyt_B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR000572; Euk_Mb_Oxred.
CC InterPro; IPR001709; FPN_cyt_reductase.
CC InterPro; IPR005066; Mo-Co_dimer.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).
CC Pfam; PF00970; FAD_binding_6; 1.
CC Pfam; PF00173; heme_1; 1.
CC Pfam; PF03404; Mo-Co_dimer; 1.
CC Pfam; PF00175; NAD_binding_1; 1.
CC Pfam; PF00174; oxidored_molyb; 1.
CC PRINTS; PR00406; CYTB5RDTASE.
CC PRINTS; PR00363; CYTOCHROMEBS.
CC PRINTS; PR00407; EUMOPTERIN.
CC PRINTS; PR00371; FPCR.
CC PRODOM; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS00255; CYTOCHROME_B5_2; 1.
CC PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
CC Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation.
FT METAL 185 185 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 239 239 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 424 424 INTERCHAIN (POTENTIAL)..
FT METAL 569 569 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 592 592 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 920 AA; 103519 MW; FE1E332CC9A4D58 CRC64;

Query Match 5.4%; Score 131; DB 1; Length 920;
Best Local Similarity 29.3%; Pred.No.0.0047;
Matches 41; Conservative 15; Mismatches 48; Indels 36; Gaps 5;

Oy 5 GNQGGGAERE-----VSP-----TFSWEETQKNLRDTSGLVID 40
Db 497 GNQGGGWAREKHLEISSELAHPTLKKSVSPPFWNTSLTFTTSEVKCKNSADSAMIVVH 556
```

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Oy 41 RKYVNTKSIQHGGGQGVIGHYAGEDATDAFRAHPDLEFVGKFKPLLIGEL----- 94
Db 557 GHYDCTSFVKDHPGSDSILLNAGTCTEEDAIHSDK--AKLLEEVYRVGELITMGYS 614
Oy 95 ---APEEPSQD-HGKNSKIT 110
Db 615 SDSAASSPNNNSVHGATNYLT 634
```

Search completed: December 9, 2003, 10:18.08
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: December 9, 2003, 10:16:46 ; Search time 21 Seconds
(without alignments)
2033.281 Million cell updates/sec

Title: US-09-719-601-5
Perfect score: 2438
Sequence: 1 MGKGGNQGGAAREVSVPT.....DIIRSLKSKGLWLDAYLHK 444

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2425	99.5	444	T13155	linoleoyl-CoA desaturase
2	2190	99.8	444	J00180	Delta6 fatty acid
3	453.5	18.6	458	S68358	Delta8 sphingolip
4	431.5	17.7	449	A84900	hypothetical prote
5	426.5	17.5	449	T47950	delta-8 sphingolip
6	422.5	17.3	449	T50555	delta-8 sphingolip
7	371.5	15.2	473	T26280	linoleoyl-CoA desaturase
8	366.5	15.0	447	T43319	Delta5 fatty acid
9	356	14.6	454	H88791	protein fl3f2.1 [i
10	347.5	14.3	523	UC7556	linoleoyl-CoA desaturase
11	277.5	11.4	345	T36617	probable Delta6 fa
12	245.5	8.6	368	S54809	linoleoyl-CoA desaturase
13	210	8.6	359	S35157	Delta6 fatty acid
14	173	7.1	134	CB05	cytochrome b5, mic
15	172	7.1	134	CBPG5	cytochrome b5, mic
16	170	7.0	370	B33034	conserved hypothe
17	169.5	7.0	134	CBRB5	cytochrome b5, mic
18	164	6.7	133	CBH05	cytochrome b5, mic
19	160	6.6	134	CBRT5	cytochrome b5, mic
20	159	6.5	134	CBHU5	cytochrome b5, mic
21	158.5	6.5	98	JK0316	cytochrome b5, ery
22	158	6.5	573	S06600	L-lactate dehydrog
23	157.5	6.5	98	J05783	cytochrome b5, ery
24	156	6.4	427	G70590	probable desA3 pro
25	155.5	6.4	351	S54259	Delta12 fatty acid
26	154.5	6.3	98	CBHU5	cytochrome b5, ery
27	154.5	6.3	359	AQ2005	omega-3 fatty acid
28	153.5	6.3	881	S25445	nitrate reductase
29	150.5	6.2	87	S07959	cytochrome b5, mic

ALIGNMENTS

RESULT 1

T13155
linoleoyl-CoA desaturase (EC 1.14.19.3) [validated] - human
N;Alternate names: Delta6 fatty acid desaturase; protein DKFZp586C201.1
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
C;Accession: T13155; T08765
R;Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
J. Biol. Chem. 274, 471-477, 1999
A;Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase
A;Reference number: Z16471; M01D:99085046; PMID:9967867
A;Accession: T13155
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-444 <CHO>
A;Cross-references: EMBL:AF126799; NID:G4406527; PID:G4406528; PIDN:AAD20018.1
R;Rambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z16471
A;Accession: T08765
A;Molecule type: mRNA
A;Residues: 'RTG', 138-428, 'D', 430, 'M', 432-444 <WAM>
A;Cross-references: EMBL:AL050118
A;Experimental source: adult uterus; clone DKFZp586C201
C;Genetics:
A;Gene: GDB:FADS6
A;Cross-references: GDB:9956652
A;Note: DKFZp586C201.1
C;Superfamily: cytochrome b5 core homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid; heme iron (heme) (axial ligands) #status predicted
F;53,76/Binding site: heme iron (heme) (axial ligands) #status predicted

Query Match 99.5%; Score 2425; DB 2; Length 444;
Best Local Similarity 99.5%; Pred. No. 2.3e-197;
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MGKGGNQGGAAREVSVPTSWERIQXHNLTDSGLVIDRKVNITKWSIQHPGQQRVI	60
DB	1	MGKGGNQGGAAREVSVPTSWERIQXHNLTDSGLVIDRKVNITKWSIQHPGQQRVI	60
QY	61	GHYAGEDATDAFRAHPDLEFVGKFLKPLIGELAPEPSQDHGKNSKITEDFRALRKTA	120
DB	61	GHYAGEDATDAFRAHPDLEFVGKFLKPLIGELAPEPSQDHGKNSKITEDFRALRKTA	120
QY	121	EDMNLKTNHVFELLLAHITALESIANFTVYFGNGHITPLITAFVLATSOAQAGNLQH	180
DB	121	EDMNLKTNHVFELLLAHITALESIANFTVYFGNGHITPLITAFVLATSOAQAGNLQH	180
QY	181	DYGHLSVVRKPKWNHLVHKFVIGHLKGSANWNHRRHQHAKPNIHKDPDNNMLHFV	240
DB	181	DYGHLSVVRKPKWNHLVHKFVIGHLKGSANWNHRRHQHAKPNIHKDPDNNMLHFV	240

241 LGWQPIEYGGKKLKYLPYNHGHVEYFFLIGPPLIPMYFOYQIIMTMVHKWVDLAWAV 300
Db LGWQPIEYGGKKLKYLPYNHGHVEYFFLIGPPLIPMYFOYQIIMTMVHKWVDLAWAV 300
301 SYIRFFIYIPFYGILGALLFLNFRFLESFVWVVTQNMHIVMEIDQAYRDWFSQ 360
Db SYIRFFIYIPFYGILGALLFLNFRFLESFVWVVTQNMHIVMEIDQAYRDWFSQ 360
361 TATCNVQSFNDWFSGHNLFOIEHLLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPL 420
Db TATCNVQSFNDWFSGHNLFOIEHLLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPL 420
421 RALLDIIRSLKSGKMLDAYLHK 444
Db RALLDIIRSLKSGKMLDAYLHK 444

RESULT 2
JG0180
Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C:Accession: JG0180
R:Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.
Biochem. Biophys. Res. Commun. 255, 575-579, 1999
A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid desaturase
A:Reference number: JG0180; MUID:99160394; PMID:10049752
A:Accession: JG0180
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-444 <AKI>
A:Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BAA75496.1; PID:g4514722
C:Superfamily: cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthesis
F:16-94/Domain: cytochrome b5 core homology <CB5>
F:53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 89.8%; Score 2190; DB 2; Length 444;
Best Local Similarity 87.8%; Pred. No. 1.8e-177;
Matches 390; Conservative 26; Mismatches 177; Indels 0; Gaps 0;

QY 1 MGKGGNGEAGAAEVSVPFSEIEQKNLRTDGLVIDRKYNITKWSIQHPGQORVI 60
Db 1 MGKGGNGEAGSTLQAPMPTFRNEEQKNLRTDRLVIDRKYNITKWSIQHPGHRVI 60
61 GHYAGEDATDAFRAHPDLFVGKFLKPLIGELAPEEPSQDHGKNSKITEDFRALKTA 120
Db 61 GHYSGEDATDAFRAHLDLDFVGKFLKPLIGELAPEEPSLDRGKSSQITEDFRALKTA 120
121 EDWNLFTNNHVFLLIAHIALESIAWFTVYFGNGWPTLTITAFVLATSOAQAGWLQ 180
Db 121 EDWNLFTNNHVFLLSHIIVNESIAWFTILSVFGNGWPTLTITAFVLATSOAQAGWLQ 180
181 DYGHLSVYRKPKNNHLVHKFVIGHLKGASANNWNRHFFQHAKPNIFHKDPPVNMMLHVF 240
Db 181 DYGHLSVYKKSINWNIHVKFVIGHLKGASANNWNRHFFQHAKPNIFHKDPPDKSLHVF 240
241 LGWQPIEYGGKKLKYLPYNHGHVEYFFLIGPPLIPMYFOYQIIMTMVHKWVDLAWAV 300
Db LGWQPIEYGGKKLKYLPYNHGHVEYFFLIGPPLIPMYFOYQIIMTMVHKWVDLAWAV 300
301 SYIRFFIYIPFYGILGALLFLNFRFLESFVWVVTQNMHIVMEIDQAYRDWFSQ 360
Db 301 SYARFFVYIPFYGILGALLFLNFRFLESFVWVVTQNMHIVMEIDLDHYRDWFSQ 360
361 TATCNVQSFNDWFSGHNLFOIEHLLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPL 420
Db 361 AATCNVQSFNDWFSGHNLFOIEHLLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPL 420
421 RALLDIIRSLKSGKMLDAYLHK 444
Db 421 RALLDIIVSLKSGKMLDAYLHK 444

RESULT 3

S68358
Delta8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - common sunflower
C:Species: Helianthus annuus (common sunflower)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C:Accession: S68358
R:Sperling, P.; Schmidt, H.; Heinz, E.
Eur. J. Biochem. 232, 798-805, 1995
A:Title: A cytochrome-b(5)-containing fusion protein similar to plant acyl lipid desaturase
A:Reference number: S68358; MUID:96028121; PMID:7588718
A:Accession: S68358
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-458 <SPE>
A:Cross-references: EMBL:X87143; NID:G1040728; PIDN:CAA60621.1; PID:GI040729
C:Superfamily: cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein; oxidoreductase
F:16-90/Domain: cytochrome b5 core homology <CB5>
F:51,74/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 18.6%; Score 453.5; DB 2; Length 458;
Best Local Similarity 27.7%; Pred. No. 1.6e-30;
Matches 124; Conservative 68; Mismatches 179; Indels 77; Gaps 12;

QY 24 EEIQKHLRTDGLVIDRKYNITKWSIQHPGQORVIGHYAGEDATDAFRAHP----- 77
Db 22 KELKKNPNNDLWISILGKYNVTEWAKEHPGGDAPLINLAGQDVTDAFIAHPGTAWKH 81
QY 78 -DLEFVGKFLKPLIGELAPEEPSQDHGKNSKITEDFRALKTAEDNMLFKTNHVFLL 136
Db 82 LDKLFTGYHLKDYQV-----SDISRYRKLASEFAKAGFEKKGHGVYS 126
137 LAHTIALESIAWFTVYFGNGWPTLTITAFVLATSOAQAGWLQDVGHLISVYRKPKNNHL 196
Db 127 LCFVSLLSACVYGVLYSGSFWI-HMLSGAILLAWMQIAYLGDHAGHYQMATRGWKNF 185
QY 197 VHKFVIGHLKGASANNWNRHFFQHAKPNIFHKDPPVNMMLHVF-----VLGEWQPIEY 251
Db 186 AGIFGNCITGISTAWKWTNNAHNAACNSLDYDPLQHLPLMLAVSKLFSNITSVFG- 244
252 KKLKYL-----YNH0HEYFFLIGPPLIPMYFOYQIIMTMVHKWVDLAWAVSYIRF 306
Db 245 RQLFDFELARFFVSQYQYLYVPMCVARNLYL--QTILLISKRK----- 288
QY 307 FITVIFPYG--IICALLFLNFIREFSHWFW-----VTQNMHIVMEIDQ--- 349
Db 289 ----IPDRGNILGTLITWTFPLLSRLNPNWPERVAVLVSCVTGIIQIQTILNHFSG 344
350 EAY-----RDWFSQSLTATCNVQSFNDWFSGHNLFOIEHLLFPTMPRHNLKIAPLV 403
Db 345 DVYVGPCKGDNWFEKQTRGTIDTACSSMDWDFGGQLQFLEHLLFPLRPLRCHLSRISPIC 404
QY 404 KSLCAKHGIEYQEKPLRALLDIIRSLK 431
Db 405 RELCKKNLPYVSLVSFDYDANVTTLKTLR 432

RESULT 4

A84900
Hypothetical protein At2g46210 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: A84900
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I.;
eius, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84900
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-449 <STO>
A:Cross-references: GB:AE002093; NID:G3702328; PIDN:AA62885.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g46210
A:Map position: 2

Query Match 17.7%; Score 431.5; DB 2; Length 449;
Best Local Similarity 28.0%; Pred. No. 1.1e-28;
Matches 124; Conservative 72; Mismatches 184; Indels 63; Gaps 15;

QY 24 BEIQKHNLRDGLVIDRKVNITKWSIOHPGQGVVGHYAGEDATDAFRPHPLDFVVG 83
DB 13 EDLKGNKPGDLWISIOGVYDVSWVAKSHPGGEAAILNLAQDQVDTDAFIAYHFGTAW-- 70
QY 84 KFLKPLLIGELAPEEPPSOHQGNKSKITDFRALRKTAEDMNLK-KTNHVFVFLLLAHIA 142
DB 71 HHLEKLNHYGV-----RDH-HVSDVSDYRRLAAEFKRGGLFDKKGHTVLTTCVGVM 124
QY 143 LESIAWTFVYFGNGWITPLITAFVLATSOAQAGLQHDYGHLSYRKPKNHLVHKFVI 202
DB 125 LAANL-YGVLACTSIW-AHLISAVLLGLLWISAVVGHDSGHYTVTSTKPCNKLIIQLSG 182
QY 203 GHLKASANNWNRHFQHKAKENIFHKDPDVNMLHVFVL-----GEWQPIEYKGLKYL 257
DB 183 NCLTGISTAWKWTNAHIAACNSLDHDPDQHIPIFAVSTKFFNSMTSRFYG-RKLTFD 241
QY 258 P-----YNHOHEYFFLIGPPLIPMYFOYQIIM-----TMIVHKNWVDL-- 296
DB 242 PLARELISYQHWTFYVNCVGRINLFITQELLFSKRVHVPDRALNIAGILVFWTFPLV 301
QY 297 AWAVSYIRFFITYIPFYGILGALLFLNFIPLFLESHFWVWQMNHIVMEIDQAY----- 352
DB 302 SFLPNQERFIPVFSF-----AVTAIOHQVFC-----LNHFAADV-----YTGPP 342
QY 353 --RDWFSSQLTACNVESFFNDFSGHLNFOIEHLEFPTPRNHLKIAPLVSKLAKH 410
DB 343 NGNDWFEXQTAGTLDISCRSFMDFGGLQFQLEHHLFPLRCHLRTVSPVVKELCKH 402
QY 411 GHEYQEKPLLRALLDIIRSLKX 433
DB 403 NLPYRSLGWNEANVTIRTKNA 425

RESULT 5
T47950
delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana
N:Alternate names: protein F2A19.180
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T47950; T51848
R:De Haan, M.; Maatse, A.C.; Grivelli, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.P.X.; Quer
submitted to the Protein Sequence Database, January 2000
A:Reference number: 224480
A:Accession: T47950
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <DEH>
A:Cross-references: EMBL:AL132962; PIDN:CAE71088.1
A:Experimental source: cultivar Columbia; BAC clone F2A19
R:Spelling, P.; Zaehring, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A:Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome
A:Reference number: 222986; MUID:99003197; PMID:9786850
A:Accession: T51848
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-449 <SPE>
A:Cross-references: EMBL:AJ224161; PIDN:CAA11858.1
A:Experimental source: cultivar Columbia; mainly green parts, some flowers, few roots
C:Genetics:
A:Gene: slid
A:Map position: 3

A>Note: F2A19.180
C:Function:
A:Description: (EC 1.14.99.-); delta-8 sphingolipid desaturase [validated, MUID:9900319
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 17.5%; Score 426.5; DB 2; Length 449;
Best Local Similarity 25.8%; Pred. No. 3e-28;
Matches 118; Conservative 70; Mismatches 174; Indels 95; Gaps 14;

QY 24 BEIQKHNLRDGLVIDRKVNITKWSIOHPGQGVVGHYAGEDATDAFRPHPLDFVVG 77
DB 13 EDLKGNKPGDLWISIOGVYDVSWVAKSHPGGEAAILNLAQDQVDTDAFIAYHFGTAWH 72
QY 78 -DLFEVGFELKPLLIGELAPEEPPSOHQGNKSKITDFRALRKTAEDMNLKFT-NHV----- 131
DB 73 LDHLFTGYHIDPQV-----SEVSRDYRERMAAEFRKGLGFENKGHVTLTY 117
QY 132 -----FFLLLAHIIALESIAWTFVYFGNGWITPLITAFVLATSOAQAGLQHDYGH 185
DB 118 LAFVAAMFGLVGLVLACTSV-----FAHQIAAALLGLLWISAVIGHDSGHY 165
QY 186 SVYRKPKNHLVHKFVIGHLKASANNWNRHFQHKAKENIFHKDPDVNMLHVFVLG--- 242
DB 166 VINSKSYNRFALGSLGNCITGISIAWKTENAHILACNSLDYDPLQHIPFAVSTKF 225
QY 243 -EQPIEYKGLKYL-----YNHOHEYFFLIGPPL-----IPMYFOYQIIM----- 285
DB 226 FSSLTSRFYDRKLTDFVARFLVSYQHFTY-----PVMCFGRINLFITQELLFSKREVP 281
QY 286 -----TMIVHKNWVDL--AWAVSYIRFFITYIPFYGILGALLFLNFIPLFLESHFWV 336
DB 282 DRALNAGILVFWTFPLVSVCLPNWPERFFVFTSF-----TVTALQHIQF----- 328
QY 337 VTQMNHIVME-IDQAYRDWFSQTLATCNVEQSFNDFSGHLNFOIEHLEFPTPRNHL 394
DB 329 --TLNFAADVYVGPPTGSDWFEKQAGTIDISCRSFMDFGGLQFQLEHHLFPLRPRC 386
QY 395 NLHKIAPLVKSLCAKHGIEVQEKPLLRALLDIIRSLK 431
DB 387 HLKRVSVQELCKKKNLPIRSMVSEANVLINTLK 423

RESULT 6
T50555
delta-8 sphingolipid desaturase [imported] - rape
C:Species: Brassica napus (rape)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Sep-2000
C:Accession: T50555
R:Spelling, P.; Zaehring, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A:Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome
A:Reference number: 222986; MUID:99003197; PMID:9786850
A:Accession: T50555
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-449 <SPE>
A:Cross-references: EMBL:AJ224160; PIDN:CAA11857.1
A:Experimental source: cultivar Drakkar
C:Genetics:
A:Gene: slid

Query Match 17.3%; Score 422.5; DB 2; Length 449;
Best Local Similarity 28.2%; Pred. No. 6.6e-28;
Matches 125; Conservative 73; Mismatches 182; Indels 63; Gaps 15;

QY 24 BEIQKHNLRDGLVIDRKVNITKWSIOHPGQGVVGHYAGEDATDAFRPHPLDFVVG 83
DB 13 DLKKNQPCDLWISIOGVYDVSWVAKSHPGGEAAILNLAQDQVDTDAFIAYHFGTAW-- 70
QY 84 KFLKPLLIGELAPEEPPSOHQGNKSKITDFRALRKTAEDMNLK-KTNHVFVFLLLAHIA 142
DB 71 RHLENLHNGYHV-----KDH-HVSDVSDYRRLAAEFKRGGLFDKKGHV-TLYTLTCVAA 123

Db 254 HVHTWMLPFLRLSWLQSIIFVSQMPHTHYDYRNTAIVEQVGLSLHAWLSGLQLYFLP 313
QY 306 FFITYIPFY---GILGALLFLAFIRELSHFWFWVQTMHIVME---IDQAYRWDFSSQ 359
Db 314 DWSTRIMFLVSLVGG-----FLLSH---VTFNHYSEKFAUSSNMTMSYACLIQ 361
QY 360 LTATCNVEQSFNDWFSGHNFQIEHLLPPTPRHNLHKLAPLVKSLCAKHGIEY 414
Db 362 IMTRNRWPGRFIDMLWGLNGLYQIEHLLPPTPRHNLHKLAPLVKFAAANGLPY 416

RESULT 9
H88791
A:Title: T13F2.1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: H88791
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A:Reference number: A75000; PMID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999
A:Accession: H88791
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <STO>
A:Cross-references: GB:chr_IV; PIDN:CAB03352.1; PID:G379828; GSPDB:GN00022; CBSP:T13F2.
C:Genetics:
A:Map position: 4
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase

Query Match 14.6%; Score 356; DB 2; Length 454;
Best Local Similarity 26.3%; Pred. No. 2.8e-22;
Matches 111; Conservative 67; Mismatches 156; Indels 88; Gaps 16;

QY 53 HPGQGVGHYAGEDATDAFRAPDLEFVGKFLKLLIGELAPEPSOD-----102
Db 30 HPGGS-AITTKNDATTVFHTGSKRAYOWLT-----ELKSCPTQEPIDIKDDP 83
QY 103 -----HGKSKITDPRLRKTAEADNFKTNHVFLLLAHIALESIA 147
Db 84 IKGIDVNMGTFNISEKSAQINKSPTDLRMVRAEGLMDGSPFVIRKI-----LETI- 137
QY 148 WFTV---FY---FNGHWPILITAFVLTSAQAQWLOHDYGHLSVYRKPKWHLVHKFY- 201
Db 138 -FTILFAFYQVHTYLP---SAILMGVAQQLGLHIEFAHQFQKNRYNDLASFYVG 193
QY 202 ---IGHL--KGASANNHRRHFOHAKPNI FHKDPDVMNLHV FVLGEWQPIEYKXKLLK 255
Db 194 NFIQVSHIFNNGPSSGKWEQHNHVAATNVVGRDGLDLPFYATVAEHLNYSQDSWV 253
QY 256 YLPYNQHEYFFLIGPLIIPMYQIIM-----TWLVHKNWVDLAWVS- 301
Db 254 MTLFRQWVHTMPLPFLRLSWLQSIIFVSQMPHTHYDYRNTAIVEQVGLSLHAWLSL 313
QY 302 ---YIRFFITYIPFY---GILGALLFLAFIRELSHFWFWVQTMHIVME---IDQAY 352
Db 314 GQLYFPDSTRIMFLVSLVGG-----FLLSH---VTFNHYSEKFAUSSNMTMSYACLIQ 361
QY 353 RWFSSQLTATCNVEQSFNDWFSGHNFQIEHLLPPTPRHNLHKLAPLVKSLCAKHGIEY 412
Db 362 SNYACLIQIMTRNRWPGRFIDMLWGLNGLYQIEHLLPPTPRHNLHKLAPLVKFAAANGLPY 416
QY 413 EY 414
Db 422 PY 423

RESULT 10
JC7556

linoleoyl-CoA desaturase (EC 1.14.19.3) - Mucor rouxii
N:Alternate names: delta6-desaturase
C:Species: Mucor rouxii
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Jun-2002
C:Accession: JC7556
R:Lacteng, K.; Manontarat, R.; Tanticharoen, M.; Cheevadhanarak, S.
Biochem. Biophys. Res. Commun. 279, 17-22, 2000
A:Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desaturase
A:Reference number: JC7556; MUID: 20563795; PMID:11112411
A:Accession: JC7556
A:Molecule type: DNA
A:Residues: 1-523 <JAO>
A:Cross-references: GB:AF290983
A:Experimental source: strain ATCC 24905
C:Comment: This enzyme, a membrane-bound key enzyme, is responsible for the transformation of linoleic acid to gamma-linolenic acid.
C:Keywords: oxidoreductase; transformation

Query Match 14.3%; Score 347.5; DB 2; Length 523;
Best Local Similarity 23.4%; Pred. No. 1.8e-21;
Matches 112; Conservative 76; Mismatches 178; Indels 113; Gaps 17;

QY 24 BEIQKHLRTDGLVIDRKYVNTKWSIQHPGGQGVGHYAGEDATDAFRAPDLEFVG 83
Db 25 EKFDLKLQGDVFIYEQKYRVNNFMFKHPGGEALRSALGRDVTDEIRTMHP- QVYE 83
QY 84 KFLKPLLIGELAPE-----EPSQD-----HGK 105
Db 84 KLINLYCIGDYMFDVIRPASMKQOHTFKPKEDKPVLTATWEGFTVQAYDDAIQDLHKH 143
QY 106 NS-----KITEFRLRKTAEADNFKTNH-----VFLLLL 137
Db 144 HSHDLIKDAVLQKDLNGDQIRNAYKLEALYKGLFKCNKYKAREGCRYTLLIFLSL- 202
QY 138 AHIALESIAWFTV-----FYFNGHWPILITAFVLTSAQAQWLOHDYGHLSVYRKPK 192
Db 203 -----WFLTKGTETWYVAG-----AAFMAFWHQVLTFAHADAGHNEITKSE 245
QY 193 WNLHVKFVIGHLKGASANNHRRHFOHAKPNI FHKDPDVMNLHV---FVLGEWQPIEY 249
Db 246 IDHVGIVIANFGLGLGSLGWKNHVNHHVTHNPEHDPDIO--HVFFMAITTKFFNNIY 303
QY 250 GKXKLYLPYN-----HQEYFFLI---GPPILIPMYQIIMTMIHKNWVDLAW 298
Db 304 STYKRVLPDPAASRPFVRHQVLYLILSFGFNLHRLSFAY-LTCKNVRTTLELVG 362
QY 299 AVSYIIF--FITVPIFYGILGALLFLNFRFLESFWFWVQTMHIVMEIDQAYEDWF 356
Db 363 ITFFVWFGSLSTLPTNIRIATVWSYMLTTPPLH--VOIT-LSHFGMSTEDRGDPDP 419
QY 357 -SSQLTATCNVEQSFNDWFSGHNFQIEHLLPPTPRHNLHKLAPLVKSLCAKHGIEY 414
Db 420 PAKMLRTMDVDCPEWHDWFHGGIYQAVHHLFRLPRLHRLRQCVPVLKFCDEVLHY 478

RESULT 11
T36617
A:Title: Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C:Accession: T36617
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A:Reference number: Z21610
A:Accession: T36617
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-345 <OLI>
A:Cross-references: EMBL:AL078610; PIDN:CAB44385.1; GSPDB:GN00070; SCOEDB:SCH35.42c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB: SCH35.42c
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 11.4%; Score 277.5; DB 2; Length 345;
Best Local Similarity 27.4%; Pred. No. 8.9e-16;
Matches 95; Conservative 39; Mismatches 162; Indels 51; Gaps 11;

QY 112 DFRALRKTADNMFLKTNHVFLLAHIALESIAWFTVFGNGWIFTLITAFVATS 171
DB 16 DFRALRKTADNMFLKTNHVFLLAHIALESIAWFTVFGNGWIFTLITAFVATS 171

QY 172 QAQAGMLQHDYGHLSVYRKPMNHLVHKFVIGHLKGSANWNHRRFQHHAKPNIFHKDP 231
DB 75 YGOVALVAHDMHROVFRRRRSELSGR-IGASIGSWGVMQDKTRHHAENTEDLDP 133

QY 232 DVNM-LHVF-----VLGEWQPIEYKGLKYLPHNQHIEYFFELGPPILLPM 277
DB 134 DIGPDLVWSPDQARAATGPRLLGRWQAF-----LFF-----PLTUE 172

QY 278 YFQVQI-----INTMIVKHNVQD-----LAWAVYIRFFITYIPFYGILGALLFNFI 328
DB 173 GFNLHVASGRAMNRRLKRALDQALLAHCAVYLTALFWLPP--GM--AIAFLAVHQC 228

QY 329 LESHWFVWVQMNHVMEI-DOEAYRDMFSSQLTATCNVEQSPFNDFWFGHLNFQIEHL 387
DB 229 LFGYLGSAFAPNKHGKMPILTADDPDLRQVLTSRNVNGGLFTDLALGGLNHQIEHL 288

QY 388 FPTWERNLHKIAPLVKSLCAKGEYQEKPLRALLDIIRSLKKG 434
DB 289 FPNPSPNLKARAIVRYCDLGDVDAETGLVASYELATSLHDAG 335

RESULT 12
S54809
linoleoyl-CoA desaturase (EC 1.14.19.3) - *Spirulina platensis*
N:Alternate names: Delta δ -desaturase
C:Species: *Spirulina platensis*
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 03-Jun-2002
C:Accession: S54809
R:Tasaka, Y.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54809
A:Accession: S54809
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 <IAS>
A:Cross-references: EMBL:X87094; NID:g9809109; PIDN:CAA60573.1; PID:g9809110
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.8%; Score 215.5; DB 2; Length 368;
Best Local Similarity 23.9%; Pred. No. 1.7e-10;
Matches 87; Conservative 57; Mismatches 129; Indels 91; Gaps 19;

QY 107 SKIT-----BDFRALRKTADNMFLKTNHVFLLAHIALESIAW-FTVYFGN 156
DB 6 SKVTFGKSIGPRKELNRVNAYLEAENISPRDNPMLKTAAILAWVVSAMTFVFGPDV 65

QY 157 GWIPTLITAFVATSQAQAGW-LOHDYGHLSVYRKPMNHLVHKFVIGHLKGSAN 211
DB 66 LWM-KLCCIVLGVSVAIGNISHDGNH-CGYKYQWVYLSGLTHDAI-----GVSSY 118

QY 212 WNNHRR-FQHHAKPNIFHKDPDVMNLHVFVLGEWQPIEYKGLKYL-----YNHQH 263
DB 119 LWKFRHNVLLHNTYTNILGHVDEI-----HGDELVRMSPSMEYRWYHYQH 163

QY 264 EYFFLIGPPLIPYFQYQIIMTWIVHK-----NWVDLAW-----AVSYI 304
DB 164 WFIWVYF--FIPYFWSLADVTQMLFRKQYHDHIEPSTWVDIATLAFKAFGVAVFLLI 221

QY 305 RFFITYIPFYGILGA-LLEFLNFIRESHNFV--WVTQMNHIV-----MEIDQEA 351
DB 222 PIAVGYSPLAIVAGISIVM-----THGLVACVWFMLAHVIERPABFLDPDNLHIDDE- 273

QY 352 YRDWFSQLTATCN-VEQSPFNDFWFGHLNFQIEHLFPTWERNLHKIAPLVKSLCAK 410
DB 274 ---WAIQVKTVDVFPANNPINWYVGLNGYQTVHLLFFPHICHYHPKRIAPILAEVCEE 330

QY 411 GIEY 414
DB 331 GVN 334

RESULT 13

S35157

Deltas fatty acid desaturase (EC 1.14.99.-) [imported] - *Synechocystis* sp.
C:Species: *Synechocystis* sp.

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000

C:Accession: S35157; S76243

R:Reddy, A.S.; Nucio, M.L.; Gross, L.M.; Thomas, T.L.

Plant Mol. Biol. 22, 293-300, 1993

A:Title: Isolation of a Delta δ (6)-desaturase gene from the cyanobacterium *Synechocystis*

A:Reference number: S35157; MUID:93283633; PMID:8389613

A:Accession: S35157

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-359 <RED>

A:Cross-references: GB:I11421; NID:G349562; PIDN:AAA27286.1; PID:G349563

R:Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasu

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

S.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76243

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-359 <KAN>

A:Cross-references: EMBL:D90914; GB:AB001339; NID:G1653477; PIDN:BA18502.1; PID:d10191

A:Experimental source: PCC 6803

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.6%; Score 210; DB 2; Length 359;

Best Local Similarity 23.5%; Pred. No. 4.8e-10;

Matches 85; Conservative 53; Mismatches 135; Indels 88; Gaps 18;

RESULT 14

CB05

cytochrome b5, microsomal form [validated] - bovine

N:Contains: cytochrome b5, erythrocyte form

C:Species: Bos primigenius taurus (cattle)
C>Date: 12-Aug-1981 #sequence revision 05-May-1995 #text change 15-Sep-2000
A:Accession: A47215; S03428; F24211; A90383; A92053; B93774; A92231; A00170
R:Cristiano, R.J.; Giordano, S.J.; Steggle, A.W.
Genomics 17, 348-354, 1993
A>Title: The isolation and characterization of the bovine cytochrome b5 gene, and a transcribed alternative form of the bovine cytochrome b5 gene.
A:Reference number: A47215; MUID:94010928; PMID:8406485
A:Accession: A47215
A:Molecule type: DNA
A:Residues: 1-134 <CR1>
A:Cross-references: GB:M63226; GB:M63227; GB:M63228; GB:M63329; GB:L22966; NID:G987590
A>Note: Sequence extracted from NCBI backbone and corrected to correspond with the published sequence.
A>Note: The authors conclude that the erythrocyte form is generated by posttranslational modification.
R:Cristiano, R.J.; Steggle, A.W.
Nucleic Acids Res. 17, 799, 1989
A>Title: The complete nucleotide sequence of bovine liver cytochrome b(5) mRNA.
A:Reference number: S03428; MUID:89128451; PMID:2915932
A:Accession: S03428
A:Molecule type: mRNA
A:Residues: 1-134 <CR2>
A:Cross-references: EMBL:X13617; NID:G297; PIDN:CAA1949.1; PID:G298
R:Abe, K.; Kimura, S.; Kizawa, R.; Anan, P.K.; Sugita, Y.
J. Biochem. 97, 1659-1668, 1985
A>Title: Amino acid sequences of cytochrome b5 from human, porcine, and bovine erythrocytes.
A:Reference number: A91992; MUID:85289161; PMID:4030743
A:Accession: F24211
A:Molecule type: protein
A:Residues: 2, '2', '4-98 <ABE>
A:Experimental source: erythrocyte
A>Note: residues 2-3 were positioned by homology with the bovine liver sequence R:Ozols, J.
Biochim. Biophys. Acta 997, 121-130, 1989
A>Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.
A:Reference number: S04976; MUID:89323209; PMID:2752049
A:Accession: S07963
A:Molecule type: protein
A:Residues: 2-61; 15-18 <OZ01>
R:Ozols, J.
Biochemistry 13, 426-434, 1974
A>Title: Cytochrome beta-5 from microsomal membranes of equine, bovine, and porcine liver.
A:Reference number: A90383; MUID:74080219; PMID:4810060
A:Accession: A90383
A:Molecule type: protein
A:Residues: 'ZB', '2', 'ZZ', '5-11', '131-133', 'D', 'OZ02' <OZ02>
R:Ozols, J.; Strittmatter, P.
J. Biol. Chem. 244, 6617-6618, 1969
A>Title: Correction of the amino acid sequence of calf liver microsomal cytochrome b5.
A:Reference number: A92053; MUID:70067001; PMID:5391285
A:Accession: A92053
A:Molecule type: protein
A:Residues: 6-15, 'QBI', '19-61', 'D', '63-97 <OZ03>
A:Experimental source: liver
R:Tsugita, A.; Kobayashi, M.; Tani, S.; Kyo, S.; Rashid, M.A.; Yoshida, Y.; Kajihara, T.
Proc. Natl. Acad. Sci. U.S.A. 67, 442-447, 1970
A>Title: Comparative study of the primary structures of cytochrome b-5 from four species.
A:Reference number: A93774; MUID:70289989; PMID:5272324
A:Accession: B93774
A:Molecule type: protein
A:Residues: 6-17, 'E', '13-61', 'D', '63-96 <TSU>
R:Fleming, P.J.; Dailey, H.A.; Corcoran, D.; Strittmatter, P.
J. Biol. Chem. 253, 5369-5372, 1978
A>Title: The primary structure of the nonpolar segment of bovine cytochrome b5.
A:Reference number: A92231; MUID:78218214; PMID:670203
A:Accession: A92231
A:Molecule type: protein
A:Residues: 32-134 <FLR>
R:Muskett, F.W.; Kelly, G.P.; Whitford, D.
submitted to the Brookhaven Protein Data Bank, February 1996
A:Reference number: A66921; PDB:1WDB
A:Contents: annotation; conformation by (1)H-, (15)N-NMR, residues 6-89
R:Muskett, F.W.; Kelly, G.P.; Whitford, D.
J. Mol. Biol. 258, 172-189, 1996
A>Title: The solution structure of bovine ferricytochrome b5 determined using heteronuclear

A:Reference number: A58628; MUID:96200988; PMID:8613986
A:Contents: annotation; conformation by (1)H-, (15)N-NMR
R:Durley, R.C.E.; Mathews, F.S.
submitted to the Brookhaven Protein Data Bank, August 1994
A:Reference number: A52769; PDB:1CYO
A:Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 6-93
R:Mathews, F.S.; Durley, R.C.E.
submitted to the Brookhaven Protein Data Bank, January 1990
A:Reference number: A50568; PDB:3B5C
A:Contents: annotation; X-ray crystallography, 1.5 angstroms, 8-92
R:Mathews, F.S.; Argos, P.; Levine, M.
Cold Spring Harb. Symp. Quant. Biol. 37, 387-395, 1971
A>Title: The structure of cytochrome b-5 at 2.0 angstrom resolution.
A:Reference number: A90922
A:Contents: annotation; oxidized form, X-ray crystallography, 2.0 angstroms; revision 1
R:Argos, P.; Mathews, F.S.
J. Biol. Chem. 250, 747-751, 1975
A>Title: The structure of ferrocyclochrome b5 at 2.8 A resolution.
A:Reference number: A92186; MUID:7509526; PMID:1167544
A:Contents: annotation; reduced form, X-ray crystallography, 2.8 angstroms
A>Note: the structure of the reduced form was found to be the same as that of the oxidized form of the heme crevice
C:Comment: This protein contains two domains: a hydrophilic, catalytic, amino-terminal domain and a hydrophobic, catalytic, amino-terminal domain.
C:Genetics: CYB5
A:Gene: CYB5
A:Introns: 43/3; 86/3; 96/3; 108/2
C:Function: <MIC>
A:Description: acts as an electron carrier for membrane bound oxygenases; with cytochrome b5
C:Function: <ERY>
A:Description: acts to reduce methemoglobin to functional hemoglobin; the oxidized form of cytochrome b5; cytochrome b5 core homology
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; membrane
P:2-134/Product: cytochrome b5, microsomal form #status experimental <MAT>
P:2-98/Product: cytochrome b5, erythrocyte form #status experimental <MA2>
P:9-84/Domain: cytochrome b5 core homology <CB5>
P:105-127/Domain: membrane-bound #status predicted <MEM>
P:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
P:44,68/Binding site: heme iron (His) (axial ligands) #status experimental
Query Match 7.1%; Score 173; DB 1; Length 134;
Best Local Similarity 32.0%; Pred. No. 1.9e-07;
Matches 47; Conservative 26; Mismatches 48; Indels 26; Gaps 4;
Cy 11 AAREVSVPTFSVEEIQKLNRLTDSGLVIDRKYNITKWSIQHPGQORVIGHYAGEDATD 70
Db 2 AEESSKAVKYTLEIEIQKNNKSTWLLHYKYDITKPLEHPGGEVLRQAGGDATE 61
Cy 71 ARAAFHPDLEFVG-----KFLKPLLIGELAPEPSQDHGKSKITDFEALRKTAEDKN 124
Db 62 NF-----EDVGHSTDAEELSTFFIGELHPDD-----RSKITPSESITTTDSNP 107
Cy 125 LFTN-----HVFLLLAHIALES 145
Db 108 SWTNWMLIPALISALFVALIIVLVTSEN 134
RESULT 15
CBPGS
N:Alternate names: hepatic cytochrome b5; membrane-bound cytochrome b5
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 29-Jul-1981 #sequence revision 20-Apr-2000 #text change 05-May-2000
C:Accession: JC5782; C24211; S07962; B90383; B92077; A93813; A00171
R:VanDerMark, P.K.; Steggle, A.W.
Biochem. Biophys. Res. Commun. 240, 80-83, 1997
A>Title: The isolation and characterization of the soluble and membrane-bound porcine cytochrome b5.
A:Reference number: JC5782; MUID:98042520; PMID:9367886
A:Accession: JC5782
A:Molecule type: mRNA
A:Residues: 1-134 <VAN>

A;Cross-references: GB:AF016389; NID:G2642485; PIDN:AAC48779.1; PID:G5642486
A;Experimental source: testis
P;Abu, K.; Kimura, S.; Kizawa, R.; Anan, F.K.; Sugita, Y.
J. Biochem. 97, 1659-1668, 1985
A;Title: Amino acid sequences of cytochrome b5 from human, porcine, and bovine erythrocyte
A;Reference number: A91992; MUID:85289161; PMID:4030743
A;Contents: sequence revisions
A;Accession: C24211
A;Molecule type: protein
A;Residues: 2-134 <OZO>
P;Ozols, J.
Biochim. Biophys. Acta 997, 121-130, 1989
A;Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.
A;Reference number: S04976; MUID:89323209; PMID:2752049
A;Accession: S07962
A;Molecule type: protein
A;Residues: 2-134 <OZO>
P;Ozols, J.
Biochemistry 13, 426-434, 1974
A;Title: Cytochrome beta-5 from microsomal membranes of equine, bovine, and porcine liver
A;Reference number: A90383; MUID:74080219; PMID:4810060
A;Accession: B90383
A;Molecule type: protein
A;Residues: 'ZZDA', 7 <OZO>
P;Nobrega, F.G.; Ozols, J.
J. Biol. Chem. 246, 1706-1717, 1971
A;Title: Amino acid sequences of tryptic peptides of cytochromes b-5 from microsomes of
A;Reference number: A92077; MUID:71134790; PMID:4993957
A;Accession: B92077
A;Molecule type: protein
A;Residues: 8-14, 'ZZ', 17, 'Z', 19-89 <NOB>
P;Ozols, J.; Gerard, C.
Proc. Natl. Acad. Sci. U.S.A. 74, 3725-3729, 1977
A;Title: Primary structure of the membranous segment of cytochrome b-5.
A;Reference number: A93813; MUID:78012290; PMID:269425
A;Accession: A93813
A;Molecule type: protein
A;Residues: 15-16, 'D', 90-134 <OZO>
A;Note: the residue 62 was identified as Asp
C;Superfamily: cytochrome b5; cytochrome b5 core homology
C;Keywords: acetylated amino end; alternative splicing; chromoprotein; electron transfer
F;9-84/Domain: cytochrome b5 core homology <CB5>
F;109-130/Domain: transmembrane #status predicted <TRM>
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F;44,68/Binding site: heme iron (His) (axial ligands) #status predicted
Query Match 7.1%; Score 172; DB 1; Length 134;
Best Local Similarity 31.3%; Pred. No. 2.4e-07;
Matches 47; Conservative 28; Mismatches 47; Indels 28; Gaps 4;
QY 11 AAEREVSYPFTSWEEIQKHLNRLDGLVDKYNITKWSIQHPGQGVICHVAGEDATD 70
Db 2 AEQSDKAVKYITLBEIQKNNKSTWLLIHHKVVYDLTKFLEHPGGEVLREQAGDATE 61
QY 71 AFRAFHPDLEFVG-----KFLKLLIGELAPEPSQDHGKNKSKITFDRLAKRTAEDMN 124
Db 62 NF-----EDVGHSTDAEELSKTIIIGELHPD-----RSKIAPSETLITTVESN 107
QY 125 LFKTNHVFELLLAHIIALEGIANFTVTFYF 154
Db 108 SWTNWV-----IPALSIVSLMYHF 129
RESULT 16
B93034
conserved hypothetical protein PA4888 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B93034
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Kuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984643
A;Accession: B93034
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-370 <STO>
A;Cross-references: GB:AE004092; GB:AE004091; NID:G9951162; PIDN:AAG08273.1; GSPDB:GN01
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4888

Query Match 7.0%; Score 170; DB 2; Length 370;
Best Local Similarity 21.7%; Pred. No. 1.2e-06;
Matches 70; Conservative 51; Mismatches 129; Indels 72; Gaps 15;

QY 157 GWIPT--LITAFVLTSAQAAGM--LQHD--YGHLSVVRKPKWNHVLVHKFVIGHLKGASAN 211
Db 67 GWLPPTWLLGSLGLGKILENMELGHNVMHGQYDWNDFEFAGRAYEWDI----AGPSD 122
QY 212 WNNRHFO-HHAKNIFHKDDPV--NMLHVFVCEWOPFYGKKLKYLPNNHCHYEFFL 268
Db 123 FWRHETHNHHHTYTNVLGKDDVGVGVRFPPEQRWKP-----YRWQ----- 165
QY 269 IGPPJ---LIPWYFOYQIIMTM-----VHKWVDLA-----WAVSYVIR 305
Db 166 ---PLWTVLQALLFOYAVAIQHRLDKYAKGRDLKABMLPLRLRAKLGEQWTKDYLL- 221
QY 306 FFITYIPYIGLALLFNFI-REFSHWVFWVMNHVME-----IDQAYRDWF 356
Db 222 -PLLGLFAGGFGAVFVGNLLANVLRLWTFTFCGHTEKAVVFPFVLEGETRGHWY 280
QY 357 SSQLTATCNVQSFDFNDFSGHLEFQIEHHLFPMRPHNLHKAFLPKVLSLCAKHGIEYQE 416
Db 281 LRQAGSNNLGGFLPHLLTGNLSHQIEHLLYFDLPARRYAALSREVRREIARRVGOYVNS 340
QY 417 KPLLRALLDIIRSLKSGKML 438
Db 341 GRLGROFLTVLR-----RIWV 356

RESULT 17

CBRS5
cytochrome b5, microsomal splice form [validated] - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jul-1981 #sequence_revision 31-Dec-1993 #text_change 20-Apr-2000
C;Accession: S03373; S07961; A91920; A93774; A92068; A91953; A92269; A61482; A00168; A
R;Dariush, N.; Fisher, C.W.; Steggles, A.W.
Protein Seq. Data Anal. 1, 351-353, 1988
A;Title: The nucleotide sequence of rabbit liver cytochrome b(5) mRNA.
A;Reference number: S03373; MUID:89128816; PMID:3222252
A;Accession: S03373
A;Molecule type: mRNA
A;Residues: 1-134 <DAR>
A;Cross-references: GB:M24844; NID:G1431635; PIDN:AAB03878.1; PID:G164785
A;Note: the authors translated the codon GAC for residues 6 and 8 as Asn, AAC for resi
R;Ozols, J.
Biochim. Biophys. Acta 997, 121-130, 1989
A;Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.
A;Reference number: S04976; MUID:89323209; PMID:2752049
A;Accession: S07961
A;Molecule type: protein
A;Residues: 2-4 <OZO>
R;Tsugita, A.; Kobayashi, M.; Kajihara, T.; Hagihara, B.
J. Biochem. 64, 727-730, 1968
A;Title: Primary structure of rabbit liver cytochrome b5.
A;Reference number: A91920; MUID:69108767; PMID:5709273
A;Accession: A91920
A;Molecule type: protein
A;Residues: 9-46, 40-61, 'D', 63-91 <TS1>
R;Tsugita, A.; Kobayashi, M.; Tani, S.; Kyo, S.; Rashid, M.A.; Yoshida, Y.; Kajihara,
Proc. Natl. Acad. Sci. U.S.A. 67, 442-447, 1970
A;Title: Comparative study of the primary structures of cytochrome b-5 from four speci
A;Reference number: A93774; MUID:70289989; PMID:5272324

A;Accession: A93774

A;Molecule type: protein

A;Residues: 7-8,47-49 <TS2>

R;Ozols, J.

J. Biol. Chem. 245, 4863-4874, 1970

A;Title: Amino acid sequence of rabbit liver microsomal cytochrome b-5.

A;Reference number: A92068; MUID:71001482; PMID:5506260

A;Accession: A92068

A;Molecule type: protein

A;Residues: 5-15,'O',17-98 <O22>

A;Note: the two minor components have either 11-Phe and 14-Clu or 96-Thr and an addition

R;Kondo, K.; Tajima, S.; Sato, R.; Narita, K.

J. Biochem. 86, 1119-1128, 1979

A;Title: Primary structure of the membrane-binding segment of rabbit cytochrome b-5.

A;Reference number: A91953; MUID:80049603; PMID:500581

A;Accession: A91953

A;Molecule type: protein

A;Residues: 92-103,'N',105-134 <KON>

A;Note: this segment corresponds to the membrane-binding carboxyl end of the molecule

R;Takagaki, Y.; Gerber, G.E.; Nihei, K.; Khorana, H.G.

J. Biol. Chem. 255, 1536-1541, 1980

A;Title: Amino acid sequence of the membraneous segment of rabbit liver cytochrome b-5.

A;Reference number: A92269; MUID:80115672; PMID:7354043

A;Accession: A92269

A;Molecule type: protein

A;Residues: 99-134 <TAK>

R;Gibson, B.W.; Fallick, A.M.; Lipka, J.J.; Waskell, L.A.

J. Protein Chem. 9, 695-703, 1990

A;Title: Mass spectrometric analysis of rabbit and bovine trypsin-solubilized cytochrome

A;Reference number: A61482; MUID:91158806; PMID:2073321

A;Accession: A61482

A;Molecule type: protein

A;Residues: 2-3,'E',5-16 <GIB>

C;Superfamily: cytochrome b5; cytochrome b5 core homology

C;Keywords: acetylated amino end; alternative splicing; chromoprotein; heme; iron; metal

F;2-134/Product: cytochrome b5 #status experimental <MAT>

F;9-84/Domain: cytochrome b5 core homology <CB5>

F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

F;44,68/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match

Best Local Similarity 7.0%; Score 169.5; DB 1; Length 134;

Matches 46; Conservative 27; Mismatches 45; Indels 21; Gaps 4;

QY 11 AAREVSVPTFSEIEIKNLRDTSGLVIDRKYNITKMSIOHPGQORVIGHAGEDATD 70

DB 2 AASDQDKVYTYLEIEIKNHSKSTWLILHHKYVDLTKFLEHPGGEVLRQAGGDAT 61

QY 71 AFRAFPDLEFVG-----KFLKPLLIGELAPEPSQDHGKSKITEDFRALRKTAEDMN 124

DB 62 NF-----EDVGHSTDAEELSKTFIIGELHPDD-----RSKLSKPMETLITTVDSNS 107

QY 125 LFKTNHVFLLLAHIAL 143

DB 108 SWTNWV-IPASALIVAL 125

RESULT 18

CBH05

N;Alternate names: hepatocytic cytochrome b5; membrane-bound cytochrome b5

C;Species: Equus caballus (domestic horse)

C;Date: 29-Jul-1981 #sequence revision 20-Apr-2000 #text_change 05-May-2000

C;Accession: S07964; A92196; A92218; A00169

R;Ozols, J.

Biochim. Biophys. Acta 997, 121-130, 1989

A;Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.

A;Reference number: S04976; MUID:89323209; PMID:2752049

A;Accession: S07964

A;Molecule type: protein

A;Residues: 1-133 <OZOL>

R;Ozols, J.; Gerard, C.; Nobrega, F.G.

J. Biol. Chem. 251, 6767-6774, 1976

A;Title: Proteolytic cleavage of horse liver cytochrome b5.

A;Reference number: A92196; MUID:77028943; PMID:977596

A;Accession: A92196

A;Molecule type: protein

A;Residues: 'Z',2,'DAS',6-41,'D',43-98 <OZ02>

A;Note: the amino terminal is shown to be blocked by acetylation and not pyroglutamic

R;Ozols, J.; Gerard, C.

J. Biol. Chem. 252, 8549-8553, 1977

A;Title: Covalent structure of the membraneous segment of horse cytochrome b-5. Chemical

A;Reference number: A92218; MUID:78045981; PMID:562879

A;Accession: A92218

A;Molecule type: protein

A;Residues: 89-133 <OZ03>

C;Superfamily: cytochrome b5; cytochrome b5 core homology

C;Keywords: acetylated amino end; alternative splicing; chromoprotein; electron transfer

F;8-83/Domain: cytochrome b5 core homology <CB5>

F;108-129/Domain: transmembrane #status predicted <TRM>

F;1/Modified site: acetylated amino end (Ala) #status experimental

F;43,67/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match

Best Local Similarity 6.7%; Score 164; DB 1; Length 133;

Matches 45; Conservative 29; Mismatches 43; Indels 48; Gaps 5;

QY 11 AAREVSVPTFSEIEIKNLRDTSGLVIDRKYNITKMSIOHPGQORVIGHAGEDATD 70

DB 1 AEQSDKAVKYTYLEIEIKNHSKSTWLILHHKYVDLTKFLEHPGGEVLRQAGGDAT 60

QY 71 AFRAFPDLEFVG-----KFLKPLLIGELAPEPSQDHGKSKITEDFRALRKTAEDMN 124

DB 61 NF-----EDIGHSTDAEELSKTFIIGELHPDD-----RSKIAKPVETLITTVD--- 103

QY 125 LFKTNHVFLLLAHIAL 169

DB 104 -----SNSSWMT-----NNVIPAISAVVVA 123

RESULT 19

CBRT5

N;Alternate names: cytochrome b5, microsomal splice form [validated] - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 15-Oct-1982 #sequence revision 31-Dec-1992 #text_change 16-Jun-2000

C;Accession: S28404; A00172; A23338; JC5597; JS0745; S07960

R;Mitoma, J.; Ito, A.

EMBO J. 11, 4157-4203, 1992

A;Title: The carboxy-terminal 10 amino acid residues of cytochrome b(5) are necessary i

A;Reference number: S28404; MUID:93011015; PMID:1396600

A;Accession: S28404

A;Molecule type: mRNA

A;Residues: 1-134 <MIT>

A;Cross-references: EMBL:D13205; NID:g220729; PIDN:BAA02492.1; PID:g220730

R;Ozols, J.; Heinsmann, F.S.

Biochim. Biophys. Acta 704, 163-173, 1982

A;Title: Chemical structure of rat liver cytochrome b-5. Isolation of peptides by high-

A;Reference number: A00172; MUID:82232110; PMID:7093287

A;Accession: A00172

A;Molecule type: protein

A;Residues: 2-134 <OZO>

R;Lederer, F.; Ghir, R.; Guillard, B.; Cortial, S.; Ito, A.

Eur. J. Biochem. 132, 95-102, 1983

A;Title: Two homologous cytochromes b-5 in a single cell.

A;Reference number: A91128; MUID:83182449; PMID:6840088

A;Accession: A23338

A;Molecule type: protein

A;Residues: 7,'B',9-17,'E',19-89 <LED>

R;Yoo, M.

Biochem. Biophys. Res. Commun. 235, 641-642, 1997

A;Title: Identification of two homologous cytochrome b5s in rat brain.

A;Reference number: JC5596; MUID:97396150; PMID:9245704

A;Accession: JC5597

A;Molecule type: mRNA

A;Residues: 1-134 <YOO>

A;Cross-references: DDBJ:AF007108; NID:g2257956; PIDN:AB567610.1; PID:g2257957

A:Experimental source: brain
 C:Comment: This protein is a small heme-containing protein which supplies electrons for 1.
 C:Superfamily: cytochrome b5; cytochrome b5 core homology
 F:2-134/Product: cytochrome b5 #status experimental <MAT>
 F:9-84/Domain: cytochrome b5 core homology <CB5>
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
 F:44,68/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.6%; Score 160; DB 1; Length 134;
 Best Local Similarity 27.9%; Pred. No. 2.4e-06;
 Matches 46; Conservative 26; Mismatches 45; Indels 48; Gaps 5;

QY 11 AAREVSVPTSWIEIQKHNLRTDSGLVDRKVNITKWSIQHPGQGVIGHVAGEDATD 70
 DB 2 AEQSDKVYTYLEIEIQKHNSKSTWILHKKYDITKFLERPGGEVLREQAGGDATE 61

QY 71 AFRAFPDLEFVG-----KFLKPLLIGELAPEPSQDHGKNKSKITDFPALRKTAE DMN 124
 DB 62 NF-----EDVGHSTDAEELSKTYIIGELHPDD-----RSKIAPSETLITVE--- 104

QY 125 LFKTNHVFLLLAHIALESIAFTVFYFCGWIPTLITAFVLA 169
 DB 105 -----SNSSWT-----NWIPIAISALVVA 124

RESULT 20
 CBHUS
 Cytochrome b5, microsomal splice form [validated] - human
 C:Species: Homo sapiens (man)
 C:Date: 29-Jul-1991 #sequence_revision 05-Apr-1995 #text_change 20-Apr-2000
 C:Accession: A28936; S04976; A91933; A00167; A24211; A32912
 R:Yoo, M.; Steggle, A.W.
 Biochem. Biophys. Res. Commun. 156, 576-580, 1988
 A:Title: The complete nucleotide sequence of human liver cytochrome b5 mRNA.
 A:Reference number: A28936; MUID:89025904; PMID:3178851
 A:Accession: A28936
 A:Molecule type: mRNA
 A:Residues: 1-134 <YOO>
 A:Cross-references: GB:M22865; NID:G181226; PIDN:AAA35729.1; PID:G181227
 A:Experimental source: liver
 R:Ozols, J.
 Biochim. Biophys. Acta 997, 121-130, 1989
 A:Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.
 A:Reference number: S04976; MUID:89323209; PMID:2752049
 A:Accession: S04976
 A:Molecule type: protein
 A:Residues: 2-3,'E','5-36;84-121,'V',123-134 <OZO>
 A:Experimental source: liver
 R:Rashid, M.A.; Hagihara, B.; Kobayashi, M.; Tani, S.; Tsugita, A.
 J. Biochem. 74, 985-1002, 1973
 A:Title: Structural studies of cytochrome b-5. III. Sequential studies on human liver cy
 A:Reference number: A91933; MUID:74074962; PMID:4770377
 A:Accession: A91933
 A:Molecule type: protein
 A:Residues: 'QZA','5-14','Q','16-17','E','19-21,23-61,'D','63-88,'K','90,'R' <RAS>
 A:Experimental source: liver
 A:Note: blocked amino-terminal peptide attributed to pyrrolidone carboxylic acid
 R:Nobrega, F.G.; Ozols, J.
 J. Biol. Chem. 246, 1706-1717, 1971
 A:Title: Amino acid sequences of tryptic peptides of cytochromes b-5 from microsomes of
 A:Reference number: A32077; MUID:71134790; PMID:4993957
 A:Accession: A00167
 A:Molecule type: protein
 A:Residues: 5-14,'Q','16-17','E','19-61,'D','63-88,'K','90,'R' <NOB>
 A:Experimental source: liver
 R:Yoo, M.; Steggle, A.W.
 Biochem. Biophys. Res. Commun. 163, 18-24, 1989
 A:Title: The characterization of three types of partially processed mRNA and two pseudo
 A:Reference number: A32912; MUID:89374222; PMID:2775258
 A:Contents: annotation; introns
 R:Abe, K.; Kimura, S.; Kizawa, R.; Anan, F.K.; Sugita, Y.

J. Biochem. 97, 1659-1668, 1985
 A:Title: Amino acid sequences of cytochrome b5 from human, porcine, and bovine erythro
 A:Reference number: A9192; MUID:85289161; PMID:4030743
 A:Contents: annotation; amino-terminal acetylation
 R:Ozols, J.
 J. Biol. Chem. 247, 2242-2245, 1972
 A:Title: Cytochrome b-5 from a normal human liver. Isolation and the partial amino acid
 A:Reference number: A92103; MUID:72154531; PMID:5062820
 A:Contents: annotation
 C:Comment: Cytochrome b5 exists in at least two alternative splice forms. This longer 1
 m (see PIR:CBHUSE) is found in erythrocytes.
 C:Genetics:
 A:Gene: GDB:CYB5
 A:Cross-references: GDB:125236; OMIM:250790
 A:Map position: 18q22.3-18q23
 A:Introns: 86/3
 A:Note: the list of introns may be incomplete
 C:Function:
 A:Description: acts as an electron carrier for membrane bound oxygenases; with cytochrome
 C:Superfamily: cytochrome b5; cytochrome b5 core homology
 C:Keywords: acetylated amino end; alternative splicing; chromoprotein; electron transf
 F:2-134/Product: cytochrome b5, microsomal splice form #status experimental <MAT>
 F:9-84/Domain: cytochrome b5 core homology <CB5>
 F:119-131/Domain: transmembrane #status predicted <TRM>
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
 F:44,68/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.5%; Score 159; DB 1; Length 134;
 Best Local Similarity 30.8%; Pred. No. 3e-06;
 Matches 44; Conservative 27; Mismatches 44; Indels 28; Gaps 4;

QY 11 AAREVSVPTSWIEIQKHNLRTDSGLVDRKVNITKWSIQHPGQGVIGHVAGEDATD 70
 DB 2 AEQSDKVYTYLEIEIQKHNSKSTWILHKKYDITKFLERPGGEVLREQAGGDATE 61

QY 71 AFRAFPDLEFVG-----KFLKPLLIGELAPEPSQDHGKNKSKITDFRALRKTAE DMN 124
 DB 62 NF-----EDVGHSTDAEELSKTYIIGELHPDD-----RPLNKPPETLITIDSS 107

QY 125 LFKTNHVFLLLAHIALESIA 147
 DB 108 SWMTNW-----IPAISAVA 122

RESULT 21
 JN0316
 cytochrome b5, erythrocyte splice form [validated] - rabbit
 N:Alternate names: soluble cytochrome b5
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
 C:Accession: JN0316; S29841
 R:Takematsu, H.; Kozutsumi, Y.; Suzuki, A.; Kawasaki, T.
 Biochem. Biophys. Res. Commun. 185, 845-851, 1992
 A:Title: Molecular cloning of rabbit cytochrome b5 genes; evidence for the occurrence
 A:Reference number: JN0316; MUID:92328788; PMID:1627141
 A:Accession: JN0316
 A:Molecule type: mRNA
 A:Residues: 1-98 <RAK>
 A:Cross-references: GB:D10901; NID:G471149; PIDN:BA01712.1; PID:G471150
 A:Note: Thr-96 was also found
 R:Giordano, S.J.; Steggle, A.W.
 Biochim. Biophys. Acta 1172, 95-100, 1993
 A:Title: Differential expression of the mRNAs for the soluble and membrane-bound forms
 A:Reference number: S29841; MUID:93176833; PMID:8439576
 A:Accession: S29841
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-98 <GIO>
 A:Cross-references: EXBL:214091; NID:G1542
 A:Note: this translation is not annotated in GenBank entry OCCVTB5, release 113.0
 C:Superfamily: cytochrome b5; cytochrome b5 core homology
 C:Keywords: acetylated amino end; alternative splicing; chromoprotein; electron transf
 F:9-84/Domain: cytochrome b5 core homology <CB5>

```
Qy      110 ---TEDFRALRK-----TAEDMNLFKTNH-----VFLLLAHLIALESIAW 148
          || : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dp      187 MINLHDFFETAROIILPPPALAYCYGAADDEVTLRNNHNAVHRIFNPKI--LIDVKKVDI 244
```

Matches	80;	Conservative	55;	Mismatches	146;	Indels	90;	Gaps	15;
---------	-----	--------------	-----	------------	------	--------	-----	------	-----

105	QY	QY	KN SKITEDFRALRKTADNM LKTNHVFFULLLAHIALESIAWFTVFVFGHGWIPTLIT	164
32	Db	Db	EE SRGERDARYIRRTIAAQRAL E---VSGRLLAG--SSRLAWMT-----GAL-TLGV	79
165	QY	QY	AFVLATSQ-----AQA GMLQHDYDGHLSVYRKPNNHLVHKFVIGHLKGASANNWNRH	17
80	Db	Db	AKIHENMEIGHNVHGGQNDNDPEIHSSTW-----EWD-----MSGSKHRYTHN	126
218	QY	QY	FQHHAKPNIFHKDPV---NMLHVFLG EWOPIEYGGKKLKYLPYNEHQHEYFFLGPPLLI	275
127	Db	Db	FVHHKYTNLGMDDDDVGVM LRVTRDQRK-----RYNIFENVMTILAIG----	172
276	QY	QY	PWYFOYQIIMTWI-----VHKWDLAVAVSYIRF-----FIYIFYGI-----	316
173	Db	Db	---FEWGVALQHEIGIKTIFKGRADREAAKTRLEFS SAKAGRQVFKDYVAFPA LITSUGA	229
317	QY	QY	---LGALLFLNFRFL ESHFWFVVTQM-----NHIW EIDOEAYDRWFFSOLTATCNV	366
230	Db	Db	TYRSTLTANVANVRJNVWSNAVIFCGHFPDGA BKFTKTDNIGEPGQWYLRQMLGSANF	289
367	QY	QY	EQSFENDWFSGHLPQIEHHLFPMPRHNHLKIAPLVKS LCAKHGIEYOEKPLLRALLDI	426
290	Db	Db	NAGPALRPMWSGNLCHQIEHHLV PDLPSNRNLHEISVRVCDRYDLPTTGTSE-----	342
427	QY	QY	IRSLKXSGKIW	437
343	Db	Db	---LVOYGGKTW	350

RESULT 25

S54259
Detailed fatty acid desaturase (EC 1.14.99.-) [imported] - *Spirulina platensis*
C:Species: *Spirulina platensis*
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jun-2000
C:Accession: S54259
R:Murata, N.; Deshnum, P.; Tasaka, Y.
submitted to the EMBL Data Library, April 1995
A:Description: Biosynthesis of gamma-linolenic acid in the cyanobacterium *Spirulina platensis*
A:Reference number: S54259
A:Accession: S54259
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-351 <MUR>
A:Cross-references: EMBL:X86736; NID:g805063; PIDN:CAA60415.1; PID:g805064
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match	6.4%;	Score 155.5;	DB 2;	Length 351;
Best Local Similarity	24.0%;	Pred. No. 1.9e-05;		
Matches	74;	Conservative 35;	Mismatches 122;	Indels 77; Gaps 16;
QY	147	AWFTVF----	YFGNGWIPTLTITAFVLA-----	TSOAQAGW---LQDYGHLSVYRKPKWN 194
Db	44	ANMTVIINVMVGLCMLGIAIAPWFLFPVVMVFTGTALTGFFVIGHDCGHRFSFR--	N 99	
QY	195	HLVHREVIQHLKGAGANW----	WNERHFQHHAKENI FHKDPDYNMLHVFLGWOP--	I 247
Db	100	VWVNDWV-GHILFLPIIIPFHSWRIGHNQHHKYNRWELD-----	NAWQFWRKE 147	
QY	248	EY-GKKKLYLPYNHQHSEYFFLIGPLLPIMYFOYIIMTWVHKWVDLANAVSYIRP 306		
Db	148	EYONACKFMQVTYDLFRGAMWIG-----	SILHWASIFHWMTKFEQKQOVKF 196	
QY	307	-----FTVIPPYGLGALLFLNFIRFLESHWFV----	WV---TOMNHIWEID 348	
Db	197	SSLIVTGAARAAFPMTLTIGVWG-----	EVKFWVLPVLVPHFWNMTFLLHHTIADIP 250	
QY	349	QEAYRWPF--SSOLTATCNVQSGFTNDWPSGHLNFQIEHHLFPTMPRHNLHKIAPVKSJ 406		
Db	251	FRPEQWHEAESQSGTVHCNYSRWGSEFLCHDINH:PHAVTIAIPMYNLRTPPYR--	308	
QY	407	CAKHGIEY 414		

Db 309 --KIGGEY 314

RESULT 26
CBHUSE
cytochrome b5, erythrocyte splice form [validated] - human
C:Species: Homo sapiens (man)
C:Date: 08-Aug-1987 #sequence_revision 05-Apr-1995 #text_cl
C:Accession: JN0075, B24211
F:Giordano, S.J.; Steggles, A.W.
Biochem. Biophys. Res. Commun. 178, 38-44, 1991
A:Title: The human liver and reticulocyte cytochrome b5 mR
A:Reference number: JN0075; MUID:91298976; PMID:1712589
A:Accession: JN0075
A:Molecule type: mRNA
A:Residues: 1-98 <GIO>
A:Cross-references: GB:M60174; NID:9181391; PIDN:AAA52165.
A:Experimental source: Erythrocyte
F:Abe, K.; Kimura, S.; Kizawa, R.; Anan, F.K.; Sugita, Y.
J. Biochem. 97, 1659-1668, 1985
A:Title: Amino acid sequences of cytochrome b5 from human,
A:Reference number: A91992; MUID:85289161; PMID:4030743
A:Accession: B24211
A:Molecule type: protein
A:Residues: 2-88, 'K', 90, 'R', 92-98 <ABE>
A:Experimental source: Erythrocyte
C:Comment: Cytochrome b5 exists in at least two alternativ
C:Genetics:

A; Cross-r

A:Map position: 18q23-18q23
A:Introns: 86/3
A>Note: the list of introns may be incomplete
C:Description:
A:description: acts to reduce methemoglobin to functional hemoglobin; the oxidized form
A>Note: A deficiency of this protein causes type IV hereditary methemoglobinemia
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: acetylated amino end; alternative splicing; chromoprotein; electron transfer;
F:2-9a/Product: cytochrome b5, erythrocyte splice form #status experimental <MAT>
F:3-9a/Domains: cytochrome b5 core homology <CB5>
F:7/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F:44,68/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.3%; Score 154.5; DB 1; Length 98;
Best Local Similarity 37.2%; Pred. No. 4.9e-06;
Matches 35; Conservative 19; Mismatches 27; Indels 13; Gaps 2;

QY 11 AAERVSVPSTSWBIQHNLTDSGLVIDRKVNITKWSIQHPCGQRVIGHYAGEDND 70
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2 AEQSDAVKYVTLEEIKQHNSKSTLWLIHHKVYDLTKFLPEHPGGVEVRQAGGDAT 61
: : : : : : : : : : : : : : : : : : : : : : : : : :
QY 71 AFRAFPHDLEFVG-----KFLKPLLLIGELAPEE 98
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 62 NF-----EDVGHSTDAREMSKTFIIGELHDD 88
: : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 27
AG2005
omega-3 fatty acid desaturase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG2005
Rfkaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A
A:Reference number: AB1807; PMID:21595285; PMID:11759840
A:Accession: AG2005
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <KUR>

A;Cross-references: GB:BA000019; PIDN:BA077963.1; PID:g17135417; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all1597
C;Superfamily: omega-3 fatty acid desaturase

Query Match 6.3%; Score 154.5; DB 2; Length 359;
Best Local Similarity 20.6%; Pred. No. 2.4e-05;
Matches 80; Conservative 54; Mismatches 131; Indels 123; Gaps 20;
QY 96 PEEPSQDHGKSKITDFRALRKAEDM-----NLFTKTHVFF-----LLL 136
DB 7 PSDNSPFGQSGENT-----TLPTQLDQAIPAECQPNVSKSLFFPFDVLIVGLIYA 62
QY 137 LAHIALESIAWFTVFYVNGNMIPLITA-FVLATSOAQAGWLOHDYCHLSVVRKPKW-- 193
DB 63 VAHY--LDSWYFWFIWLIQ--TMEWALFVVG-----HDCGHQS-FSKHKWLN 106
QY 194 ---NHLVHKFVIGHLKGSANWNRHFOHAKENIFHKOPDYNMLHVFVLGSEWQIEYG 250
DB 107 DLIGHLTHFTFLVPHYG-----WISRTHHKNTGNINDE-----SWYPTQS 150
QY 251 KKXLYLPYNHQBHYFFFLIGPL-----LTPMYFQYQIIMTMIVHK 291
DB 151 QYKEMPLGQKIGRYVFLAYPVVLFKESPNKESGSHLPSSSLFKPKSEKWDVITSLWS 210
QY 292 NWVDL-----ANAVSYIREFITYIPFYGILGALLFLNFIRLESHWFVWVQMN 341
DB 211 CMVGLLGELTYQGMWMLLKYYAAPYIVF-----IWLDLVTLFH 250
QY 342 HIVMEIDQAYR--DWFSQLTATCNVQSPFNDFWFGHLNFQI-----EHLPTMPRHN 395
DB 251 H--TEADLPWRGEDM-TFLKGLASSIDRNY--GLVNHIIHHDIGTHVAHIFLNPYHN 304
QY 396 LHKIAPLVKSLCAKHGEYQKPLRLAL 423
DB 305 LKKAIEAKPYMGY-YRKSEPIWKSIL 331

RESULT 28

S25445
nitrate reductase (NADH) (EC 1.7.1.1) 1 - kidney bean
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 22-Nov-1993 #sequence_revision 08-Sep-1995 #text_change 03-Jun-2002
C;Accession: S25445
R;Hoff, T.; Stummann, B.M.; Henningsen, K.W.
Physiol. Plantarum 82, 197-204, 1991
A;Title: Cloning and expression of a gene encoding a root specific nitrate reductase in
A;Reference number: S25445
A;Accession: S25445
A;Molecule type: DNA
A;Residues: 1-881 <HOF>
A;Cross-references: EMBL:X53603; NID:g21018; PIDN:CAA37672.1; PID:g21019
A;Experimental source: cv. Saxonia
C;Genetics:
A;Introns: 322/1; 369/1; 446/3
C;Complex: homodimer
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 redu
C;Keywords: electron transfer; FAD; flavoprotein; heme; homodimer; iron; metalloprotein;
F;63-455/Domain: molybdopterin-binding domain homology <PCO>
F;515-589/Domain: cytochrome b5 core homology <CB5>
F;632-881/Domain: cytochrome-b5 reductase homology <CBR>
F;167/Binding site: molybdopterin (Cy9) (covalent) #status predicted
F;550,573/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.3%; Score 153.5; DB 2; Length 881;
Best Local Similarity 25.2%; Pred. No. 8.7e-05;
Matches 69; Conservative 40; Mismatches 78; Indels 87; Gaps 14;
QY 5 GNQCGGAARE-----VSVP-----TFSWBIQKHNRDTSGLVIDR 41
DB 479 GNQSGGWAREKQLEKSESNPILKKSVSFPMTATKSYSLSEVRHNRDSAWIIVNG 538

QY 42 KYVNIITKWSIQHGGQGVIGHYAGEDATDAFRAHFDLEFVKFKPLKPLIGELAPEESQ 101
DB 539 HYVDCRFLKHPGGEDSILLNAGDCTEEFEAIHSDK--AKKULEDYRIGELMTDITS 596
QY 102 D-----HGKV-----SKITEDFRALR--KTRAD--M 123
DB 597 DSSSNNNSVHGNSETHLAPIREVALNPREKIPCKLLSKTISHDVRLRLPALPAEDQVM 656
QY 124 NLFTKTHVFF-----LILLAH--IIALESIAWF-----TVFY-----FGNGMPTL-I 163
DB 657 GLPVGNHVFLCATVDEKLCMRAYTSTSSVDVGFDFLVVYFKGVHFNFGNGIMSQHL 716
QY 164 TAFVLATSOAQAGWLOH-DY---GHLVSVVRKPKW 193
DB 717 DSLPIGVSVDVVRKPLGHIEYTCRGNFLVHGKPRF 750

RESULT 29

S07959
cytochrome b5, microsomal splice form [validated] - brown howler monkey (fragment)
N;Alternate names: hepatic cytochrome b5
C;Species: Alouatta fusca (brown howler monkey)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-May-2000
C;Accession: S07959; A92077; A00167
R;Ozols, J.
Biochim. Biophys. Acta 997, 121-130, 1989
A;Title: Structure of cytochrome b5 and its topology in the microsomal membrane.
A;Reference number: S04976; MUID:89323209; PMID:2752049
A;Accession: S07959
A;Molecule type: protein
A;Residues: 1-87 <OZO>
R;Nobrega, F.G.; Ozols, J.
J. Biol. Chem. 246, 1706-1717, 1971
A;Title: Amino acid sequences of tryptic peptides of cytochromes b-5 from microsomes of
A;Reference number: A92077; MUID:71134790; PMID:4993957
A;Accession: A92077
A;Molecule type: protein
A;Residues: 1-10, 'Q', '12-13, 'E', '15-57, 'D', '59-74, 'Y', '76-84, 'K', '86, 'R' <NOB>
C;Superfamily: cytochrome b5; cytochrome b5 core homology
C;Keywords: electron transfer; heme; iron; liver; metalloprotein
F;5-80/Domain: cytochrome b5 core homology <CB5>
F;40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match

Best Local Similarity 6.2%; Score 150.5; DB 2; Length 87;
Matches 34; Conservative 17; Mismatches 24; Indels 13; Gaps 2;
QY 17 SVPTFSWBIQKHNRDTSGLVIDRKYVNIKWSIQHGGQGVIGHYAGEDATDAFRAH 76
DB 4 AVKYITLSEIQKHNSKSTWLILHHKVYDLTKFLEHPGGBEVLRBOAGGDATENF---- 59
QY 77 PDLEFVG-----KFLKPLIGELAPEE 98
DB 60 ---EDVGHSTDAEISLKTFFIIGLHPDD 84

RESULT 30

JQ2337
omega-3 fatty acid desaturase (EC 1.14.99.-) BN3 [similarity] - rape
C;Species: Brassica napus (rape)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: JQ2337
R;Radav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.;
J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browne, J.
Plant Physiol. 103, 467-476, 1993
A;Title: Cloning of higher plant omega-3 fatty acid desaturases.
A;Reference number: JQ2335; MUID:94302147; PMID:8029334
A;Contents: cDNA:BN3
A;Accession: JQ2337
A;Molecule type: mRNA
A;Residues: 1-377 <YAD>
A;Cross-references: GB:L22962; NID:g408491; PIDN:AAA61775.1; PID:g408492
C;Comment: This enzyme introduces the third double bond in the biosynthesis of 18:2 and

C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 6.1%; Score 148.5; DB 1; Length 377;
Best Local Similarity 23.6%; Pred. No. 8.1e-05;
Matches 91; Conservative 58; Mismatches 137; Indels 99; Gaps 25;

QY 88 PLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNLFKTNHVFLLAHIALESIA 147
DB 24 PFKIGDIRAAIP-----KHCWKSPLRSMYSVARD-----IFAVVALLA-VAAYVYFDS 69

QY 148 WF--TVFPGNGWITLITA-FVLATSOAQAGWLOHDYCHLSVYRKPKWN-----HLVHKF 200
DB 70 WFFWFLYAAQAQ---TLFWAIFVLG-----HDCGHSFSDIPLLNTAVGHILHSF 116

QY 201 VTCHLKGASANNWNRHFFOHAHPNI FHKDPDNNLHVFLGEMOPIEYGGKCLKLPYN 260
DB 117 ILVPYHG-----WRISHRTHH---QNHGHNDES-----WVPLP--EKLYKNLSHS 158

QY 261 HQHEVFFLIGPPLIPMFQOIIMTVHKH-----WDLAWAV 300

DB 159 TMLRYTVPLPMLAYPLVLYWSPGKSGSHYNYPSLFPAPSERKLIATSTTCW-SIMLAT 217

QY 301 SVYIRFP---ITVIFPGYIGLALLFLNFIREFSHFVMTOMNHVMEIDQAYR--DW 355
DB 218 LVYLSFLVCPVTVLVKYG---PYIIFWMLDA-----VTVLHHGHDDKLPWYRGKEW 268

QY 356 --FSSQLTATCNVEGSPFNDFSGHNLFOIEHLLPPTPRNLHKLAPLVKSLCAKH--G 411
DB 269 SVYRGGLT-TIDRDYGIFFNN-IHHDIGTHVHHLFQIPFHYHL-----VDAKTS--AKHVLG 321

QY 412 IEVOKPPLRAL-LDIIRSLKSGK 435
DB 322 RYREPKTSGLPIHLVESLVAISK 346

RESULT 31

A44227
omega-3 fatty acid desaturase (EC 1.14.99.-) [similarity] - rape
N:Alternate names: omega-3 linoleate desaturase
C:Species: Brassica napus (rape)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: A44227
R:Arondel, V.; Lemieux, B.; Hwang, I.; Gibson, S.; Goodman, H.M.; Somerville, C.R.
Science 258, 1353-1355, 1992
A:Title: Map-based cloning of a gene controlling omega-3 fatty acid desaturation in Arab
A:Reference number: A44227; MUID:93088059; PMID:1455229
A:Accession: A44227
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-383 <ARO>
A:Cross-references: GB:I01418; NID:G167147; PIDN:AAA32994.1; PID:G167148
A:Experimental source: developing seed
A:Note: sequence extracted from NCBI backbone (NCBIP:119842)
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 6.1%; Score 148.5; DB 1; Length 383;
Best Local Similarity 22.5%; Pred. No. 8.3e-05;
Matches 92; Conservative 62; Mismatches 149; Indels 105; Gaps 25;

QY 65 GEDATDAFAFHFDLEFVGKFLPLJIGELAPEEPSQDHGKNSKITEDFRALRKTAEADN 124
DB 13 GDSGARKEBGFDSQAQ-----PPFKIGDIRAIP-----KHCWKSPLRSMYS-----54

QY 125 LFTKNHVFLLAHIALESIAWF--TVFPGNGWITLITA-FVLATSOAQAGWLOHD 181
DB 55 -YVTRDIFAVALA-NAAYVYFDSWFLWPLYWVAQAQ---TLFWAIFVLG-----HD 99

QY 182 YGHSVYRKPKWN-----HLVHKFVIGHLKASANNWNRHFFOHAHPNI FHKDPDNNLH 237
DB 100 CGHGSFSDIPLLNSVVGHLHSFILVPYHG-----WRISHRTHH---QNHGHNDES---149

QY 238 VFVLGEMOPIEYGGKCLKLPYNHQHEVFFLIGPPLIPMFQOIIMTVHKH-----292
DB 150 -----WVPLP--EKLYKNLSHSTMLRYTVPLPMLAYPIYLWYSPGKSGSHYNYPSL 201

QY 293 -----WDLAWAVSYIRFP-----ITVIFPGYIGLALLFLNFIREFSHF 334
DB 202 FAPSERKLIATSTTCW-SIMLATVLSFLVDPVTVLVKYG---PYIIFWMLDA-----253

QY 335 VWYTONNHVMEIDQAYR--DW--FSSQLTATCNVEGSPFNDFSGHNLFOIEHLLPPT 390
DB 254 --VTVLHHGHDEKLPWYRGKSWYLRGLT-TIDRDYGIFFNN-IHHDIGTHVHHLFPQ 309

QY 391 MPRNLHKLAPLVKSLCAKH--GIEYOKPPLRAL-LDIIRSLKSGK 435
DB 310 IPHYHL-----VDATRAAKHVLGRIYREPKTSGLPIHLVESLVAISK 352

RESULT 32
S43771
phosphatidylcholine desaturase (EC 1.3.1.35) - Synecococcus sp. (strain PCC 7002)
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) [misidenti
C:Species: Synecococcus sp.
A:Variety: PCC 7002
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S43771
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
Plant Mol. Biol. 24, 643-650, 1994
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobacter
A:Reference number: S43770; MUID:94207189; PMID:8155883
A:Accession: S43771
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <SAK>
A:Cross-references: GB:D13779; NID:G488510; PIDN:BAA02922.1; PID:G488511
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 6.1%; Score 148; DB 2; Length 347;
Best Local Similarity 22.5%; Pred. No. 8.1e-05;
Matches 75; Conservative 58; Mismatches 120; Indels 80; Gaps 18;

QY 106 NSKITEDFRALRKTAEADNLFKTNHVFLLAHIAII---ALESIA-WFTVFP--YFGNGW 158
DB 19 NLKLRDILDTLPSVTEINPLKASRV--LLSVAVVGCVALLAIAFVWLLPWLGTG-75

QY 159 IPTLITAFVLATSOAQAGWLOHDYCHLSVYRKPKWNHVLHKFVIGHLKASANNW----WN 214
DB 76 --ITLTGFPV-----IGHDCGHSFSPSRKWNWNLV-----GHAFLEPLIYPFHSWR 119

QY 215 HRHFQHHAKENIFHKDPDNNLHVFLGEMOPIEYGGKCLKLP--YNNHQHEVFFLIGPP 272
DB 120 ILNHHHRYTNNMDED-----NAWAP-----FTELYDSDPAFIKAVYRA 159

QY 273 LLIPMFQOIIMTVHKHWN-----VDLAWAVSYIRFFITYIPFYG 315
DB 160 IRGKLWNLASVIHQLKLFHNFNFAFEGKQREQVRSALFVIAAGAIAPVPMFYT-----LG 214

QY 316 ILGALLFLNFIREFSHFVWYTONNHVMEIDQAYRDFWS---SOLTATCNVEGSPFF 371
DB 215 VWGVYKFW-LMPVLGVHFMWSTFTLVHHTVPEI-PFSYRDKWNEA-AQSGTVHCDPYKW 272

QY 372 NDFSGHNLFOIEHLLPPTPRNLHKLAPLVK 404
DB 273 VEVLCHDINVHPHLLSTGIPSYNLKAYASIK 305

RESULT 33

T10063
Omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - castor bean
N:Alternate names: linoleoyl desaturase
C:Species: Ricinus communis (castor bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T10063

```
C;Keywords: chloroplast; oxidoreductase  
F;1-40/Domain: transit peptide (chloroplast) #status predicted <TP>  
  
Query Match      6.0%; Score 147; DB 2; Length 424;  
Best Local Similarity 20.2%; Pred.No.0.00013;  
Matches 78; Conservative 61; Mismatches 136; Indels 112; Gaps 21;
```

QY 90 LIGELAPEPSODHGKNSKITEDFRALRKTAEDMNLFTKNHVFFLLLAHIIALESTIAWF 149

Dd ||| : : : ||| : : : ||| : : : ||| : : :
Db LARELGYSIGRELPDONSITDIKSM-----PAEVFKLDHGKAWRACLTIIAACSACYW 117

QY 150 TVTYFCNGWIPTLIATFLVATSQAAGW-----LOHDYGHLVSVPKPKNHVLHKFVI 202

Dd : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 118 LI-----SISPYILLPAAWALGATGTCFGVFIGHDCGRHSFFE----NNLIED-IV 163

QY 203 GHLKGSANW---WNHRHFQHAKENIFPKDPVNMLHVFLGEWPQIEYGGKKLYPL 258

Dd : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 164 CHIFFAPLIYPPEPWRIKINHHHAHTNKLVEDT-----AWHPVT--EADMAKW D 210

QY 259 YNHQEHYEFELGPPLLIPMYFOQIIMTVLVKHVKWDLA-WAYSYY-----IRFF 307

Dd : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 211 STSAMLYKVFLGTPL-----KLWASGVGHWLWHFDLNKYTKPKQRTRVV 253

QY 308 ITVIPFYGI LG-----ALLFLN-----PIRF-----LESH-WFVMVTOMNVIMEIDOEAYR 353

Dd : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 254 ISLAVVYGFMATAFPALLYEGGWFAVKYLMPGLWGVEFWMSFTVVHHTAPHI PPKAE 313

QY 354 DW-FSSQLTAINVZQSFPNDW--FSGH-LNFQIEHHLFPTWPRHNLHKIAP----- 401

Dd : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 314 ENNAACAQLSGTVHCDD--FPNWVELTDISHVPHPVHAPKIPTWNLNKATESLENWG 370

QY 402 -----LVKSCLKAHGIEYOEK 417

Dd : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 371 QYMTECTFNVRVVYNICTSCHV-YDEK 396

RESULT 35

S53309

N-6 fatty acid desaturase precursor - spinach

C;Species: Spinacia oleracea (spinach)

C;Date: 28-Oct-1996 #sequence revision 27-Feb-1997 #text_change 07-Dec-1999

C;Accession: S53309; S73100; S49331

R;Schmidt, H.; Dresselhaus, T.; Buck, F.; Heinz, B.

Plant Mol. Biol. 26, 631-642, 1994

A;Title: Purification and PCR-based cDNA cloning of a plastidial n-6 desaturase

A;Reference number: S53309; UID:95036044; PMID:7948918

A;Accession: S53309

A:Molecule type: mRNA

A;Residues: 1-447 <SCH>

A;Cross-references: EMBL:X78311; NID:G623343; PIDN:CAA55121.1; PID:G623344

A;Accession: S73100

A:Molecule type: protein

A;Residues: 66-78 <SCH2>

C;Genetics:

A;Genome: nuclear

C;Superfamily: omega-3 fatty acid desaturase

C;Keywords: chloroplast

F;1-65/Domain: transit peptide (chloroplast) #status predicted <TNP>

F;66-447/Product: n-6 fatty acid desaturase #status experimental <MAT>

Query Match 6.0%; Score 146; DB 2; Length 447;
Best Local Similarity 20.4%; Pred.No.0.00016;
Matches 79; Conservative 60; Mismatches 142; Indels 106; Gaps 19;

QY 91 IGGLEAPEEPSODHGKNSKITEDFRALRKTAEDMNLFTKNHVFFLLLAHIIALESTIA--- 147

Dd : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 97 IGEP LPD VDT-----NRDIITSLPKQVFENDTKMGCTVLVISVTSVALGFIAMIAKAP 148

QY 148 WFTVTFVGNGWIPTLIATFLVATSQAAGWLOHDYGHLVSVPKPKNHVLHKFVIIGHLKG 207

Dd : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 149 WY-LLLPLAWATWTGTAITGFV-----IGHDCARHGFSK-----NKLVED-IVGTAF 193

QY 208 ASANW---WNHRHFQHAKPNIFIHKD-----PDNMMLHVFVLG---EWQP 246

Db 194 MFLIYPEPWRPKQHQHTKTNMLREDTAWLPIMKEDIESSPGLRKALIIYAVGLRTWMS 253
Qy 247 IEYGGKKLKYLPYNHNEY- - - - -PFLIGPPLLIPMYFOYQIIMTMIVHKNWV 294
Db 254 IAHWLKLVHFNKDFQSEVKRATISLAFAFPMVIGWPL- - - - -IYKTGI 299
Qy 295 DIAMAVSYVIRFFIYIPFYIGLALLFLNFIREFLESFHWVVTQMHVMEIDQEAIRD 354
Db 300 -VGW- - - - -IKFWL- - - - -MPWLG- - - - -HFMSTFTIVHTAPHIPKSSKE 337
Qy 355 W- - - - -FSSQATATCNVQSFNDWFSGLHNFQIEHLLFPMPRHNLKIAPIVKSICAKHGI 412
Db 338 MNAQAQLSGTVCHDPRWIEITLCHDISVPHPHISPKIPSYNLRAN- - - - -OSLNENWG- 393
Qy 413 EYCEXP- - - - -LLRALLDIIRSLKSG 434
Db 394 EYLNPKSNWRLMRTIMTCHYIDKG 420

RESULT 36

JC5596
cytochrome b5, brain splice form - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 05-May-2000
C:Accession: JC5596
R;Yoo, M.
Biochem. Biophys. Res. Commun. 236, 641-642, 1997
A:Title: Identification of two homologous cytochrome b5s in rat brain.
A:Reference number: JC5596; MUID:97396150; PMID:9245704

A:Accession: JC5596

A:Molecule type: mRNA

A:Residues: 1-100 <FOO>

A:Cross-references: DDBJ:AF007107; NID:92257954; PIDN:AAB67609.1; PID:92257955

A:Experimental source: brain

C:Superfamily: cytochrome b5; cytochrome b5 core homology

C:Keywords: alternative splicing; heme; iron; metalloprotein

F:9-84/Domain: cytochrome b5 core homology <CB5>

F:44,68/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.0%; Score 145.5; DB 2; Length 100;

Best Local Similarity 35.1%; Pred. No. 2.9e-05;

Matches 34; Conservative 20; Mismatches 30; Indels 13; Gaps 2;

Qy 11 AAREVSVPTFSWEIEQKHLNLTDSGLVIDRKVNITKWSIOHPGGQGVGHYAGEDATD 70

Db 2 AGQSDKVKYVLEIEIQKDKSKSTWVILHKKVYDLTKLEHPSGSEVLRQAGDATE 61

Qy 71 AFRAPHPLDFVG- - - - -KFLKPLLIGELAPEEPSQ 101

Db 62 NF- - - - -EDVGHSTDAEELSKVTIIGELHPDRSK 91

RESULT 37

T19614
probable cytochrome b5 C31E10.7 [similarity] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: T19614
R;Swihurne, J.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19151

A:Accession: T19614

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-138 <WIL>

A:Cross-references: EMBL:Z78539; PIDN:CAB01732.1; GSPDB:GN000028; CESP:C31E10.7

A:Experimental source: clone C31E10

C:Genetics:

A:Gene: CESP:C31E10.7

A:Map position: X

A:Introns: 42/3; 85/3; 111/2

C:Superfamily: cytochrome b5; cytochrome b5 core homology

C:Keywords: heme; iron; metalloprotein
F:43,67/Binding site: heme iron (His) (axial ligands) #status predicted
Query Match 6.0%; Score 145.5; DB 2; Length 138;
Best Local Similarity 30.9%; Pred. No. 4.3e-05;
Matches 46; Conservative 26; Mismatches 50; Indels 27; Gaps 6;
Qy 14 REVSVFTFSWEIEQKHLNLTDSGLVIDRKVNITKWSIOHPGGQGVGHYAGEDATDAPR 73
Db 4 RMADLQKITLKEIAEHTNKSAWLIVGNKVFDTFLDEHPGCGCEVLLQAGSDGTEAPE 63
Qy 74 - - - - -AHPDLEFVGKFLKPLLIGE-LAPEEPSODHGKNS-KITEPFRALKTAEDNN 124
Db 64 DVGHSTDAHKMDEY- - - - -LGEVVASERKYSYDVKQWKSTTEQDNKQRGESM- 114
Qy 125 LFKTNHVFVFLLLAHIIALESIAWFTVFY 153
Db 115 - - - - -QTDNIVVFALLAVIVAL- - - - -VYY 134

RESULT 38

JC2555
omega-3 fatty acid desaturase - common tobacco (cv. SR1)
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 20-Jun-2000
C:Accession: JC2555
R;Hamada, T.; Kodama, H.; Nishimura, M.; Iba, K.
Gene 147, 293-294, 1994
A:Title: Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.
A:Reference number: JC2555; MUID:95011632; PMID:7926817
A:Accession: JC2555
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <HAM>

A:Cross-references: DDBJ:D26509; NID:91311480; PIDN:BAA05515.1; PID:G599592

C:Superfamily: omega-3 fatty acid desaturase

Query Match 6.0%; Score 145.5; DB 2; Length 379;

Best Local Similarity 21.3%; Pred. No. 0.00015;

Matches 86; Conservative 56; Mismatches 143; Indels 119; Gaps 23;

Qy 78 DLFEVSKFLKPLLIGELAPEEPSODHGKNSKITEDPRALKTAEDNNLTKTNHVFLLLL 137

Db 19 EFEPDPSAPPPFLAIBIRNIP- - - - -KHCWKDPLRSLSVVRDV- - - - -IFVATLI 66

Qy 138 AHIIALESIAWFTVFYFGNGWIPTLITA-FVLATSOAQAGWLQHDYGHLSVYRKPKWN- 194

Db 67 GIAIHLDNLFFLYWAIQ- - - - -TMFWAIFVLG- - - - -HDCGHGSPSDSOLLNV 113

Qy 195 - - - - -HLVHKFVIGHLKASANNWNRHFOHAKPNI-FKQPDVNMHLVFLVGEWQP- - - - - 246

Db 114 VGHILHSAILVPYHG- - - - -WRISHKTHQNGNVTDE- - - - -SWVPMPEKLY 157

Qy 247 - - - - -IEYGGKKLKY-LPYNHQHEYFLLIGPPLLIPMYF- - - - - 279

Db 158 NKVGYSTKFLRYKIPP- - - - -PFLAYPMYLMKSPGKSGSHENPYSLDLPOFHER 206

Qy 280 QYQIIMTMIVHKNWDLAWAVSYVIRFFIYIPFYIGLGA- - - - -LLFLNFIREFLESFHWV 337

Db 207 KYVVTSTLC- - - - -WTVMA-ALLYLCTAFGSLQMFKIYGAPYLIFV- - - - -MWLDVF 253

Qy 338 TOMNHIWMEIDQEAIR- - - - -FSSQATATCNVQSFNDWFSGLHNFQIEHLLFPTMPR 393

Db 254 TYLHHGYEKKLPYRGKESYLRGGLT-JVDRDYGLFNN-IHHDIGTHVHLLFPQIPH 311

Qy 394 HNLKIAPLVKSICAKHGEYQEK- - - - -PL-LRALLDIIRSLKK 432

Db 312 YHLREATKAAKPVLGKY- - - - -YREPKKSGPIPFHLVKDLTRSMQ 352

RESULT 39

CECH5

cytochrome b5 precursor - chicken

Search completed: December 9, 2003, 10:19:34
Job time : 23 secs

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DD007CE05QP1.

FEATURES

source
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD007YJ09"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 261 a 345 c 240 t 19 others
ORIGIN
Query Match 34.9%; Score 1110.6; DB 9; Length 1201;
Best Local Similarity 97.3%; Pred. No. 1.1e-221;
Matches 1109; Conservative 17; Mismatches 14; Indels 0; Gaps 0;
QY 97 CCGGCTGGAGGCGGCTGTGTGACGACGACCGCGCGGGAGGCGGCGGCGGCGG 156
DB 61 CCGGCTGGAGGCGGCTGTGTGACGACGACCGCGCGGGAGGCGGCGGCGGCGG 120
QY 157 GGGGCTCACAGTCGCGGAGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 216
DB 121 GGGGCTCACAGTCGCGGAGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 217 AGCGCGAGGTGTGGTGGCCACCTTACGCTGGGAGGAGATTCAGAACATTAACCTGGCA 276
DB 181 AGCGCGAGGTGTGGTGGCCACCTTACGCTGGGAGGAGATTCAGAACATTAACCTGGCA 240
QY 277 CGGAGTGGGCTGTGTATTCACGCGAGGTTTACACATCACCAATGCTTCCATCCAGC 336
DB 241 CCGCAGGKGTGTGTATTCACGCGAGGTTTACACATCACCAATGCTTCCATCCAGC 300
QY 337 ACCCGGGGGCCAGCGGCTCATCGGGCACTACGCTGGAGAGATSCAACGATGCTTCC 396
DB 301 ACCCGGGGGCCAGCGGCTCATCGGGCACTACGCTGGAGAGATSCAACGATGCTTCC 360
QY 397 GGGCTTCCACCTGACCTGAAATTCGTGGCAAGTTCTTGAACCCCTGCTGATTCGTG 456
DB 361 GGGCTTCCACCTGACCTGAAATTCGTGGCAAGTTCTTGAACCCCTGCTGATTCGTG 420
QY 457 AACTGGCCCGGAGAGCCAGCCAGGACCCAGGCAAGAACTCAAGATCACTGAGGACT 516
DB 421 AACTGGCCCGGAGAGCCAGCCAGGACCCAGGCAAGAACTCAAGATCACTGAGGACT 480
QY 517 TCCGGGCTTGAGGAGAGCGGTGAGGACATGAACCTGTTCAAGACCAACACAGTGTCT 576
DB 481 TCCGGGCTTGAGGAGAGCGGTGAGGACATGAACCTGTTCAAGACCAACACAGTGTCT 540
QY 577 TCTCTCTCTCTGCGCCACATCATCGCCCTGGAGAGCATTCGATGGTTCACTGCTTCT 636
DB 541 TCTCTCTCTCTGCGCCACATCATCGCCCTGGAGAGCATTCGATGGTTCACTGCTTCT 600
QY 637 ACTTTGGCAATGGCTGATTCCTACCTCATCAGGCGCTTGTCTTCTGCTACCTCTCAGG 696
DB 601 ACTTTGGCAATGGCTGATTCCTACCTCATCAGGCGCTTGTCTTCTGCTACCTCTCAGG 660
QY 697 CCCAGCTGGATGGCTGCAACATGATTATGGCCACTGCTCTCTACAGAAACCCCAAGT 756
DB 661 CCCAGCTGGATGGCTGCAACATGATTATGGCCACTGCTCTCTCTACAGAAACCCCAAGT 720
QY 757 GGAACCACTTGTCCAAATTTGTCATTGGCCACTTAAGGGTGCCTCTGCCAACTGGT 816
DB 721 GGAACCACTTGTCCAAATTTGTCATTGGCCACTTAAGGGTGCCTCTGCCAACTGGT 780
QY 817 GGAATCATGCCACTTCCAGGACCCAGCCAGCCTTAACATCTTCCAGAGGATCCCGATG 876
DB 781 GGAATCATGCCACTTCCAGGACCCAGCCAGCCTTAACATCTTCCAGAGGATCCCGATG 840

QY 877 TGAACATGCTGCACGCTTTGTTCTGGGCGAATGGCGACCCATCGAGTACGGCAAGAGA 936
DB 841 TGAACATGCTGCACGCTTTGTTCTGGGCGAATGGCGACCCATCGAGTACGGCAAGAGA 900
QY 937 AGCTGAAATACCTGCTCCCTACAAATCACCAGACAGCAATATCTTCTCTGATTTGGGCGGCGC 996
DB 901 AGCTGAAATACCTGCTCCCTACAAATCACCAGACAGCAATATCTTCTCTGATTTGGGCGGCGC 960
QY 997 TGCTCATCCCCCATGTAATTCAGTACAGATCATCATGACATGATGCTCATTAAGAACT 1056
DB 961 TGCTCATCCCCCATGTAATTCAGTACAGATCATCATGACATGATGCTCATTAAGAACT 1020
QY 1057 GGTGGACCTGCTGCGCGCTGAGCTACTACATCCGCTTCTTCTCATCACCTTACATCCCTT 1116
DB 1021 GGTGGACCTGCTGCGCGCTGAGCTACTACATCCGCTTCTTCTCATCACCTTACATCCCTT 1080
QY 1117 TCTACGGCATCTGGAGCCCTCTCTTCTCAATCTCATCAGGTTCTCTGGAGAGCACT 1176
DB 1081 TCTACGGCATCTGGAGCCCTCTCTTCTCAATCTCATCAGGTTCTCTGGAGAGCACT 1140
QY 1177 GGTGGTGTGGTGCACAGATGAATCATCATGCTGATGAGATTCAGCAGGAGGCTTACC 1236
DB 1141 GKTITGTGTGGTGAACAAAWRAAWAAWCGTCATGAGATGAAACAAGAGGCGCHCCB 1200

RESULT 2
ALS30345 1201 bp mRNA linear EST 23-MAY-2003
LOCUS ALS30345 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DD007YJ09 3-PRIME, mRNA sequence.
ACCESSION ALS30345
VERSION ALS30345.2 GI:31068178
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12793838.
Contact: Genoscope
Genoscope - Centre National de Sequenage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6148.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DD007CE05NP1&cluster=6148.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DD007CE05NP1.

FEATURES
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD007YJ09"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 235 a 375 c 344 g 200 t 47 others
ORIGIN

Query Match 32.9%; Score 1049; DB 9; Length 1201;
Best Local Similarity 93.0%; Pred. No. 8.1e-209;
Matches 1096; Conservative 38; Mismatches 38; Indels 6; Gaps 4;

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2862)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inctani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-3216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers

source 1. 2862

organism="Mus musculus"

mol_type="mRNA"

strain="C57BL/6J"

db_xref="FANTOM_DB.C630034B17"

db_xref="taxon:10090"

clone="C630034B17"

sex="male"

tissue_type="hippocampus"

clone_lib="RIKEN full-length enriched mouse cDNA library"

dev_stage="adult"

115..1376

note="fatty acid desaturase 2 (MGD|MGI:1930079, GI|NM_019699, evidence: BLASTN, 100%, match=1266) putative"

2845..2850

note="putative"

2862

note="putative"

BASE COUNT 637 a 779 c 758 g 688 t

ORIGIN

Query Match 32.2%; Score 1023.8; DB 11; Length 2862;

Best Local Similarity 78.5%; Pred. No. 1.6e-203;

Matches 1310; Conservative 0; Mismatches 282; Indels 77; Gaps 4;

QY 68 GAAGCGAAGAGGCGCGGCTGCACACACCGGCTGGAG-GCAGCGGCTGTGCAGCGA 126

Db 2 GAAGCGAGAGGCGCGGCGGCTGCACACACCGGCTGGAG-GCAGCGGCTGTGCAGCGA 61

QY 127 GCAGCGGCGCGGCGGAGCGCGAGTCACAGCGGCGGTCACAGTCGGCAGGCGAGCATGGGGA 186

Db 62 GCAGCGGCGCGCGGAGCGGCTAGCGCACAGCGGCGATCCGGGTAGACTGGCAGCATGGGGA 121

QY 187 AGGAGGGAACACAGCGGAGGGGCGCGCGAGCGGAGGTGTCGTGCCACCTTCAGCT 246

Db 122 AGGAGGGAACACAGCGGAGGGGAGGACCGAGCGCGGCGGCTCCGATGCCACCTCCGTT 181

QY 247 GGGAGGAGATTTCAGAACATAACCTGCGCACCGACAGTGGGCTGGTCAATTGACCGCAAG 306

Db 182 GGGAGGAGATTTCAGAACATAACCTGCGCACCGACAGTGGGCTGGTCAATTGACCGCAAG 212

QY 307 TTTTACAAATACACAAATGGTCCATCCAGCACCGCGGGGGCCAGCGGGTCAATCGGCACT 366

Db 213 -----CGTGTTCATCGGCACT 228

QY 367 ACCTGGAGAGATGCAACCGATGCTTCGCGCCTTCCACACCTGACCTGGATTCGTTGG 426

Db 229 ATTGCGGAGAGATGCTACCGATGCTTCGCGCCTTCCATCTGGACCTGGATTCGTTGG 288

QY 427 GCAAGTTCTTTAAACCCCTCTGATTGGTGAATGCGCCCGGAGGAGCCAGCAGGAC 486

Db 289 GCAAGTTCTTTAAAGCCCTCTGATTGGTGAATGCGCCCGGAGGAGCCAGCAGGAC 348

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QY 547 TGAACCTGTTTCAAGACCAACACCGTGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 606

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Db 469 TGGAAAGCCTTGGCTGGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 528

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QY 727 GCCACCTGTCTGTCTACAGAAACCCAGTGGAGAACCCCTTGTTCACAAATTCGTCTAT 786

Db 589 GCCACCTTCTGTCTATAGAAATTCATATGGAATTCATATGGAATTCATATGGAATTC 648

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QY 907 AATGGAGCCCATCGAGTACGCAAGAGAGTGAATACCTGCCCTTACCAATCAGCAGC 966

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QY 1027 TCATCATGACATGATCGTCCATAAGAACTGGGTGGACCTGGCTGGGCGTCAAGTACT 1086

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QY 1327 TTGAGCACCACTCTTCTCCCACTATGCCCGGCGCACTTACACAGATCGCCCGCTGG 1386

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DEFINITION clone CSOD1040YK05 3-PRIME, mRNA sequence.
ACCESSION BX397627
VERSION BX397627.1 GI:30629236
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1127)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1040AF03NP1&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1040AF03NP1.
FEATURES
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primer="Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Query Match 31.1%; Score 990.8; DB 13; Length 1127;
Best Local Similarity 97.4%; Pred. No. 1.2e-196;
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Qy 2352 CCTCAGGGGTGCTGAGGTCCAAGATTCTGAGCAATCTGACCCCTTTCTCAAGGCTCTG 2411
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Db 753 TTATCAGCTGGGCAAGTCCAGCCCAATCCTCGCCATTCTGGGCCCA-GGGGAGCTGGGCC 695
Qy 2472 TGCAGGCTGCAGGAGGGCACTGGAGCTGGGAGGTCTGCTCCAGCCCTCCCATCTCGG 2531
Db 694 TGCAGGCTGCAGGAGGGCACTGGAGCTGGGAGGTCTGCTCCAGCCCTCCCATCTCGG 635
Qy 2532 GCTGCTGTGTGAGGGGCTGCTCAGCACTCTCTGCTGTGAACTGCTTACTGTGT 2591
Db 634 GCTGCTGTGTGAGGGGCTGCTCAGCACTCTCTGCTGTGAACTGCTTACTGTGT 575
Qy 2592 TTAACCTGCTTCCAGGATGCATCTGATAGGAGGGGCGGAGGCTGGGCTTGTGA 2651
Db 574 TTAACCTGCTTCCAGGATGCATCTGATAGGAGGGGCGGAGGCTGGGCTTGTGA 515
Qy 2652 CAATCTGCTTTTCAACCATGCTTGCCTCGTGGGCCCTGACTGTTCAGGAGGGCCAGG 2711
Db 514 CAATCTGCTTTTCAACCATGCTTGCCTCGTGGGCCCTGACTGTTCAGGAGGGCCAGG 455
Qy 2712 GAGCAGAGCGGGAGGAGTCTCAGGAGGAGCTGCTTGGGCTGAGGGCTGGGAGGGGTAC 2771
Db 454 GAGCAGAGCGGGAGGAGTCTCAGGAGGAGCTGCTTGGGCTGAGGGCTGGGAGGGGTAC 395
Qy 2772 CTCATGAGGACAGGGGTGAGCTGAGAGAGAGAGGTGGGGCTGGAGGTGCTGTAG 2831
Db 394 CTCATGAGGACAGGGGTGAGCTGAGAGAGAGAGGTGGGGCTGGAGGTGCTGTAG 335
Qy 2832 TTGAGGGACCGGCAAGTGTGAGGGGAGGAGGAGTCTCTGGGAGGATCTCTGAGTGTCT 2891
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Db 274 GTTGAGTCTAACCCACTTAATCAGTCTTATGATTTCAGGGGAGGGCAGGACCAACACT 215
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Db 154 CTTGATCTAAGCATCTGGGTTGCATGCGCAATGGCATGCCCGCCAGCTACTGTATGCC 95
Qy 3072 CCGACCCCGCAGAGGCAAGATGAACCCATAGGAGGCTGATCGTAATGTTTATCATGTTA 3131
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Db 35 CTTCCCGCACCCCTACATTTTGTGAATAATAATAA 2
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clone CSOD1001YH12 5-PRIME, mRNA sequence.
ACCESSION BX355607
VERSION BX355607.1 GI:30375985
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1001DD06QPI&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1001DD06QPI.
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1. 1201
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 217 a 361 c 353 g 251 t 19 others
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Best Local Similarity 98.1%; Pred. No. 2.4e-194;
Matches 1017; Conservative 5; Mismatches 12; Indels 3; Gaps 3;
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QY 1813 ACCTCCACTCTGCTCCCTTAAAGATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1872
DB 181 ACCTCCACTCTGCTCCCTTAAAGATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 1873 AGCTCCCTTACGCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1932
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QY 1933 TGGGGTTCATAGGGGAGAGTCTAGTCCGGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1992
DB 301 TGGGGTTCATAGGGGAGAGTCTAGTCCGGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 1993 ACTCTCCCTGAGCGGTGCATGTGTCACCTTTTCATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2052
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DB 1078 AAGCARAAGCGGAGGAA 1094
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DEFINITION AL520270 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
cDNA clone CSODB006YM17 5-PRIME, mRNA sequence.
ACCESSION AL520270
VERSION AL520270.2 GI:31038611
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12783763.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
```

AL520270 1201 bp mRNA linear EST 22-MAY-2003
cDNA clone CSODB006YM17 5-PRIME, mRNA sequence.

AL520270
VERSION AL520270.2 GI:31038611
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12783763.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see


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Db 68 AGGACGGCTCTGTGACGAGCAGCGCGCGCGGAGCGCGAGTCACAGGGCGCTCAC 127
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Qy 226 TGTGGTGGCCACCTTCAGCTGGGAGGAGATTCAGAGCATTAACCTCGGCACGACAGTG 285
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Qy 466 CGGAGGAGCCACGAGGACACGCGCAAGAACTCAAGATCACTGAGGACTTCGCGGCC 525
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RESULT 8

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clone CS0D1001YH12 3-PRIME, mRNA sequence.
ACCESSION
BX355606
VERSION
BX355606.1 GI:30373970
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1. (bases 1 to 1201)
AUTHORS
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1001YH12&cluster=6148.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID: CS0D1001YH12
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/db_xref="taxon:9606"
/clone="CS0D1001YH12"
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
```

BASE COUNT
235 a 359 c 337 g 219 t

Query Match

Best Local Similarity 28.7%; Score 913.4; DB 13; Length 1201;

Matches 96.2%; Pred. No. 1.9e-180;

Mismatches 17; Conservative 15; Indels 7; Gaps 6;

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Db 1015 SCCAACCTTGGGCGCTGGAGAGTCTCCACCCCATCTAGAGTCTCTGACCTGGGC 959

Qy 2199 TTTCACGGGCGCCATTCACCGCTCCCAACTTGGAGCTGTGACCTTGGGACCAAGGG 2258

Db 958 TTTCACGGGCGCCATTCACCGCTCCCAACTTGGAGCTGTGACCTTGGGACCAAGGG 899

Qy 2259 GGAGTCCCTCGTCTTGTGACTCAGAGGAGTGGCCACGTTTCAGGAGGCGGCGGC 2318

Db 898 GGAGTCCCTCGTCTTGTGACTCAGAGGAGTGGCCACGTTTCAGGAGGCGGCGGC 840

Qy 2319 TGGCTCGAGGCTCAGCCCATCTCCAGCTTTTCTCAGGCTGTCTGAGGCTCAAGATT 2378

Db 839 TGGCTCGAGGCTCAGCCCATCTCCAGCTTTTCTCAGGCTGTCTGAGGCTCAAGATT 780

Qy 2379 CTGGAGCAATCTGACCTTCTCCAAAGGCTCTGTTATCAGTGGGAGTGCAGGCCAATC 2438

Db 779 CTGGAGCAATCTGACCTTCTCCAAAGGCTCTGTTATCAGTGGGAGTGCAGGCCAATC 720

Qy 2439 CTTGGCATTTGGGCGGAGCTGGGCGCTTGGAGGCTTGGAGGAGGCTTGGAGCT 2498

Db 719 CTTGGCATTTGGGCGGAGCTGGGCGCTTGGAGGCTTGGAGGAGGCTTGGAGCT 661

Qy 2499 GGGAGGCTCTCGTCCAGGCTTCCCATCTCGGGGCTGCTGTGTGGAAGGCGCTCGCTCAG 2558

Db 660 GGGAGGCTCTCGTCCAGGCTTCCCATCTCGGGGCTGCTGTGTGGAAGGCGCTCGCTCAG 601

more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC005DD09QPI&cluster=6148.f>. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DC005DD09QPI.

FEATURES

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/clone="CS0DC005YH18"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR.V sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 168 a 302 c 250 g 208 t 1 others
ORIGIN

Query Match 26.9%; Score 855.8; DB 9; Length 929;

Best Local Similarity 98.9%; Pred. No. 2.1e-168;

Matches 871; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY	1373	GATCGCCCGCTGCTGAGTCTCTATGTCACAGCATGGCAATTAATACAGGAGAGCC	1432
DB	50	GAATCCCGGATGGAAGTCTCTATGTCACAGCATGGCAATTAATACAGGAGAGCC	109
QY	1433	GCTACTGAGGCGCTGCTGAGCATCATCAGTCTCCTGAAGAAGTCTGGGAAGCTGTGGCT	1492
DB	110	GCTACTGAGGCGCTGCTGAGCATCATCAGTCTCCTGAAGAAGTCTGGGAAGCTGTGGCT	169
QY	1493	GGAGCCTTACCTTCAATGAAGCAGACAGCCCGGGACACCTGTGGGAGGGTGCAG	1552
DB	170	GGAGCCTTACCTTCAATGAAGCAGACAGCCCGGGACACCTGTGGGAGGGTGCAG	229
QY	1553	GTGGGGTGATGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCAGAGGCTGGT	1612
DB	230	GTGGGGTGATGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCAGAGGCTGGT	289
QY	1613	GTATGACTGTTCAGGACCCGATGTTGGATCTTCTCCCTTCTCCTCTCTCTTTTCTC	1672
DB	290	GTATGACTGTTCAGGACCCGATGTTGGATCTTCTCCCTTCTCCTCTCTCTTTTCTC	349
QY	1673	TTACATCTCCCCATAGCACCTCCCTCATGGACCTGCCTCCCTCAGCCCTCAGCC	1732
DB	350	TTACATCTCCCCATAGCACCTCCCTCATGGACCTGCCTCCCTCAGCCCTCAGCC	409
QY	1733	ATCAGCATGCGCTCCAGTGCCTCTAGCCCTTTTCAAGAGCAGAGAGTGCC	1792
DB	410	ATCAGCATGCGCTCCAGTGCCTCTAGCCCTTTTCAAGAGCAGAGAGTGCC	469
QY	1793	ACCGGGGTGGCTGTCTACTCTCATCTCTGCCCCCTAAAGATGGGAGAGACGAGC	1852
DB	470	ACCGGGGTGGCTGTCTACTCTCATCTCTGCCCCCTAAAGATGGGAGAGACGAGC	529
QY	1853	GTCCATGGTCTGGCTGTGAGTCTCCCTTTGACGCTGGTCACTAGGCATCACCCCGC	1912
DB	530	GTCCATGGTCTGGCTGTGAGTCTCCCTTTGACGCTGGTCACTAGGCATCACCCCGC	589
QY	1913	TTTGGTCTTCAGATGCTCTTGGGGTTTATAGGGGAGGCTCTAGTCGGGAGGGCCCT	1972
DB	590	TTTGGTCTTCAGATGCTCTTGGGGTTTATAGGGGAGGCTCTAGTCGGGAGGGCCCT	649
QY	1973	GACCTTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCATTTGTCACCCCTTTTATAGA	2032
DB	650	GACCTTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCATTTGTCACCCCTTTTATAGA	709
QY	2033	GAGGCTGCTTTGTTACAAAGCTCGGGTCTCCCTCTCTGAGCTCGTTTAACTACCGAGG	2092
DB	710	GAGGCTGCTTTGTTACAAARCTCGGGTCTCCCTCTCTGAGCTCGTTTAACTACCGAGG	769

QY	2093	CCTCTCTTAAGATGTCCAGGGCCCCAGCCCGCGGCGACAGCCACCAACCTTTGGGCC	2152
DB	770	CCTCTCTTAAGATGTCCAGGGCCCCAGG-CGCGGGGACACAGCCAGCCCAACCTTTGGGCC	828
QY	2153	CTGGGAAGTCTCTCCACCCCATCACTAGAGTCTCTGACCTTGGGCTTTTCAGGGGCCCA	2212
DB	829	CTGGGAAGTCTCTCCACCCCATCACTAGAGTCTCTGACCTTGGGCTTTTCAGGGGCCCA	888
QY	2213	TTCCACCGCTCCCAACTTGAGCCTGTGACCTTGGGACCA	2253
DB	889	TTCCACCGCTCCCAACTTGAGCCTGTGACCTTGGGACCA	929
RESULT 12			
LOCUS	EX441083	952 bp	mRNA linear EST 15-MAY-2003
DEFINITION	EX441083 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone		
	CS0DF014YM11 5-PRIME, mRNA sequence.		
ACCESSION	EX441083		
VERSION	EX441083.1	GI:30787936	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 952)		
AUTHORS	Li W.B., Gruber C., Jessee J. and Polayes D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6148.f For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF014AG06QPI&cluster=6148.f . Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paradise Avenue Genoscope sequence ID : CS0DF014AG06QPI.		
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	/clone="CS0DF014YM11"		
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	/dev_stage="fetal"		
	/clone_lib="Homo sapiens FETAL BRAIN"		
	/note="Organ: Brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."		
BASE COUNT	237 a 280 c 236 g 168 t	31 others	
ORIGIN			
Query Match	26.7%;	Score 851.2; DB 13; Length 952;	
Best Local Similarity	95.0%;	Pred. No. 1.9e-167;	
Matches	861; Conservative 23; Mismatches 21; Indels 1; Gaps 1;		
QY	81	GCCCGGGCTGCACACACCGGCTGGGAGGCGAGCGCTGTGTGACGAGCAGCGCGCGG	140
DB	48	GCCCGGACAGCAGACACACCGGCTGGGAGGCGAGCGCTGTGTGACGAGCAGCGCGG	107
QY	141	GAGCGCGCAGTGCACCGGGCGCTCACAGTCGGCAGCAGCATGGGAAGGAGGACACCA	200
DB	108	GAGCGCGCAGTGCACCGGGCGCTCACAGTCGGCAGCAGCATGGGAAGGAGGACACCA	167
QY	201	GGCAGAGGGGCGCGCCAGCGGAGGTGTGGTGGCCACCTTCAGCTGGGAGGATTCAG	260
DB	168	GGCRAAGGGGCGCGCCAGACGAAAGTGTGGTACCCACCTTCARCTGGGAGGATTCAA	227

QY 1302 TTCACTGACACCTTAACTTCAGATTGAGCACCACTCTTCCACCATGCCCGGCAC 1361
 Db 718 TTCACTGACACCTTAACTTCAGATTGAGCACCACTCTTCCACCATGCCCGGCAC 777
 QY 1362 AACTTACACAGATCGCCCGCTGTGTGAAGTCTCTATGTGCAGAGCATGGGATGAATAC 1421
 Db 778 AACTTACACAGATCGCCCGCTGTGTGAAGTCTCTATGTGCAGAGCATGGGATGAATAC 837
 QY 1422 CAGGAGAGCCGCTACTGAGGCGCTGTGTGACATCATCAGTCCCTGAAGAGTCTGGG 1481
 Db 838 CAGGAGAGCCGCTACTGAGGCGCTGTGTGACATCATCAGTCCCTGAAGAGTCTGGG 897
 QY 1482 AGCTGTGTGGTGGAGCCCTACTCTTCAAAAAGAAGC 1517
 Db 898 AAGCTGTGTGGTGGAGCCCTACTCTTCAAAAAGAAGC 933

RESULT 14
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 LOCUS 602659806F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803192 5',
 DEFINITION mRNA sequence.
 ACCESSION BG696762
 VERSION BG696762.1 GI:13962248
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 CONTACT: Robert Strausberg, Ph.D.
 Email: c9apb3-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10698 row: k column: 01
 High quality sequence start: 3
 High quality sequence stop: 876.
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 /db_xref="taxon:9606"
 /clone="IMAGE:4803192"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI CGAP Skn3"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site: 2: SalI; Cloned unidirectionally. Primer: Oligo.dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI CGAP Library."
 BASE COUNT 148 a 305 c 258 g 200 t
 ORIGIN

Query Match 26.5%; Score 845; DB 10; Length 912;
 Best Local Similarity 96.7%; Pred. No. 3.7e-166;
 Matches 884; Conservative 0; Mismatches 26; Indels 4; Gaps 2;

QY 1431 CCGTACTGAGGCGCCCTGTGTGACATCATCAGTCCCTGAAGAGTCTGGGAGCTGTGG 1490
 Db 1 CCGTACTGAGGCGCCCTGTGTGACATCATCAGTCCCTGAAGAGTCTGGGAGCTGTGG 60
 QY 1491 CTGGAGCCCTACTTCAAAATGAAGCCACAGCCCCCGGACACCGTGGGAGAGGGTGC 1550
 Db 61 CTGGAGCCCTACTTCAAAATGAAGCCACAGCCCCCGGACACCGTGGGAGAGGGTGC 120

FEATURES
 source

QY 1551 AGTGGGGTCATGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCTG 1610
 Db 121 AGTGGGGTCATGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCTG 180
 QY 1611 GTGTATGCACTGCTCAGGACCCCATGTTGGATCTTTCTCCCTTTCTCCTCTCCTTTTC 1670
 Db 181 GTGTATGCACTGCTCAGGACCCCATGTTGGATCTTTCTCCCTTTCTCCTCTCCTTTTC 240
 QY 1671 TCTTTCATCTCCCTCCCATAGCACCTTGCCTCATGGGACCTGCCCTCCCTCCCTCAGCGTCTAG 1730
 Db 241 TCTTTCATCTCCCTCCCATAGCACCTTGCCTCATGGGACCTGCCCTCCCTCCCTCAGCGTCTAG 300
 QY 1731 CATTAGCATGCGCCCTCCAGTGCCTCTAGCCCTTCTCCNAGGACAGAGGCTG 1790
 Db 301 CATTAGCATGCGCCCTCCAGTGCCTCTAGCCCTTCTCCNAGGACAGAGGCTG 360
 QY 1791 CCACCGGGGGTGGCTCTGTCTTACCTTCCACTCTCTGCCCCCTAAAGATGGGAGGACACAG 1850
 Db 361 CCACCGGGGGTGGCTCTGTCTTACCTTCCACTCTCTGCCCCCTAAAGATGGGAGGACACAG 420
 QY 1851 CGGTTCATGGGTGCGCTGTGAGTCTCCCTTGCAGCCCTGCTCACTAGGCAATACCCCC 1910
 Db 421 CGGTTCATGGGTGCGCTGTGAGTCTCCCTTGCAGCCCTGCTCACTAGGCAATACCCCC 480
 QY 1911 GCTTTGGTTCTTCAGATGCTCTTGGGGTTCATAGGGGCAGGTCCTAGTCCGGCAGGGCCC 1970
 Db 481 GCTTTGGTTCTTCAGATGCTCTTGGGGTTCATAGGGGCAGGTCCTAGTCCGGCAGGGCCC 540
 QY 1971 CTGACCCCTCCCGGCTGGCTTCACTCTCCCTGACGGTCCCATTTGGTCCACCTTTTCATA 2030
 Db 541 CTGACCCCTCCCGGCTGGCTTCACTCTCCCTGACGGTCCCATTTGGTCCACCTTTTCATA 600
 QY 2031 GAGAGGCTCTTTGTTTACAAAGCTCGGGTCTCCCTCTGACGCTCGGTAAAGTACCCGA 2090
 Db 601 GAGAGGCTCTTTGTTTACAAAGCTCGGGTCTCCCTCTGACGCTCGGTAAAGTACCCGA 660
 QY 2091 GGCTCTCTTAAGATGTCAGGGCCCGCCAGGCGGGGACAGCCAGCCAAACCTTTGGG 2150
 Db 661 GGCTCTCTTAAGATGTCAGGGCCCGCCAGGCGGGGACAGCCAGCCAAACCTTTGGG 720
 QY 2151 CCTGGAAGAGTCTCCACCCATCACTAGAGTGTCTGACCTGGGCTTTTCAC-GGGCC 2209
 Db 721 CCTGGAAGAGTCTCCACCCATCACTAGAGTGTCTGACCTGGGCTTTTCACGGGGCC 780
 QY 2210 CATTTCACCGCTCCCGCAACTGTGACCTTGGGACCAAGGGGGAGTCCCTCG 2269
 Db 781 CATTTCACCGCTCCCGCAACTGTGACCTTGGGACCAAGGGGGAGTCCCTCG 840
 QY 2270 TCTTGTGACTCAGCAGGAGGAGTGGCCAGTTCAGGGAGGGCGCGCTGGCTGGAGG 2329
 Db 841 TCTTGTGACTCAGCAGGAGGAGTGGCCAGTTCAGGGAGGGCGCGCTGGCTGGAGG 2397
 QY 2330 CTCAGCCCACTTC 2343
 Db 898 CTCAGCCCACTTC 911

RESULT 15
 BG696015
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 DEFINITION mRNA sequence.
 ACCESSION BG696015
 VERSION BG696015.1 GI:13960717
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10692 row: p column: 15
 High quality sequence stop: 867.
 Location/Qualifiers

FEATURES

source

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 /lab_host="DH10B (TI phage-resistant)"
 /clone_lib="NCI CGAP Skn3"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."
 166 a 268 c 315 g 178 t

BASE COUNT
 ORIGIN

Query Match 26.4%; Score 841.6; DB 10; Length 927;
 Best Local Similarity 98.3%; Pred. No. 1.9e-165;
 Matches 914; Conservative 0; Mismatches 9; Indels 7; Gaps 6;

2065 CTCCTGACGTCGGTTAAGTACCCGAGGCTCTCTTAAGATGTCAGGGGCCAGGGCCG 2124
 1 CTCCTGACGTCGGTTAAGTACCCGAGGCTCTCTTAAGATGTCAGGGGCCAGGGCCG 59

2125 CGGACACACCCAGCCCAACCTTGGGCTCGAGAGATCTCCACCCCATCACTAGAGTG 2184
 60 CGGACACACCCAGCCCAACCTTGGGCTCGAGAGATCTCCACCCCATCACTAGAGTG 119

2185 CTCTGACCTGGCTTTACGGGCCCCATTCCACGGCTCCGCCAATCTGAGCTGTGACC 2244
 120 CTCTGACCTGGCTTTACGGGCCCCATTCCACGGCTCCGCCAATCTGAGCTGTGACC 179

2245 TTGGGACCAAGGGGAGTCCCTCTCTCTGTGACTCAGAGGAGGAGTGGCCAGTTTC 2304
 180 TTGGGACCAAGGGGAGTCCCTCTCTCTGTGACTCAGAGGAGGAGTGGCCAGTTTC 239

2305 AGGGAGGCGCGCTGGCTGGAGGCTCAGGCCACCTCCAGCTTTTCTCAGGGTGTCC 2364
 240 AGGGAGGCGCGCTGGCTGGAGGCTCAGGCCACCTCCAGCTTTTCTCAGGGTGTCC 299

2365 TGAGGTCCAGATTCTGGAGCAATCTGACCTCTTCCAAAGGCTCTGTATCAGCTGGC 2424
 300 TGAGGTCCAGATTCTGGAGCAATCTGACCTCTTCCAAAGGCTCTGTATCAGCTGGC 359

2425 AGTGCCAGCAATCCCTGGCCATTTGGCCCCA-GGGGACGTGGGCCCTCGCAGGTCGAGG 2484
 360 AGTGCCAGCAATCCCTGGCCATTTGGCCCCA-GGGGACGTGGGCCCTCGCAGGTCGAGG 418

2485 AGGGCACTGGAGTGGAGTCTCGTCCAGCCCTCCCACTCGGGGCTGTGTGGA 2544
 419 AGGGCACTGGAGTGGAGTCTCGTCCAGCCCTCCCACTCGGGGCTGTGTGGA 478

2545 CGGCGTGGCTCAGGCACCTCTCTGTCTGAACCTGCCCTTACTGTGTTAACTGTGTCT 2604
 479 CGGCGTGGCTCAGGCACCTCTCTGTCTGAACCTGCCCTTACTGTGTTAACTGTGTCT 538

2605 CAGGATGATTTCTGATAGAGGGGCGGCGAGGCTGGGCTGTGACATCTGCCCTTC 2664
 539 CAGGATGATTTCTGATAGAGGGGCGGCGAGGCTGGGCTGTGACATCTGCCCTTC 598

2665 ACCACATGCGCTTGGCTCGGTGGCTCTGACTGTCTAGGAGGGGCCAGGAGGCGGG 2724
 599 ACCACATGCGCTTGGCTCGGTGGCTCTGACTGTCTAGGAGGGGCCAGGAGGCGGG 658

2725 AGGAGTCTCAGGAGGAGGCTGCCCTCAGGGGCTGGGGGAGGAGTACCTCATGAGACCA 2784
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2785 GGGTGGAGCTCAGAAGAGGAGGAGGTTGGGGCTGGAGGTCTGGTAGCTGAGGGGACGG 2844
 Db GGTGGAGCTCAGAAGAGGAGGAGGTTGGGGCTGGAGGTCTGGTAGCTGAGGGGACGG 777

2845 CAAGTGAAGGGGAGGAGGAGGAGTCTCGGAGGATCTCGAGCTGC-TGTTGAGTCTAA 2903
 Db CAAGTGAAGGGGAGGAGGAGGAGTCTCGGAGGATCTCGAGCTGCTTTGTCAGTCTAA 837

2904 CCCACTAATCAGTCTTTAGATTTCAGGGGAGGAGGAGG-CACCAACAACCTCAGATGGGG 2962
 Db CCCACTAATCAGTCTTTAGATTTCAGGGGAGGAGGAGGAGGAGGAGGAGGAGG 897

2963 CTTTCGGGG--AGGGCGCTAGTCCCGCCA 2990
 Db CTTTCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 927

RESULT 16
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 DEFINITION AGENCOURT_8294640 Lupski_sympathetic_trunk Homo sapiens cDNA clone
 IMAGE:6194559 5', mRNA sequence.
 ACCESSION BQ717429
 VERSION BQ717429.1 GI:21856326
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (Bases 1 to 914)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1359 row: p column: 16
 High quality sequence stop: 663.
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 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski_sympathetic_trunk"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCAACGCGTCCG-3' and 5'-GACATGTTAGATCGGAGCGGCGGCGCTT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

BASE COUNT
 ORIGIN

208 a 283 c 224 g 199 t


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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 882)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13291 row: a column: 04
High quality sequence stop: 655.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."
BASE COUNT 162 a 283 c 234 g 203 t
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Best Local Similarity 99.2%; Pred. No. 4.6e-163;
Matches 866; Conservative 0; Mismatches 3; Indels 4; Gaps 3;
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DB 1 GAGCCCTCTTTTCTCCTCACTTATCAGGTTCTCGAGGACCACTGGTTTGTGGGTC 60
QY 1192 CACAGATGAATCATCTGTCATGAGATTGACAGGAGGCGTACCGTGTGTCAGTGA 1251
DB 61 CACAGATGAATCATCTGTCATGAGATTGACAGGAGGCGTACCGTGTGTCAGTGA 120
QY 1252 GCCAGCTGACAGCCACTGCAAGCTGAGAGAGTCTTCTCAACGACTGTTCACTGGAC 1311
DB 121 GCCAGCTGACAGCCACTGCAAGCTGAGAGAGTCTTCTCAACGACTGTTCACTGGAC 180
QY 1312 ACCTTAATCTCCAGATTGAGCACACCTCTTCCACCACCATGCCCGGCAACTTACACA 1371
DB 181 ACCTTAATCTCCAGATTGAGCACACCTCTTCCACCACCATGCCCGGCAACTTACACA 240
QY 1372 AGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGCGATTGAATACAGGAGAGC 1431
DB 241 AGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGCGATTGAATACAGGAGAGC 300
QY 1432 CGCTACTGAGGGCCCTGCTGAGCATCATCAGTCCCTGGAAGTCTCGGAAGCTGTGGC 1491
DB 301 CGCTACTGAGGGCCCTGCTGAGCATCATCAGTCCCTGGAAGTCTCGGAAGCTGTGGC 360
QY 1492 TGAAGCGCTACCTTCAAAATGAAGCCACAGCCCCCGGACACCGTGGGAAAGGGTGA 1551
DB 361 TGAAGCGCTACCTTCAAAATGAAGCCACAGCCCCCGGACACCGTGGGAAAGGGTGA 420
QY 1552 GGTGGGTGATGCGCAGAGAAATGATGGGCTTTTGTCTGAGGGTGTCCGAGAGCTGG 1611
DB 421 GGTGGGTGATGCGCAGAGAAATGATGGGCTTTTGTCTGAGGGTGTCCGAGAGCTGG 480
QY 1612 TGATGACACTGCTCAGGAGCCCATGTTGATCTTCTCCCTTCTCTCTCTCTCTCTCTCT 1671

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Db 481 TGTATGCACTGCTCAGCGAGCCCAATGTTGGATCTTTCTCCCTTCTCTCTCTCTCT 540
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Db 541 CTTTCACTCTCCCTCAGATGAGCCCTGCTCAGTGGAGCTGCTCCTCCTCAGCGTCAGC 600
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Db 601 CATCAGCATGCGCTCCCAAGTGGCTCCTAGCCCTTCTTCCAGGAGCAGAGAGTGGC 660
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QY 1852 GGTCCATGGGTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGG 1911
Db 721 GGTCCATGGGTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGG 780
QY 1912 CTTTGG-TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1969
Db 781 CTTTGGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
QY 1970 CC--TGACCTCTCCCGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2000
Db 841 CCCTGGACCTTCCCGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 873
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DEFINITION clone IMAGE:6179733 5', mRNA sequence.
ACCESSION BQ883702
VERSION BQ883702.1 GI:22275710
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 926)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13561 row: f column: 22
High quality sequence stop: 586.
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/clone_lib="Lupski dorsal root ganglion"
/notes="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACATAGTCTAGATCGGAGCGGCGGCTT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

```


Db	421	CTGTCTCACTCTCACTCTCTGTCCCTTAAAGATGGAGGACACGAGCGGTCCATGGGCTTG	480
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Db	481	GCCTGTGAGTCTCCCTCTTGAGCCCTGGTGTCACTAGGCATCACCCCGCTTTTGGTTCCTTCAG	540
Qy	1926	ATGCTCTTTGGGTTTCATAGGGCAGTTCCTAGTCGGCAGGCGCCCTGACCTCCCGGCC	1985
Db	541	ATGCTCTTTGGGTTTCATAGGGCAGTTCCTAGTCGGCAGGCGCCCTGACCTCCCGGCC	600
Qy	1986	TGGCTTCACCTCTCCCTCAGCGCTGCCATTTGGTCCACCCCTTTCATAGAGAGCGCTGCTTTC	2045
Db	601	TGGCTTCACCTCTCCCTCAGCGCTGCCATTTGGTCCACCCCTTTCATAGAGAGCGCTGCTTTC	660
Qy	2046	TTACAAAGCTCGGGTCTCCCTCTCTGAGCTCGGTTAAGTACCGAGGCTCTCTTAAGAT	2105
Db	661	TTACAAAGCTCGGGTCTCCCTCTCTGAGCTCGGTTAAGTACCGAGGCTCTCTTAAGAT	720
Qy	2106	GTCAGGGGCCAGCGCCGGGGCACAGCCAGCCAAACCTTGGGCCCTCGAAGAGTCCCT	2165
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Db	781	CCGACCCATCCTAGAGTGTCTGTACCCCTGGGTTTCACGGGCCCATTCACCGGCTCC	840
Qy	2226	C	2226
Db	841	C	841
RESULT	22		
LOCUS	BG674567	931 bp	mRNA
DEFINITION	602620383F1 NCI_CGAP_skn3 Homo sapiens cDNA clone IMAGE:4745853	5'	linear EST 01-MAY-2001
ACCESSION	BG674567		mRNA sequence.
VERSION	BG674567.1	GI:13905963	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 931)		
JOURNAL	NIH-MGSC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapsb@mail.nih.gov		
	Tissue Procurement: James Cleaver, M.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA		
	Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLAM10593 row: e column: 22		
	High quality sequence start: 22		
	High quality sequence stop: 864.		
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	Average insert size 1.5kb. Library constructed by Life		
	Technologies. Note: this is a NCI CGAP Library."		
BASE COUNT	151 a	301 c	273 g 206 t
ORIGIN			

[illegible]

Site 2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT	196 a	319 c	320 g	213 t	
ORIGIN					
Query Match	25.8%; Score 820; DB 13; Length 1048;				
Best Local Similarity	96.6%; Pred. No. 6.4e-161;				
Matches	891; Conservative	0; Mismatches	25; Indels	6; Gaps	5;
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Db	1	GTCTAGTCGGGAGGCGCCCTGACCTCCCGGCTGGCTTCACCTCTCCCTGACGGCTGC	60		
QY	2011	CATTGTCACCCCTTCATAGAGAGGCGCTGTTGTTACAAAGCTCGGGTCTCCCTCTG	2070		
Db	61	CATTGTCACCCCTTCATAGAGAGGCGCTGTTGTTACAAAGCTCGGGTCTCCCTCTG	120		
QY	2071	CAGCTCGGTTAGTACCCGAGGCTCTCTTAAGATGTCAGGGCCCGAGGCCGCGGCA	2130		
Db	121	CAGCTCGGTTAGTACCCGAGGCTCTCTTAAGATGTCAGGGCCCGAGGCCGCGGCA	180		
QY	2131	CAGCCAGCCCAACCTTGGGCGCTGGAAGAGTCTCCACCCCATCACTAGAGTGTCTGA	2190		
Db	181	CAGCCAGCCCAACCTTGGGCGCTGGAAGAGTCTCCACCCCATCACTAGAGTGTCTGA	240		
QY	2191	CCCTGGGCTTCACGGGCGCCATTCCACCGCTCCCACTTGGAGCTGTGACCTTGGGA	2250		
Db	241	CCCTGGGCTTCACGGGCGCCATTCCACCGCTCCCACTTGGAGCTGTGACCTTGGGA	300		
QY	2251	CCAAAGGGGAGTCCCTCTCTTGTGACTCAGCAGAGGAGTGGCCACGTTTCAGGGAG	2310		
Db	301	CCAAAGGGGAGTCCCTCTCTTGTGACTCAGCAGAGGAGTGGCCACGTTTCAGGGAG	360		
QY	2311	GGGCCGCTGGCTGAGGCTGACCCACCTCCAGCTTTCTCTCAGGGTGTCTGAGGT	2370		
Db	361	GGGCCGCTGGCTGAGGCTGACCCACCTCCAGCTTTCTCTCAGGGTGTCTGAGGT	420		
QY	2371	CCAAGATTCTGGAGCAATCTGACCTCTCCAAAGGCTCTGTATCAGCTGGGAGTGC	2430		
Db	421	CCAAGATTCTGGAGCAATCTGACCTCTCCAAAGGCTCTGTATCAGCTGGGAGTGC	480		
QY	2431	AGCCAAATCCCTGGCCATTTGGCCCGAGGGGAGTGGGCCCTGCGAGGCTGCGAGGGCA	2490		
Db	481	AGCCAAATCCCTGGCCATTTGGCCCGAGGGGAGTGGGCCCTGCGAGGCTGCGAGGGCA	539		
QY	2491	CTGGAGCTGGAGTCTCTGTCAGGCTCCCGCTCTGGGCTGCTGTGAGGAGCGGC	2550		
Db	540	CTGGAGCTGGAGTCTCTGTCAGGCTCCCGCTCTGGGCTGCTGTGAGGAGCGGC	599		
QY	2551	TGCCTCAGGCACTCTCTCTGTGAACCTGCGCTTACTGTGTTAACTGTCTCCAGGA	2610		
Db	600	TGCCTCAGGCACTCTCTCTGTGAACCTGCGCTTACTGTGTTAACTGTCTCCAGGA	659		
QY	2611	TGCATTTCTATAGAGGGGCGGAGGCTGGGCTTGTCGCAATCTGCTTTTCCACCA	2670		
Db	660	TGCATTTCTATAGAGGGGCGGAGGCTGGGCTTGTCGCAATCTGCTTTTCCACCA	719		
QY	2671	TGGCCTTGCTCTCGTGGCCCTGACTGTCTGAGGAGGGCCAGGAGCGGAGGG	2728		
Db	720	TGGCCTTGCTCTCGTGGCCCTGACTGTCTGAGGAGGGCCAGGAGCGGAGGG	779		
QY	2729	AGTCTCAGGAGGAGCTG-CCCTGAGGGCTGGGAGGGGTACCTCATGAGACAGGG	2787		
Db	780	AGTCTCAGGAGGAGCTGCGCCCTGAGGGCTGGGAGGGGTACCTCATGAGACAGGG	839		
QY	2788	TGGAGCTGGAAGAGGAGGAGTGGGGGCTGG-AGGTCTGTGTAGCTGAGGGGAGCGGC	2845		
Db	840	TGGAGCTGGAAGAGGAGGAGTGGGGGCTTGAAGTGTCTGTGTAAGTGGGGAGCGGT	899		

QY	2846	AAGTGAGAGGGAGGGAGGAGGAA	2867		
Db	900	AATTGAAGGAGGAGGAGGAA	921		
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LOCUS	BG743088	894 bp	mRNA	linear	EST 15-MAY-2001
DEFINITION	602634223F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779461 5',				
ACCESSION	BG743088				
VERSION	BG743088.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 894)				
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: rsapbs@mail.nih.gov Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: L4M10636 row: n column: 06 High quality sequence stop: 845.				
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BASE COUNT	170 a	282 c	239 g	203 t	
ORIGIN					
Query Match	25.7%; Score 819.2; DB 10; Length 894;				
Best Local Similarity	97.5%; Pred. No. 9.3e-161;				
Matches	874; Conservative	0; Mismatches	18; Indels	4; Gaps	4;
QY	1192	CACAGATGAATCATCATGTCATGAGATTGACAGGAGGCTACCGTACTGTTTCACTA	1251		
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QY	1252	GCACAGCTGACAGCACCACTGCAAGCTGGAGCAGTCTTCTTCAACGACTGTTTCACTG	1311		
Db	61	GCACAGCTGACAGCACCACTGCAAGCTGGAGCAGTCTTCTTCAACGACTGTTTCACTG	120		
QY	1312	ACCTTAACTTCCAGATTGAGCACCACTTTCCTCCCACTGCTCCCGGACCACTTACACA	1371		
Db	121	ACCTTAACTTCCAGATTGAGCACCACTTTCCTCCCACTGCTCCCGGACCACTTACACA	180		
QY	1372	AGATCGCCCGCTGGTGAAGTCTCTATGTCGAAGCATGCAATGATACCGAGGAGAC	1431		
Db	181	AGATCGCCCGCTGGTGAAGTCTCTATGTCGAAGCATGCAATGATACCGAGGAGAC	240		
QY	1432	CGTACTGAGGGCCCTGCTGGACATCATCAGTTCCTGTGAAGAGTCTGGGAAGCTGTGGC	1491		
Db	241	CGTACTGAGGGCCCTGCTGGACATCATCAGTTCCTGTGAAGAGTCTGGGAAGCTGTGGC	300		
QY	1492	TGGACGCTACCTTTCACAAATGAAGCCACAGCCCGGGGACACCGTGGGAGGGGTGCA	1551		

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Db 301 TGAAGCCTACCTTCAAAATGAAGCAACAGCCCCGGGACACCGTGGGGAAGGGGTGA 360
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Db 361 GGTGGGGTATGACCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCTGG 419
Qy 1612 TGTATGACATCTCAGGAGCCCATGTTGGATCTTTCTCCCTTCTCCTCTCTCTTTTCT 1671
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Qy 1852 GGTCCATGGTCTGGCCCTGTAGTCTCCCTTGGAGCCCTGCTCACTAGGATCACCCCG 1911
Db 660 GGTCCATGGTCTGGCCCTGTAGTCTCCCTTGGAGCCCTGCTCACTAGGATCACCCCG 719
Qy 1912 CTTTGGTCTTTCAGATCTCTTGGGGTTCATAGGGCA-GGTCTAGTGGGAGGGCC 1970
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Qy 1971 CTGACCTCCCGCTGGCTTCACTCTCCCTGACGGCTGCATGTGTCACCTTTTATA 2030
Db 780 CTGACCTCCCGG-CTGGCTTCACTCTCCCTGACGGTGGCATGTGTCACCTTTTATA 838
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VERSION BX440551.1 GI:30781858
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 868)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DF008BF03QF1.
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vector. Library was not normalized."
BASE COUNT 180 a 272 c 216 g 199 t 1 others
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Query Match 25.6%; Score 814.6; DB 13; Length 868;
Best Local Similarity 99.9%; Pred. No. 8.5e-160;
Matches 814; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1080 AGCTACTACATCCGGTCTTTCATCACCTACATCCCTTCTACGSCATCTTGGGAGCCCTC 1139
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Qy 1140 CTTTTCCTCAACTTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGGGTACACAGATG 1199
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Qy 1200 AATCAGATCGTCATGAGATTGACAGAGGCTTACCGTGACTGGTTCAGTAGCCAGCTG 1259
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Qy 1260 ACAGCCACTGCAACGCTGGAGCAGTCTTCTTCAACGACTGGTTTCAGTGGACACTTAAC 1319
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Qy 1320 TTCAGATTGACAGCCACTCTTCCACCATGCCCCGGGACACTTACACAGATCGCC 1379
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RESULT 27
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LOCUS
DEFINITION BQ880510 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6339071

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linear EST 16-AUG-2002
BQ880510
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ACCESSION BQ880510
VERSION BQ880510.1 GI:22272518
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 936)
AUTHORS Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgs.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2533 row: e column: 24
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            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GGACACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: This is a NIH MGC Library."
        166 a 279 c 300 g 186 t 5 others
BASE COUNT
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Best Local Similarity 96.7%; Pred. NO. 2.2e-159;
Matches 882; Conservative 0; Mismatches 22; Indels 8; Gaps 5;
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Db 361 CTGSCCTGGAGGCTCAGCCCCACCTCTCCAGCTTTTCTCAGGGTGTCTCAGGTCACAGAT 420
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Db 421 TCTGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTTATCAGCTGGGAGTCCAGCCCAAT 480
Qy 2438 CCCTTGGCCATTGTCGCCCGGAGGACCTGGGCCCTGCGAGGCTGCAGAGGCGCACTGGAGC 2497
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Db 839 AAAAAGNAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 898
Qy 2852 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 898
Db 899 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 910
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VERSION BX354479.1 GI:30379876
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ORGANISM Homo sapiens
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Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
1 (bases 1 to 948)
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0DC020BH1IQ1&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      157 a      296 c      281 g      209 t
ORIGIN
Query Match      25.5%; Score 811.4; DB 13; Length 948;
Best Local Similarity 97.5%; Pred. No. 4e-159;
Matches 861; Conservative 5; Mismatches 11; Indels 6; Gaps 4;
QY 1840 GAGGAGCAGCGGTCCATGGCTCTGGCTGTGAGCTCCCTTGAGCGCTGGTCACTAG 1899
Db |-----|-----|-----|-----|-----|-----|-----|
QY 67 GAGGAGCAGCGGTCCATGGCTCTGGCTGTGAGCTCCCTTGAGCGCTGGTCACTAG 126
Db |-----|-----|-----|-----|-----|-----|-----|
QY 1900 GCATCACCCCGCTTTGGTCTTTCAGATGCTCTTGGGTTTCATAGGGCAGTCTCTAGTC 1959
Db |-----|-----|-----|-----|-----|-----|-----|
QY 127 GCATCACCCCGCTTTGGTCTTTCAGATGCTCTTGGGTTTCATAGGGCAGTCTCTAGTC 186
Db |-----|-----|-----|-----|-----|-----|-----|
QY 1960 GGGCAGGGCCCTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCCATTGGTCC 2019
Db |-----|-----|-----|-----|-----|-----|-----|
QY 187 GGGCAGGGCCCTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCCATTGGTCC 246
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2020 ACCCTTTTCATAGAGAGCGCTCTTTGTTCAAAAGCTCGGCTCTCCCTCTGAGCTCGGT 2079
Db |-----|-----|-----|-----|-----|-----|-----|
QY 247 ACCCTTTTCATAGAGAGCGCTCTTTGTTCAAAAGCTCGGCTCTCCCTCTGAGCTCGGT 306
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2080 TAAGTACCCAGGCTCTCTTAGATGTCACAGGGCCCGAGCCCGGGCAGACAGCCAGC- 2138
Db |-----|-----|-----|-----|-----|-----|-----|
QY 307 TAAGTACCCAGGCTCTCTTAGATGTCACAGGGCCCGAGCCCGGGCAGACAGCCAGC 366
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2139 --CCAAACCTTGGCCCTGGAAGAGTCTCCACCCCATCACTAGTGTCTGACCCCTGG 2196
Db |-----|-----|-----|-----|-----|-----|-----|
QY 367 CGCAACCGCTTGGCCCTGGAAGAGTCTCCACCCCATCACTAGTGTCTGACCCCTGG 426
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2197 GCTTTACGGGCCCCCATTCACCGCTCCCGCACTTGAGCTGTGAGCTTGGACCCAAAG 2256
Db |-----|-----|-----|-----|-----|-----|-----|
QY 427 GCTTTACGGGCCCCCATTCACCGCTCCCGCACTTGAGCTGTGAGCTTGGACCCAAAG 486
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2257 GGGAGTCCCTGCTCTCTGTGACTCAGCAGAGCAGTGGCCACAGTTCAGGAGGGGCGG 2316
Db |-----|-----|-----|-----|-----|-----|-----|
QY 487 GGGAGTCCCTGCTCTCTGTGACTCAGCAGAGCAGTGGCCACAGTTCAGGAGGGGCGG 546
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2317 GCTGGCTGAGGCTCAGCCCAACCTCCAGCTTTTCTCAGGTGTCTGAGTCTCAAGA 2376
Db |-----|-----|-----|-----|-----|-----|-----|
QY 547 GCTGGCTGAGGCTCAGCCCAACCTCCAGCTTTTCTCAGGTGTCTGAGTCTCAAGA 606
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2377 TTCTGGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTTATCAGCTGGGCACTGCCACAA 2436
Db |-----|-----|-----|-----|-----|-----|-----|
QY 607 TTCTGGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTTATCAGCTGGGCACTGCCACAA 666
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2437 TCCCTGGCCATTGGCCCCAGGGGAGCGTGGGCCCTCGAGCTGCAGGGGCACTGGAG 2496
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QY 667 TCCCTGGCCATTGGCCCCAGGGGAGCGTGGGCCCTCGAGCTGCAGGGGCACTGGAG 725
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QY 2497 CTGGAGGTCTGCTGCCAGCCCTCCCATCTCGGGGCTGTGTGTGAGACGGCGCTGCCTC 2556
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QY 726 CTGGAGGTCTGCTGCCAGCCCTCCCATCTCGGGGCTGTGTGTGAGACGGCGCTGCCTC 785
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2557 AGGCACTCTCTGTCTGAACCTGCGCTTACTGTGTGTTTAACTGTGTCTCAGGATGATT 2616
Db |-----|-----|-----|-----|-----|-----|-----|
QY 786 AGGCACTCTCTGTCTGAACCTGCGCTTACTGTGTGTTTAACTGTGTCTCAGGATGATT 845
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2617 CTGATAGAGGGGGGGGAGGGGCT--GGGCTGTGAGCAATCTGCTTTTCAACCATGGCC 2675
Db |-----|-----|-----|-----|-----|-----|-----|
QY 846 CTGATAGAGGGGGGGGAGGGGCTTTTGTGACAACTGCTTTTCAACCATGGCC 905
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2676 TTGCC-TCGGTGGCCCTGACTGTCTCAGGGAGGGCCAGGAGGCA 2717
Db |-----|-----|-----|-----|-----|-----|-----|
QY 906 TTGCCCTTGGTGGCCCTGACTGTCTATGTRTGGCAAGGAGGCA 948
Db |-----|-----|-----|-----|-----|-----|-----|
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RESULT 29
AL559446/c
LOCUS
DEFINITION
Homo sapiens cDNA clone CS0DJ013YD17 3-PRIME, mRNA sequence.
ACCESSION
AL559446
VERSION
AL559446.2 GI:31283578
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 928)
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12904956.
```

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COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6148.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ013CB09NP1&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DJ013CB09NP1.
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Location/Qualifiers
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10-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      185 a      312 c      249 g      163 t      19 others
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ORIGIN
Query Match      25.4%; Score 809.6; DB 9; Length 928;
Best Local Similarity 96.0%; Pred. No. 9.5e-159;
Matches 855; Conservative 8; Mismatches 18; Indels 10; Gaps 3;
QY 2262 GTCCCTCTCTCTTGTGACTCAGCAGAGCAGTGGCCACGTTACAGGAGGGCGGCTGG 2321
Db |-----|-----|-----|-----|-----|-----|-----|
QY 894 GTCCCGWATTCGCGGATCTCAGCAGAGGCGAGTGGCCACGTTACAGGAGGGCGGCTGG 835
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2322 CTGAGAGCTCAGCCACCTCCAGCTTTCTCAGGGTGTCTGAGTGTCCAGATTCTG 2381
Db |-----|-----|-----|-----|-----|-----|-----|
QY 834 CTGAGAGCTCAGCCACCTCCAGCTTTCTCAGGGTGTCTGAGTGTCCAGATTCTG 775
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2382 GAGCAATCTGACCCCTTCTCCAAAGGCTCTGTTATCAGCTGGGCGAGTGCACCAATCCCT 2441
Db |-----|-----|-----|-----|-----|-----|-----|
QY 774 GAGCAATCTGACCCCTTCTCCAAAGGCTCTGTTATCAGCTGGGCGAGTGCACCAATCCCT 715
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2442 GGCATTTGGCCCCCAGGGGAGCGTGGGCCCTTCAGGCTGCAGGGGCGGCACTGGAGCTGG 2501
Db |-----|-----|-----|-----|-----|-----|-----|
QY 714 GGCCATTTGGCCCCA--GGGAGCGTGGGCCCTTCAGGCTGCAGGGGCGGCACTGGAGCTGG 656
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2502 AGGTCTCGTCCAGCCCTCCCATCTCGGGGCTGTGTGTGAGACGGCGCTGCCTCAGGCA 2561
Db |-----|-----|-----|-----|-----|-----|-----|
QY 655 AGGTCTCGTCCAGCCCTCCCATCTCGGGGCTGTGTGTGAGACGGCGCTGCCTCAGGCA 596
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QY 2562 CTCTCTGTCTGAACCTGCGCCCTTACTGTGTTTAACTGTGTCTCAGGATGCAATCTGAT 2621
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Db	595	CTCTCCCTGCTGAAACCTCGCCCTTACTGTGTTTAACTGTTCCTCCA-----TCTGAT	544
Qy	2622	AGGAGGGGGGGCAGAGGCGTGGCCCTTGCTGCAATCTGCCTTTTACCACATGGCCTTGCCT	2681
Db	543	AGRGGGGGGGCAGAGGCGTGGCCCTTGTGACAATCTGCCCTTACCACATGGCCTTGCCT	484
Qy	2682	CGGTG-CCCTGACTGTTCAGGAGGGCCAGGAGGCACAGCGGAGGAGTCTCAGAGG	2740
Db	483	CGGTGTGCCCTTACTGTTCAGGAGGGCCAGGAGGCACAGCGGAGGAGTCTCAGAGG	424
Qy	2741	AGGCTGCCCTCAGGGGCTGGGGAGGGGCTACCTCATGAGCACCAAGGTGTGAGCTGAGAAG	2800
Db	423	AGGCTGCCCTCAGGGGCTGGGAGGGGGTACCTCATGAGACCAAGGTGTGAGCTGAGAAG	364
Qy	2801	AGGAGGAGGTGGGGCTTGGAGGTCTCGTGTAGCTGAGGGGACGGGCAAGTCAGAGGGGAGG	2860
Db	363	RGRRGAGGTGGGGGCTTGGAGGTCTCGTGTGCTGAGGGGACGGGCAAGTCAGAGGGGAGG	304
Qy	2861	GAGGGAGTCTCTGGAGGATCCCTGAGCTGTGTGTGTCAGTCTAACCCACTAATCAGTTCCT	2920
Db	303	GRGGAGTCTCTGGAGGATCCCTGTGCTGTGTGTGTCAGTCTAACCCACTAATCAGTTCCT	244
Qy	2921	AGATTAGGGGAAAGGGCAGGCACCAAACTCAGAAATGGGGGCTTTCCGGGAGGGGGCCCT	2980
Db	243	AGATTAGGGGAAAGGGCAGGCACCAACNACTCAGAAATGGGGCTTTCCGGGAGGGGGCCT	184
Qy	2981	AGTCCCCCAGCTCTAAGCAGCCAGGAGGACCTGCATCTAAGCATCTGGGTTGCCATGG	3040
Db	183	AGTCCCCCAGCTCTAAGCAGCCAGGAGGACCTGCATCTAAGCATCTGGGTTGCCATGG	124
Qy	3041	CAATGGCATGCCCCCAGCTACTGTATGCCCCCGACCCCGCAGAGCGCAATGAACCCA	3100
Db	123	CAATGGCATGCCCCCAGCTACTGTATGCCCCCGCAGAGCGCAATGAACCCA	64
Qy	3101	TAGGAGCTGATCGTAATGTTTATCATGTGTACTTCCCAACCCCTACATTTT	3151
Db	63	TAGGAGCTGATCGTAATGTTTATCATGTGTACTTCCCAACCCCTACATTTT	13

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RESULT 30
BO891931
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
BO891931
AGENCOURT 8684379 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6377089
5', mRNA sequence.
BO891931
BO891931.1 GI:22283945
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 950)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-t@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L2CM2560 row: f column: 02
High quality sequence stop: 632.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_types="neuroblastoma, cell_line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_47" /notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8Kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life technologies). Note: this is a NIH_MGC Library."																			
Qy	1958	TCGGCAGGCGCCTGACCCCTCCGGCTGGCTTCACTCTCCCTGAGCGTGCCATTGGT	2017																
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Qy	2018	CCACCTTTTCATAGAGAGGCGCTGTTTGTACAAAGCTCGGGTCTCCCTCGACGCTCG	2077																
Db	61	CCACCTTTTCATAGAGAGGCGCTGTTTGTACAAAGCTCGGGTCTCCCTCGACGCTCG	120																
Qy	2078	GTTAAGTACCGAGGCGCTCTTTAAGATGTCAGGGGCCAGGCGCGGGGCAAGCCAG	2137																
Db	121	GTTAAGTACCGAGGCGCTCTTTAAGATGTCAGGGGCCAGGCGCGGGGCAAGCCAG	180																
Qy	2138	CCCAACCTTTGGGCGCTTGGAAAGTCTCCACCCCATCACTAGAGTGCTCTGACCTGGG	2197																
Db	181	CCCAACCTTTGGGCGCTTGGAAAGTCTCCACCCCATCACTAGAGTGCTCTGACCTGGG	240																
Qy	2198	CTTTCACGGGCCCATTCACCGCCTCCCAATTGAGGCTGTGACTTGGGACCAAAAGG	2257																
Db	241	CTTTCACGGGCCCATTCACCGCCTCCCAATTGAGGCTGTGACTTGGGACCAAAAGG	300																
Qy	2258	GGGAGTCCCTCGTCTTGTGATCTCAGCAGAGCAGTGCCACGTTTCAGGGGGGCCCG	2317																
Db	301	GGGAGTCCCTCGTCTTGTGATCTCAGCAGAGCAGTGCCACGTTTCAGGGGGGCCCG	360																
Qy	2318	CTGCGCTGGAGGCTCAGCCACCCCTCCAGTCTTCTCAGGGTGTCTCAGGTCCTAAGAT	2377																
Db	361	CTGCGCTGGAGGCTCAGCCACCCCTCCAGTCTTCTCAGGGTGTCTCAGGTCCTAAGAT	420																
Qy	2378	TCTGGAGCATCTGACCCCTCTCCAAAGGCTCTGTTATCAGCTGGCAGTGCCAGCCAT	2437																
Db	421	TCTGGAGCATCTGACCCCTCTCCAAAGGCTCTGTTATCAGCTGGCAGTGCCAGCCAT	480																
Qy	2438	CCCTGGGCATTTGGCCCCCAGGGGAGCGTGGGCCCTCGAGGCTCAGAGGGCACTGGAGC	2497																
Db	481	CCCTGGGCATTTGGCCCCCAGGGGAGCGTGGGCCCTCGAGGCTCAGAGGGCACTGGAGC	539																
Qy	2498	TGGAGGTCCTGTCACAGCCCTCCCATCTCGGGGCTGTGTGTGAACGGCGTGCCTCA	2557																
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Qy	2618	TGATAGAGGGGCGGAGGCGTGGGCGCTTGTGAACAATCTGCCCTTTTCAACACATGGCCTT	2677																
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Db      779 AGGAGCTGCTGAGGGGGCTGGGGAGGGGTACCTCATGAGGACGAGGGTGGAGCTG 838
Qy      2796 AGAA-----GAGGAGGAGGTGGGGCTGGAGGTGCTGAGTGGAGGAGCGGCAAGTGA 2851
Db      839 AGAANAAGGAGGAGGGGGGGGGCTGGGAAGGGCTGTAACCTGAGGAGCGGCAATGG 898
Qy      2852 GAGGGGAGGGAG 2863
Db      899 AAGAGGGGAGGG 910

RESULT 31
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DEFINITION
AL525169 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC005YH18 3-PRIME, mRNA sequence.
ACCESSION
AL525169
VERSION
AL525169.2 GI:31043424
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 884)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
COMMENT
On Feb 13, 2001 this sequence version replaced gi:12788662.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC005DD09NP1&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC005DD09NP1.
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 164 a 292 c 240 g 160 t 28 others
ORIGIN

Query Match 25.1%; Score 799.2; DB 9; Length 884;
Best Local Similarity 95.6%; Pred. NO. 1.4e-156;
Matches 846; Conservative 24; Mismatches 10; Indels 5; Gaps 5;

Qy      2265 CTTCTCTCTGTGTCAGAGGAGGAGTGGCCAGCTTCAGGGAGGGGGCGGTGGCT 2324
Db      884 CTTCTCTCTGTGTCAGAGGAGGAGTGGCCAGCTTCAGGGAGGGGGCGGTGGCT 825
Qy      2325 GGAGGCTCAGCCACCCCTCCAGCTTTTCTCAGGGTGTCTGAGGTCCAGATTCGAG 2384
Db      824 GGAGGCTCAGCCACCCCTCCAGCTTTTCTCAGGGTGTCTGAGGHCCAGATTCGAG 765
Qy      2385 CAATCTGACCTTCTCCAAAGCTCTGTATCAGTGGCGAGTCCAGCCATCCCTGGC 2444
Db      764 CAATCTGACCTTCTCCAAAGCTCTGTATCAGTGGCGAGTCCAGCCATCCCTGGC 705
Qy      2445 CATTTGGCCCCAGGGGAGCTGGGCCCTGTCAGGCTGCAGAGGGGACATCGAGCTGGAGG 2504

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Db      704 CATTGGCCCCCA-GGGGACGTGGGGCCCTGCAGGCTGCAGGAGGGCACTGGAGTGGGAG 646
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Db      645 TCTGCTCCSAGCCCTCCCATCTCGGGGCTGCTGTGTGGAGCGGCGCTGCMTCAGGCAM 586
Qy      2563 TCTCTGTCTGAACCTGCCCTTACTGTGTTAACTGTGTTGCTCCAGATGCAATCTTGATA 2622
Db      585 TCGCTGTCTGAACCTGCCCTCACTGTGTTTAACTGCCGCTCCAGATGCAATCTTGATA 526
Qy      2623 GGAGGGGGCGGAGGGCTGGCCCTTGTGACAACTGCTCCCTTTACACACATGGCCCTTCCTC 2682
Db      525 GGAGGGGGCGGAGGGCTGGCCCTTGTGACAACTGCTCCCTTTACACACATGGCCCTTC 466
Qy      2683 GGTGGCCCTCACTGTCTAGGAGGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2742
Db      465 GGTGGCCCTCACTGTCTAGGAGGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 406
Qy      2743 GCTGCCCTGAGGGGCTGGGGAGGGGTACCTCATGAGGACGAGGTGGAGCTGAGAAGAG 2802
Db      405 GCTGCCCTGAGGGGCTGGGGAGGGGAGGACCTCATGAGGACGAGGTGGAGCTGAGAAGAG 346
Qy      2803 GAGGAGGTGGGGGCTGGAGGTGCTGTGAGTGGAGGAGCGGCAAGTGCAGAGGGAGGGA 2862
Db      345 GAGGAGGAGGGGCTGGAGGTGCTGTGAGTGGAGGAGCGGCAAGTGCAGAGGGAGGGA 286
Qy      2863 GGGAGTCTCTGGAGGAGTCTGAGCTGCTGTGAGTCTTAACCCACTCAATCAGTTCTTAG 2922
Db      285 GSGMAGTCTCTGGAGGAGTCTGAGCTGCTGTGAGTCTTAACCCACTCAATCAGTTCTTAG 226
Qy      2923 ATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2982
Db      225 ATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 166
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Qy      3043 ATGGGATCCCCCAGCTTACTGTATGCCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3102
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 AGENCOURT_7786911 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6068929
 5', mRNA sequence.

ACCESSION BQ423614
 VERSION BQ423614.1 GI:21118929

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1. (bases 1 to 841)
 NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Prepared by: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13950 row: n column: 02

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High quality sequence stop: 633.					
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	/lab_host="DH10B (phage-resistant)"				
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	/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."				
BASE COUNT	178 a 267 c 203 g 193 t				
ORIGIN					
<hr/>					
Query Match	25.1%; Score 797.8; DB 13; Length 841;				
Best Local Similarity	98.9%; Pred. No. 2.8e-156;				
Matches	814; Conservative 0; Mismatches 7; Indels 2; Gaps 1;				
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QY	912 CAGCCCATCGAGTCGGCAAGAAGCTGAAATACCTGCCCTACAATCACAGCAGCAA	971			
Dd	1 CAGCCCATCGAGTCGGCAAGAAGCTGAAATACCTGCCCTACAATCACAGCAGCAA	60			
QY	972 TACTTTCTTCTGTATTGGCGCCGCTGCTCATCTCCCATGATNTTCCAGTACCAGATCATC	1031			
Dd	61 TACTTTCTTCTGTATTGGCGCCGCTGCTCATCCCCATGATNTTCCAGTACCAGATCATC	120			
QY	1032 ATGACCATGATCGTCCATAAAGACTGGTGGAACCTGGCCTGGGCCGTGAGCTACTACATC	1091			
Dd	121 ATGACCATGATCGTCCATAAAGACTGGTGGAACCTGGCCTGGGCCGTGAGCTACTACATC	180			
QY	1092 CGGTTCTTCATCAGCTACATCCCTTTCTACGGCATCTGGAGAGCCCTTTTCTCTCAAC	1151			
Dd	181 CGGTTCTTCATCAGCTACATCCCTTTCTACGGCATCTGGAGAGCCCTTTTCTCTCAAC	240			
QY	1152 TTCAATCAGGTTCTCTGGAGAGCACTGGTTGTGTGGGTTCACACAGATGAATCAATCGTC	1211			
Dd	241 TTCAATCAGGTTCTCTGGAGAGCACTGGTTGTGTGGGTTCACACAGATGAATCAATCGTC	300			
QY	1212 ATGAGATTTGACACAGAGAGGCTACCGTGA CTGGTTTCAGTAGCCAGCTGAAGCCACCTGC	1271			
Dd	301 ATGAGATTTGACACAGAGAGGCTACCGTGA CTGGTTTCAGTAGCCAGCTGAAGCCACCTGC	360			
QY	1272 AACGTGAGCAGTCTCTTCTTCAACGACTGGTTCA GTGAGACACCTTAATCTCCAGATTGAG	1331			
Dd	361 AACGTGAGCAGTCTCTTCTTCAACGACTGGTTCA GTGAGACACCTTAATCTCCAGATTGAG	420			
QY	1332 CACCACTCTTTCCCAACATGCCCGCGCA CAACTTTACAAAGATGCGCCCGCTGGTGAAG	1391			
Dd	421 CACCACTCTTTCCCAACATGCCCGCGCGCA CAACTTTACAAAGATGCGCCCGCTGGTGAAG	480			
QY	1392 TCTCTATGTCGCAAGCATGCAATTGATAC CAGAGAGCGCTACTTGAGGGCCCTGCTG	1451			
Dd	481 TCTCTATGTCGCAAGCATGCAATTGATAC CAGAGAGCGCTACTTGAGGGCCCTGCTG	540			
QY	1452 GACATCATCAGGTCCTTGAAAGAGCTCTG GGAAGCTGTGGGTGGACGCTTACCTTCACAAA	1511			
Dd	541 GACATCATCAGGTCCTTGAAAGAGCTCTG GGAAGCTGTGGGTGGACGCTTACCTTCACAAA	600			
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QY 481 AGGACACGCGGAGAGATCAAGATCACTGAGGACTTCGGGCGCTGAGGAAGCGGCTG 540
Db 718 AGGACACGCGGAGAGATCAAGATCACTGAGGACTTCGGGCGCTGAGGAAGCGGCTG 777
QY 541 AGGACATGACCTGTTCAAGACCAACGATGTTCTTCCTCTCTCTCTCTCTCTCT 600
Db 778 AGGACATGACCTGTTCAAGACCAACGATGTTCTTCCTCTCTCTCTCTCTCTCT 837
QY 601 TCGCCCTGGAGAGATTCATGATGTTCACTGTCCTTCTCTCTCTCTCTCTCTCT 660
Db 838 TCGCCCTGGAGAGATTCATGATGTTCACTGTCCTTCTCTCTCTCTCTCTCTCT 897
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Db 898 CCTCATACGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 957
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RESULT 34

BQ928848

LOCUS

DEFINITION

BQ928848

VERSION

BQ928848.1

KEYWORDS

SOURCE

Homo sapiens

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LUCW2667 row: b column: 15

High quality sequence stop: 647.

Location/Qualifiers

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FEATURES

source

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/notes="Organ: prostate; Vector: pOTB7; Site: 1: XhoI;
Site: 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library." 2 others

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BASE COUNT 161 a 279 c 299 g 181 t
ORIGIN

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Query Match 25.1%; Score 797.6; DB 13; Length 922;
Best Local Similarity 93.5%; Pred. No. 3.1e-156;
Matches 864; Conservative 0; Mismatches 56; Indels 4; Gaps 3;

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QY 1945 GGGCAGGTCTAGTTCGGGCGAGGCGCTGACCTCCCGGCTGGCTTCACTCTCCTGTAC 2004
Db 1 GGGCAGGTCTAGTTCGGGCGAGGCGCTGACCTCCCGGCTGGCTTCACTCTCCTGTAC 60
QY 2005 GGTGCGCATTTGCTCCACCTTTTATAGAGAGGCTCTTTTGTACAAAGCTCGGCTTC 2064
Db 61 GGTGCGCATTTGCTCCACCTTTTATAGAGAGGCTCTTTTGTACAAAGCTCGGCTTC 120
QY 2065 CTCCTGAGCTCGGTTAAGTACCGGAGGCTCTTTAAGATGTCCAGGCGCCAGGCGCG 2124
Db 121 CTCCTGAGCTCGGTTAAGTACCGGAGGCTCTTTAAGATGTCCAGGCGCCAGGCGCG 180
QY 2125 CGGCGACAGCGAGCCCAACCTTTGGGCGCTGGAAGAGTCTCTCCACCCATCATAGAGTG 2184
Db 181 CGGCGACAGCGAGCCCAACCTTTGGGCGCTGGAAGAGTCTCTCCACCCATCATAGAGTG 240
QY 2185 CTCTGACCTCGGCTTTTACGGGCGCCCATTCACCGGCTTCCCAAGCTGTGAC 2244
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QY 2245 TTGGGACAAAGGGGAGTCTCTGCTGTGTGATCAGCAGAGGAGTGCACGCTTC 2304
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QY 2783 CAGGGTGGAGCTGAGAGAGGAGGAGCTGGGGGCTGGAGTGTCTGAGCTGAGGGGACG 2842
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QY 2843 GGCAGTGTAGAGGGGAGGAGGGA 2866
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RESULT 35
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ACCESSION BG742060
VERSION BG742060.1 GI:14052713
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10634 row: f column: 05
High quality sequence stop: 841.
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 137 a 306 c 249 g 189 t
ORIGIN
Query Match 25.0%; Score 797.2; DB 10; Length 881;
Best Local Similarity 97.8%; Pred. No. 3.7e-156;
Matches 861; Conservative 0; Mismatches 13; Indels 6; Gaps 5;

QY 1706 GACCTGCTCCCTCCCTCAGCGCTGAGCCATGAGCCATGCGCCCTCCAGGCTCCCTAGGCC 1765
Db 4 GGGACTGCTCCCTCCCTCAGCGCTGAGCCATGAGCCATGCGCCCTCCAGGCTCCCTAGGCC 63

QY 1766 CTTCTTCCAGGAGCAGAGAGTGGCCACCGGGGTGGCTCTGCTACCTCCACTCTCT 1825
Db 64 CTTCTTCCAGGAGCAGAGAGTGGCCACCGGGGTGGCTCTGCTACCTCCACTCTCT 123

QY 1826 GCCCTTAAGATGGGAGGAGACGAGCGGTCCATGGGTCTGGCTGTGAGTCTCCCTTGC 1885
Db 124 GCCCTTAAGATGGGAGGAGACGAGCGGTCCATGGGTCTGGCTGTGAGTCTCCCTTGC 183

QY 1886 AGCTGGTCTACTAGGATACACCCCGCTTGGTCTTTCAGATCTCTGGGTTCATAGG 1945
Db 184 AGCTGGTCTACTAGGATACACCCCGCTTGGTCTTTCAGATCTCTGGGTTCATAGG 243

QY 1946 GGCAGTCTCTAGTCGGGAGGAGGCGCCCTGACCCCTCCGGGCTGGCTTCACTCTCCCTGACG 2005

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Db 244 GGCAGTCTCTAGTCGGGACGGGCCCTTGACCTCCCGGCTGCTCACTCTCCCTGACG 303
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QY 2066 TCCTGCAGCTCGGTTAAGTACCCGAGGCTCTCTTAAGATGTCCAGGGGCCCGAGGCCGC 2125
Db 364 TCCTGCAGCTCGGTTAAGTACCCGAGGCTCTCTTAAGATGTCCAGGGGCCCGAGGCCGC 422
QY 2126 GGGCAGACGACGACCAACCTTGGGCCCTGGAGAGTCTCCACCCCATCCTAGAGTGC 2185
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Db 483 TCTGACCTCGGCTTTCACGGGGCCCAATTCACGGCTCCCACTTGGAGCTGTGACCT 542
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QY 2306 GGGAGGGGCGGCTGGGCTGAGGCTCAGCCACCTCCAGCTTTTCTCAGGGTGTCT 2365
Db 603 GGGAGGGGCGGCTGGGCTGAGGCTCAG-CAACCTCCAGCTTTTCTCAGGGTGTCT 661
QY 2366 GAGTCCAGAGTCTGGAGCAATCTGACCTTCTCCAAAGGCTCTGTATCAGCTGGCA 2425
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RESULT 36
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LOCUS 602808526F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4940503
DEFINITION 5', mRNA sequence.
ACCESSION BG910799
VERSION BG910799.1 GI:14291275
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10879 row: d column: 08
High quality sequence stop: 794.
Location/Qualifiers
1. .909
FEATURES
source

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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 kb. Constructed by Life
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Best Local Similarity 96.8%; Pred. No. 8.8e-156;
Matches 866; Conservative 0; Mismatches 21; Indels 8; Gaps 5;
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DB 1 ACCACCTCTTCCCAACATCCCGGACAACTTACACAGATCGCCCGCTGGTGAAGT 60
QY 1393 CTATATGTGCAAGCATGGCAATTGAATACAGAGAGCGGCTACTGAGGGCCCTGCTGG 1452
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QY 1453 ACATCATCAGGTCCTTGAAGAGCTGGGAAGCTGGGTGGAGCGCTACCTTCACAAAT 1512
DB 121 ACATCATCAGGTCCTTGAAGAGCTGGGAAGCTGGGTGGAGCGCTACCTTCACAAAT 180
QY 1513 GAAGCCACAGCCCGGACACCGTGGGGAGGGGTGCAGGTGGGTGATGCGCAGAGGA 1572
DB 181 GAAGCCACAGCCCGGACACCGTGGGGAGGGGTGCAGGTGGGTGATGCGCAGAGGA 240
QY 1573 ATGATGGGCTTTGTTCTGAGGGGTGTCGAGAGGCTGGGTGATGACTGCTCACGGACC 1632
DB 241 ATGATGGGCTTTGTTCTGAGGGGTGTCGAGAGGCTGGGTGATGACTGCTCACGGACC 300
QY 1633 CCATGTTGGATCTTTCTCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1692
DB 301 CCATGTTGGATCTTTCTCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
QY 1693 CCCTGCCCTATGAGACCTGCTCCCTCCTCAGCGTACGACCATGAGCCATGGCCCTCCAG 1752
DB 361 CCCTGCCCTATGAGACCTGCTCCCTCCTCAGCGTACGACCATGAGCCATGGCCCTCCAG 420
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DB 481 ACCTCCACTCTCTGCCCTTAAGATGGAGGAGCAGCGGCTCCATGGGTCTGGCCTGTG 540
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DB 721 AGCTCGGCTCTCC--TCTGCACTCGTTAAGTACCCGAGGCTCTCTTTACGATGTCCAG 778
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VERSION BG742600.1 GI:14053253
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 877)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM10632 row: b column: 24
High quality sequence stop: 851.
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/notes="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      144 a   288 c   250 g   195 t
ORIGIN
Query Match      24.9%; Score 792.8; DB 10; Length 877;
Best Local Similarity 96.9%; Pred. No. 3.1e-155;
Matches 851; Conservative 0; Mismatches 22; Indels 5; Gaps 4;
QY 1469 GAAGAGTCTGGAGCTGTGGTGGAGCTTACCTTCAAAATGAAGCCACAGCCCGC 1528
DB 1 GAAGAGTCTGGAGCTGTGGTGGAGCTTACCTTCAAAATGAAGCCACAGCCCGC 60
QY 1529 GGACACCGTGGGAAAGGGGTGAGGTGGGTGATGCGCAGAGGAATGATGGCTTTTGT 1588
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QY 1709 CTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1768
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Qy	2556	CAGGCATCTCTCTGTCTGTGAACCTGCCCTTACTGTGTTAACTGTTGCTCCAGGATGCAT	2615
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Qy	2616	TCGTATAGGAGGGGGCGGACAGGCTGGGCC--TTGTGACAACTCTGCCCTTTCACACATGGC	2674
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Qy	2675	CTTGCTCTGGTGGCCCTGACTGTCTAGGAGGGCCAGGAGGCACAGCGGAGGAGTCTC	2734
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Qy	2735	AGGAGGAGGCTGCCCTGAGGGGCTGGGAGGGGGTACCTCATGAGGACCAAGGTTGGAGCT	2794
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Qy	2795	GAGAAGAGGAGGAG--GTGGGGCTGGAGTGTCTGTGTAGCTGAGGGGACGGGCAAGTGA-G	2852
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Qy	2853	AGGAGGAGGAGGAGTCTCTGGGAGGATCTGAGCTGCTGTGAGTCTAACCCACTAAT	2912
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RESULT 40

CA488914

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CA488914

AGNCOURT_10808311

MAPL Homo sapiens

892 bp

mRNA

linear

EST 14-NOV-2002

mRNA sequence.

CA488914

CA488914.1

GI:24951705

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 892)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Kristi A. Eglund, Ira Pastan

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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column: 15

High quality sequence stop: 650.

Location/Qualifiers

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/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1, LNCaP"

/lab_host="EMD10B"

/clone_lib="MADPCL"

FEATURES

source

/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: Oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

Job time : 4254 secs

BASE COUNT	162 a	284 c	240 g	204 t	2 others
ORIGIN					
Query Match	24.8%; Score 789.4; DB 14; Length 892;				
Best Local Similarity	99.4%; Pred. No. 1.6e-154;				
Matches 824; Conservative	0; Mismatches 1; Indels 4; Gaps 3;				
QY	1130	GGGAGCCCTCCTTTTCTCAACTTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGGGT	1189		
Db	1	GGGAGCCCTCCTTTTCTCAACTTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGGGT	60		
QY	1190	CACACAGATGAATCACATCGTCATGAGATTGACAGAGGCCTACCGTACTGGTTTCAG	1249		
Db	61	CACACAGATGAATCACATCGTCATGAGATTGACAGAGGCCTACCGTACTGGTTTCAG	120		
QY	1250	TAGCCAGCTGACAGCCACTGCAAGTGGAGAGTCTCTTCAACGACTGGTTTCAGTGG	1309		
Db	121	TAGCCAGCTGACAGCCACTGCAAGTGGAGAGTCTCTTCAACGACTGGTTTCAGTGG	180		
QY	1310	ACACCTTAACCTCCAGATTGAGCCACCACTCTTCCCAACATGCCCGGCACAACTTACA	1369		
Db	181	ACACCTTAACCTCCAGATTGAGCCACCACTCTTCCCAACATGCCCGGCACAACTTACA	240		
QY	1370	CAAGATGCCCGCTGTTGAGTCTCTATGTCGCAAGCATGGCATTAATACCAGGAGAA	1429		
Db	241	CAAGATGCCCGCTGTTGAGTCTCTATGTCGCAAGCATGGCATTAATACCAGGAGAA	300		
QY	1430	GCCTACTAGGGCCCTGTGTCATCATCAGGTCCCTGAAGAAGTCTGGAGAGCTGTG	1489		
Db	301	GCCTACTAGGGCCCTGTGTCATCATCAGGTCCCTGAAGAAGTCTGGAGAGCTGTG	360		
QY	1490	GCTGGAGCCTACTTCAATATGAGCCACAGCCCGCGGACACCTGGGAGAGGGGTG	1549		
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QY	1610	GGTGTATGCACTGCTCAGGACCCCATGTTGGATCTTTCTCCCTTTCTCTCTCTCTTTT	1669		
Db	481	GGTGTATGCACTGCTCAGGACCCCATGTTGGATCTTTCTCCCTTTCTCTCTCTCTTTT	540		
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QY	1730	GCCATGAGCCATGGCCCTCCAGTGCCTCTCTAGCCCTTTCTTC-CAAGGAGCAGAGGTT	1788		
Db	601	GCCATGAGCCATGGCCCTCCAGTGCCTCTCTAGCCCTTTCTTC-CAAGGAGCAGAGGTT	660		
QY	1789	GGCCACC--GGGGTGGTCTGTCTTACCTCCACTCTGCCCTTAAGATGGAGGAGA	1846		
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QY	1847	CCAGGGTCCATGGGTCTGGCTGTGAGTCTCCCTTGCAGCCCTGGTCACTAGGCATCAC	1906		
Db	721	CCAGGGTCCATGGGTCTGGCTGTGAGTCTCCCTTGCAGCCCTGGTCACTAGGCATCAC	780		
QY	1907	CCCGCTTTGGTCTTTCAGATGCTCTT- GGGGTTTCATAGGGGAGGTCC	1954		
Db	781	CCCGCTTTGGTCTTTCAGATGCTCTTGGGGGTTTCATAGGGGAGGTCC	829		

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus p2n model

Run on: December 10, 2003, 18:09:05 ; Search time 1951 Seconds
(without alignments)
5531.106 Million cell updates/sec

Title: US-09-719-601-5
Perfect score: 2438
Sequence: 1 MGKGNQGEAAREVSVPT.....DIIRSLKSKGLMDAYLHK 444

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-NODEL=frame+pin.model -DEV=xlh
-Q/cgn2_1/USPTO_spool/US09719601/runat_09122003_094908_21162/app_query.fasta_1.583
-DB=EST -QFMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=ext -THR MAX=100 -THR MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09719601 @CGN 1 1 2135 runat_09122003_094908_21162 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em esthum:*
3: em estin:*
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6: em estpl:*
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11: gb htc:*
12: gb est3:*
13: gb est4:*
14: gb est5:*
15: em estfun:*
16: em estom:*
17: em gss hum:*
18: em gss inv:*
19: em gss pin:*
20: em gss vrt:*
21: em gss fun:*
22: em gss mus:*
23: em gss nam:*
24: em gss pro:*
25: em gss rod:*
26: em gss phg:*
27: em gss vrl:*
28: gb gss1:*

29: gb gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	2048	84.0	2862	11	AK083282 Mus muscu
2	1826	74.9	1201	9	AL530346 AL530346
3	1602	65.7	884	13	BQ881930 AGENCOURT
4	1560	64.0	1201	13	BX417399 BX417399
5	1555.5	63.8	926	13	BQ883702 AGENCOURT
6	1553.5	63.7	924	13	BQ883702 AGENCOURT
7	1551.5	63.6	1689	11	BQ883702 AGENCOURT
8	1548	63.5	914	13	AK080414 Mus muscu
9	1545.5	63.4	3129	11	AK080414 Mus muscu
10	1482.5	60.8	3697	11	AK029318 Mus muscu
11	1471	60.3	3318	11	AK090042 Mus muscu
12	1470.5	60.3	2272	11	AK083959 Mus muscu
13	1449	59.4	820	10	AK076485 Mus muscu
14	1412	57.9	806	10	BG742318 602631469
15	1397	57.3	909	10	BG742318 602631469
16	1379	56.6	805	10	BG742318 602631469
17	1379	56.6	910	9	BG742318 602631469
18	1372	56.3	802	10	AL522956 AL522956
19	1339	54.9	933	13	BG742318 602631469
20	1336	54.8	952	13	BG742318 602631469
21	1329	54.5	745	10	BG742318 602631469
22	1325	54.3	1091	10	BG742318 602631469
23	1310.5	53.8	932	13	BG742318 602631469
24	1301.5	53.4	1246	13	BG742318 602631469
25	1286	52.7	829	13	BG742318 602631469
26	1285	52.7	938	13	BG742318 602631469
27	1282.5	52.6	802	10	BG742318 602631469
28	1278.5	52.4	764	10	BG742318 602631469
29	1277	52.4	832	10	BG742318 602631469
30	1261	51.7	589	10	BG742318 602631469
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36	1239	50.8	799	10	BG742318 602631469
37	1232	50.5	1022	13	BG742318 602631469
38	1225	50.2	755	10	BG742318 602631469
39	1214	49.8	971	14	BG742318 602631469
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45	1178	48.3	1201	13	BG742318 602631469

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Mus musculus adult male hippocampus cDNA, RIKEN full-length
enriched library, clone: C630034B17 product: fatty acid desaturase 2,
full insert sequence.
ACCESSION AK083282
VERSION AK083282.1 GI:26101164
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AK083282 2862 bp mRNA linear HTC 05-DEC-2002
Mus musculus adult male hippocampus cDNA, RIKEN full-length
enriched library, clone: C630034B17 product: fatty acid desaturase 2,
full insert sequence.

QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160
 Db 462 ATCGTCATGGAAGCGTTGCTGCTTATCTCTCTGCTATCGGACCTGGCTGGATTCCT 521
 QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
 Db 522 ACCCTCGTCACAGCGTTTGTCTCGTACCTCTCAGGCCCAAGCTGGATGCTGCACAT 581
 QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200
 Db 582 GACTATGGCCACCTTCTGCTTAAGAAATCCATATGGAAACCGAGTGTGCCAAGTTT 641
 QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
 Db 642 GTCATTTGCCACTTAAAGGGTGCCTCAGCCAACTGGTGAACCAACCCAGACATTTCCAAC 701
 QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
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 QY 241 LeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLys 260
 Db 762 CTGGCGAGTGGCAGCCCTTGTATGTCGCAAGAGAGCTGAATATACCTGCCCTCAAC 821
 QY 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
 Db 822 CACGAGCATGATATCTTCTCTGATCGGACCGCGCTGCTCATCCCTATGATCTTCAG 881
 QY 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
 Db 882 TACCAGATCATCATGACATCATCAGCGCAGGACTGGGTGGACTTGGCTGGGCCATC 941
 QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
 Db 942 AGCTACTATATGCGTTTCTTACACCTTACATCCCTTCTACCGCATCTTGGGAGCCCTG 1001
 QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
 Db 1002 GTTTTCTCTCACTTATCAGTTCTCTGAGAGCCACTGTTTGTGTGGTCACACATG 1061
 QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
 Db 1062 AACCACTTGTCTGAGATTGATCTTGTACACTACCGGACTGGTTCAGCAGCCAGCTG 1121
 QY 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
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 QY 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
 Db 1182 TTCCAGATTGAGCACCACTCTTCCCACTATGCCAGCTCAACACCTGCACAGATTGCC 1241
 QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGlyLysProLeuLeu 420
 Db 1242 CCACGTGGTGAAGTCTCTCTGCGCAAGCATGGCATTAATACCAAGAGAGCCCTTCTGT 1301
 QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
 Db 1302 AGGGCCCTGATGCACATTGTGAGTTCACTGAAGAAGTCTGGGGAGCTGTGGCTGATGCT 1361
 QY 441 TyrLeuHisLys 444
 Db 1362 TACCTCCATAAA 1373
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 LOCUS AL530346 1201 bp mRNA linear EST 23-MAY-2003
 DEFINITION AL530346 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
 cDNA clone CS0DD007J09 5-PRIME, mRNA sequence.
 ACCESSION AL530346
 VERSION AL530346.2 GI:31068179
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12793839.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 6148.f For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DD007CE05QP1&cluster=6148.f. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DD007CE05QP1.
 Location/Qualifiers
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 /clone="CS0DD007J09"
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 /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
 /note="First strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
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 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 261 a 345 c 336 g 240 t 19 others
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 Best Local Similarity: 95.73% Mismatches: 13
 Query Match: 74.90% Indels: 0
 DB: 9 Gaps: 0
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 Db 144 ATGGGGAAGGAGGAGAACCGAGGGCGCGCGAGCGGAGGTGCGGTGCCACC 203
 QY 21 PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
 Db 204 TTCAGCTGGAGGAGATTTCAGAACATACCTGCGCACCGACAGGKNGCTGTCATTGAC 263
 QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
 Db 264 CCGAAGTTTACAAATCATCCAAATGGTCCATCCAGACCCCGGGGGCGAGCGGTGTC 323
 QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
 Db 324 GGGCACTACGCTGGAGAGATGCAACGGATGCTTCCGGCGCTTCCACCTGACCTGGAA 383
 QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluProSer 100
 Db 384 TTCTGTGGCAAGTTCTTGAACCCCTGCTGTATGTGTGAACCTGCGCCCGAGAGGCCACG 443
 QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
 Db 444 CAGGACCAAGGAGAGACTCAAGATCATCTAGGACTTCCGGGCCCTGAGGAGAGCGCT 503
 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
 Db 504 GAGGACATGAACCTGTTCAGACCAACCAACGACGTGTCTTCTCTCTCTCTCTCTCTCTCT 563

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141 1leAlaLeuGluSer1leAlaThrPheThrValPheTyrPheGlyAsnGlyTrrPhePro 160
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Db 624 ACCCTCATCAGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683
Qy 181 AspTyrGlyHisLeuSerValTyrArgGlyProTyrPheAsnHisLeuValHisValPhe 200
Db 684 GATTATGGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 743
Qy 201 Val1leGlyHisLeuLysGlyAlaSerAlaAsnTrrPheAsnHisArgHisPheGlnHis 220
Db 744 GTCAITGGCCACTTAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 803
Qy 221 HisAlaLysProAsn1lePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
Db 804 CAGGCCAAGCCTAAACATCTTCCACAGGATCCCGATGTGAACATGCTGCAGTGTGTGT 863
Qy 241 LeuGlyGluTrrPheGlnPro1leGlyTrrPheGlyLysLysLysLeuLysTyrLeuProTyrAsn 260
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Qy 261 HisGlnHisGluTyrPhePheLeu1leGlyProProLeuLeu1leProMetTyrPheGln 280
Db 924 CACGACGACGAATACTTCTTCTGATTTGGCGCGCGCTGCTCATCCCATGTATTTCAG 983
Qy 281 TyrGln1le1leMetThrMet1leValHisLysAsnTrrPheValAspLeuAlaTrrPheAlaVal 300
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Qy 301 SerTyrTrrPhePhePhe1leThrTrrPhePhePheTrrPhePheTrrPheGlyLeuGlyAlaLeu 320
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Qy 341 AsnHis1leValMetGluLeuAspGlnGluAla 351
Db 1164 AAWMAAAGCTCATRGAGATGAACAAGAGGCC 1196

RESULT 3
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5', mRNA sequence.
AGENCOURT_8726156 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6340921
ACCESSION BQ881930
VERSION BQ881930.1 GI:22273938
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2538 row: c column: 02
High quality sequence stop: 689.
Location/Qualifiers

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source

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1..884
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6340921"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

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BASE COUNT 201 a 271 c 199 g 211 t

ORIGIN

Alignment Scores:

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Pred. No.: 4,81e-153 Length: 884
Score: 1602.00 Matches: 291
Percent Similarity: 98.64% Conservative: 0
Best Local Similarity: 98.64% Mismatches: 2
Query Match: 65.71% Indels: 2
DB: 13 Gaps: 0

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US-09-719-601-5 (1-444) x BQ881930 (1-884)

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Db 62 GCTACCTCTCAGGCCCAAGCTGGCTGGCTGCAACATGATTATGGCCACCTGCTGTCTAC 121
Qy 189 ArgLysProLysTrrPheAsnHisLeuValHisLysPheVal1leGlyHisLeuLysGlyAla 208
Db 122 AGAAACCCCAAGTGGAAACACCTTGTCCACAAATTCGTATTGGCCACTTAAGGGGTGCC 181
Qy 209 SerAlaAsnTrrPheAsnHisArgHisPheGlnHisAlaLysProAsn1lePheHis 228
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Qy 229 LysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrrPheGlnPro1leGlu 248
Db 242 AAGGATCCCATGTGAACATGCTGCAGCTGTTTGTTCGGCGAATGGCAGCCCATCGAG 301
Qy 249 TyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTrrPhePheLeu 268
Db 302 TACGCCAAGAAGAAGCTGAAATACCTGCCCTACCAATCACCAGCAGCAATACTTCTTCTCTG 361
Qy 269 1leGlyProProLeuLeu1leProMetTyrPheGlnTyrGln1le1leMetThrMet1le 288
Db 362 ATTGGCGCGCGCTGCTCATCCCATCCCATGATTTCCAGTACCATCATCATGACCATGATC 421
Qy 289 ValHisLysAsnTrrPheValAspLeuAlaTrrPheValSerTyrTrrPheArgPhePheLeu 308
Db 422 GTCCATAAAGAACTGGGTGGACCTGGCGCTGGCGCTGAGCTACTACATCCGTTCTTCTCATC 481
Qy 309 ThrTrrPheProPheTyrGly1leLeuGlyValAlaLeuLeuPheLeuAsnPhe1leArgPhe 328
Db 482 ACCTACATCCCTTTCTAGGCAATCCTGGAGAGCCCTCTCTTTTCTCACTTCATCAGGTTTC 541
Qy 329 LeuGluSerHisTrrPheValTrrPheValThrGlnMetAsnHis1leValMetGluLeuAsp 348
Db 542 CTGGAGAGCCACTGCTTGTGTGGGTCAACAGATGAATCAGATCATCATCGTATGGAGATTGAC 601
Qy 349 GlnGluAlaTyrArgAspTrrPheSerSerGlnLeuThrAlaThrCysAsnValGluGln 368
Db 602 CAGGAGGCCCTACCTGACTGTTTCACTAGTACAGCTGACGCCACCTGCAACAGTGGAGCAG 661

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FEATURES

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QY 369 SerPheAsnAspTrpPheSerGlyHisLeuAsnPhenGlnIleGluHisLeuPhe 388
Db 662 TCCTTCTTCAAGACTGTTTCTAGTGACACCTTAACTTCCAGATGAGCACCACTTTC 721
QY 389 ProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAla 408
Db 722 CCCACCATGCCCGGCACAACTTACAAAGATCGCCCGCTGGTGAAGTCTCTATGTGCC 781
QY 409 LysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuAspIleLeuArg 428
Db 782 AAGCATGCGATTTGAATACAGAGAGCGGCTACTGANGGCCCTTCTGGACATCATCANG 841
QY 429 SerLeuLysLysSer-GlyLysLeuTrpLeu-AspAlaTyr 441
Db 842 TCCCTGAAGAAGTCTGGGGAAGCTGTGGCTGGGAGCGCTAC 882

RESULT 4
BX417399
LOCUS
DEFINITION BX417399 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YE07
5-PRIME, mRNA sequence.
ACCESSION BX417399
VERSION BX417399.1 GI:30658393
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DE009AC04QP1&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE009AC04QP1.

FEATURES
Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE009YE07"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="vector: PCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 282 a 321 c 306 g 237 t 55 others
ORIGIN

Alignment Scores:
Pred. No.: 1.4e-148 Length: 1201
Score: 1560.00 Matches: 300
Percent Similarity: 91.54% Conservative: 3
Best Local Similarity: 90.63% Mismatches: 23
Query Match: 63.99% Indels: 8
DB: 13 Gaps: 2

US-09-719-601-5 (1-444) x BX417399 (1-1201)
QY 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaGluArgGluValSerValProThr 20
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Db 142 ATGGGGAAGGAGGAAACCCAGGGCGAGGGGGCGCGAGCGAGGTGTGGTGGCCACC 201
QY 21 PheSerTrpGluGluIleGlnLysHisLeuAsnPhenGlnIleGluValLysLeu 40
Db 202 TTCAGCTGGAGGAGATTCCAGAAAGCATACCTGCGCCAGCCAGCAGGKGKNTGGTCTATTGAC 261
QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
Db 262 CGCAAGGTTTCAACATCACCAATGGTCCATCCAGCACCCCGGGGGCGAGGGGTCTATC 321
QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
Db 322 GGGCACTAGCTGGAGAAAGATCAACGAGATGCTTCCGCGCCTTCCACCTGACCTGGAA 381
QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluLysProSer 100
Db 382 TTCGTGGGCAAGTCTTGAACCCCTGCTGATTGTTGTAACCTGGCCCGGAGGAGCCACG 441
QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
Db 442 CAGGACCAACGGCAAGAACTCAAAAGATCACTGAGGACTTCCGGGGCCTCGAGGAGACGGT 501
QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
Db 502 GAGGACATGAACCTGTTCAAGACCAACCAACGCTGTTCTCTCTCTCTCTCTCTCTCTCT 561
QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160
Db 562 ATCGCCCTGGAGAGCATTCATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 621
QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
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QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200
Db 682 GATTATGGCCACTGCTGCTCTACAGAAACCCAAAGTGGAAACCACTTGTCCACAAATTC 741
QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
Db 742 GTCAATGGCCACTTAAGGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 801
QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
Db 802 CAGCCCAAGCTTAACATCTTCCACAAAGATCCGATGTGAACATGCTGACGCTGTTGTT 861
QY 241 LeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsn 260
Db 862 CTGGGCGAATGGCAGCCCATCGAGTACGCGAAGAAAGAGCTGAAATACCTGCCCTTACAT 921
QY 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
Db 922 CACCAGCAGATACTTCTCTCTGATTGGGCGCGCTGCTCATCCCCCATGTATTTCAG 981
QY 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
Db 982 TAMCAGATCAWATCACCATCATGCTCCATAAAAN-TGGGKGAGCTG-GSCTGGGCGGTA 1039
QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleGluAlaLeu 320
Db 1040 RSTAM-TAMATCCGG---TTTYTATCACCTAAWYCCITTTWCGGSATCTYGGRSCC--- 1092
QY 321 LeuPheLeuAsnPhenIleArgPheLeuGluSer 331
Db 1093 -----YCTTTTCTCATTATATGATTCT 1116

RESULT 5
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LOCUS
DEFINITION BX417399 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YE07
5-PRIME, mRNA sequence.
ACCESSION BX417399
VERSION BX417399.1 GI:30658393
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DE009AC04QP1&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE009AC04QP1.

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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE009YE07"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="vector: PCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 282 a 321 c 306 g 237 t 55 others
ORIGIN

Alignment Scores:
Pred. No.: 1.4e-148 Length: 1201
Score: 1560.00 Matches: 300
Percent Similarity: 91.54% Conservative: 3
Best Local Similarity: 90.63% Mismatches: 23
Query Match: 63.99% Indels: 8
DB: 13 Gaps: 2

US-09-719-601-5 (1-444) x BX417399 (1-1201)
QY 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaGluArgGluValSerValProThr 20
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BQ883702 926 bp mRNA linear EST 16-AUG-2002
AGENCOURT_8152253 Lupsaki dorsal root ganglion Homo sapiens CDNA
clone IMAGE:6179733 5', mRNA sequence.
BQ883702
BQ883702.1 GI:22275710

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KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13561 row: f column: 22
            High quality sequence stop: 586.

FEATURES
source
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6179733"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski dorsal root ganglion"
/vector="pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCCG-3' and
5'-GACTAGTTTACATCGGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT  208 a 298 c 203 g 216 t 1 others

ORIGIN
Alignment Scores:
Pred. No.:      2,88e-148      Length:      926
Score:          1555.50        Matches:    287
Percent Similarity: 96.67%      Conservative: 3
Best Local Similarity: 95.67%    Mismatches: 7
Query Match:    63.80%         Indels:     3
DS:             13             Gaps:       1

US-09-719-601-5 (1-444) x BQ883702 (1-926)

QY 105 LysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsn 124
Db 2  AAGAACTCAAGATCACTAGGAGCTTCGGGCGCTCGAGGAGCGCTGAGGACATGAAC 61
QY 125 LeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGlu 144
Db 62 CTCTTCAAGACCAACACCGTGTCTTCCTCCCTCCTCGCCCGACATCATCGCCCTGGAG 121
QY 145 SerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTyrIleProThrLeuIleThr 164
Db 122 AGCATTTGCATGGTTCACCTGCTTTTACTTTGGCAATGGCTGGATTCCTACCTCATCAG 181
QY 165 AlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTyrPheLysHisAspTyrGlyHis 184
Db 182 GCCTTTGCTCTGCTACTCTCAGGCGCCAGCTGGATGGTGCACATGATTATGGCCAC 241
QY 185 LeuSerValTyrArgLysProLysTyrAsnHisLeuValHisLysPheValIleGlyHis 204
Db 242 CTGTCTGTCTACAGAAACCAACCAAGTGGACCACTTGTCCACAAATTCGTATGGCCAC 301

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205 LeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysPro 224
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QY 225 AsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyLysTrp 244
Db 362 AACATCTTCCACAAGGATCCCGATGTGAACATGTGCACGTGTGTGTCTGGCGAATGG 421
QY 245 GlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLys 264
Db 422 CAGCCCATCATGAGTGGCGCAAGAGCTGAATACCTGCCCTACCAATCACCGACACGAA 481
QY 265 TyrPhePheLeuIleGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIleIle 284
Db 482 TACTTCTTCTGATTTGGCGCGCGCTGCTCATCTCCCATGTAATTTCCAGTACCATCATC 541
QY 285 MetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTrpIle 304
Db 542 ATGACCATGATGTCATTAAGAACTGGGTGGACCTGGCGCTGGCGCTGAGCTACTACATC 601
QY 305 ArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsn 324
Db 602 CGGTTCTTTCATCACCTACATCTCTTCTACGGCATCTTGGGAGCCCTCTCTTTCCCTCAC 661
QY 325 PheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleVal 344
Db 662 TTCATCAGGTTCTCTGGAGAGCCACTGGTTGTGTGGGTGCACACAGATGAATCACATCGTC 721
QY 345 MetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCys 364
Db 722 ATGAGATTTGACAGAGGCGCTACCGTGTCTGGTGTAGTACGAGCTGACAGCCACCTGC 781
QY 365 AsnValGluGlnSerPhePheAsnAspTrp-PheSerGlyHisLeuAsnPheGlnIleGln 384
Db 782 AACGTGGAGCAGCTCTTCTTCCAGCACTGGTTCAGTGGACCCCTTAACCTTCAGATTGA 841
QY 384 uHisHisLeuPhe-ProThrMet---ProArgHisAsnLeuHisLysIleAlaPro 401
Db 842 GGCACACCTTCTTCCCGACCATGCCCCCGGGGACACAACTTACACCAAGAAATCGCCC 897

RESULT 6
BU845046 924 bp mRNA linear EST 16-OCT-2002
LOCUS
DEFINITION AGENCOURT 10412170 NIH MGC.109 Homo sapiens cDNA clone
IMAGE:657575 5', mRNA sequence.
ACCESSION BU845046
VERSION BU845046.1 GI:24029487
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 924)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ruben Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2780 row: i column: 07
High quality sequence stop: 599.
Location/Qualifiers
1..924
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

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/clone="IMAGE:6578575"
/tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_109"
/notes="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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BASE COUNT      213 a      286 c      202 g      221 t      2 others
ORIGIN

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Alignment Scores:

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Pred. No.:      4,6e-148      Length:      924
Score:          1553.50      Matches:      290
Percent Similarity: 95.44%      Conservative: 3
Best Local Similarity: 94.46%      Mismatches: 9
Query Match:      63.72%      Indels:      6
DB:              13          Gaps:      2

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US-09-719-601-5 (1-444) x BU845046 (1-924)

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QY 118 LysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeu 137
Db 2 AAGACGGGTGAGGACATGAACCTGTTCAGACCAACACCGTGTCTCTCTCTCTCTCTG 61
QY 138 AlaHisIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGly 157
Db 62 GCCACATCATCGCCCTGAGAGCATTGATGTTCACTGCTTTTATTCTTTGGCAATGGC 121
QY 158 TrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrp 177
Db 122 TGGATTCTTACCTCATCAGCGCTTTGTCCTTGTCTTCTCTCAGGCCAACAGTGGATGG 181
QY 178 LeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuVal 197
Db 182 CTGCACATGATATGCGCACCTGTCTGTCTACAGAAACCCAAAGTGAACACCTTGTCTC 241
QY 198 HisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHis 217
Db 242 CACAAATTCGTATTGGCCACTTAAGGGTGCCTCTGCCAATCGTGGATCATCGCCAC 301
QY 218 PheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHis 237
Db 302 TTCCAGCACACGCCCAAGCCTAACATCTTCCAAAGGATCCCGATGTGAACATGCTGCAC 361
QY 238 ValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeu 257
Db 362 GTGTTTGTCTGGCGAATGGCAGCCCATCGAGTACGGCAAGAGAACTGAAATACCTG 421
QY 258 ProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMet 277
Db 422 CCTACATCACAGCACCAAGAACTACTTCTCTGATTGGCGCCGCTGCTCATCCCATG 481
QY 278 TyrPheGluTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAla 297
Db 482 TATTTCAGTACAGATCATCATGACCATGTCATGATGTCATGATGATGATGATGATGATG 541
QY 298 TrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeu 317
Db 542 TGGCGCGTCAGCTACTACATCCGTTCTTCTCATCCTACCTACCTACCTTCTAGGCACTCTG 601
QY 318 GlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVal 337
Db 602 NGAGCCCTCTCTTCTCTCAACTCATCAGTTCTTCTGGAGAGCCATGTTGTGTGGGTCTC 661
QY 338 ThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSer 357
Db 662 ACACACATGAATCATCATCTGTCATGGAGATGTACAGGAGGCTACCGTGACTGGTTTCACT 721

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QY 358 SerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGly 377
Db 722 AGCCAGCTACAGCCACCTGCAACGCTGGAGCAGTCTCTTCTTCAAGACTGGTTCAGTGA 781
QY 378 HisLeuAsnPheGlnIleGluHisLeuPheProThrMet-ProArgHisAsn-LeuH 397
Db 782 CACCTTAACCTTCAAG-ATTGAGCACCACCTCTTCCGCCANCATGCCCGCGCACAACTTAC 840
QY 397 IctylsIleAlaProLeuValLys---SerLeuCysAlaLysHis-----GlyIleGlu 414
Db 841 ACGAATCCCGCCCGCTGGTGAAGTCTTATGTGCCAAGCATGGCATGGCAATTACCA 900
QY 414 yrGlnGluLysProLeu 419
Db 901 GGGAAGAAAGCCGCTT 917

RESULT 7
AK080414
LOCUS
DEFINITION
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:A730007D17 product:fatty acid desaturase 3,
full insert sequence.
ACCESSION
AK080414
VERSION
AK080414.1 GI:26348536
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
REFERENCE
3 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
REFERENCE
4 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, K.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
REFERENCE
5 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,
Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,

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Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
PUBMED
11217851

5 The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1689)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tgawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES

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US-09-719-601-5 (1-444) x AK080414 (1-1689)

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 VERSION B0717429.1 GI:21856326
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 914)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-research.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 5'-GACTAGTCTAGATCGGAGCGGCCGCT(15)-3'. Size selected >
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 library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine); available through Life
 Technologies."

BASE COUNT 208 a 283 c 224 g 199 t
 ORIGIN

Alignment Scores:
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US-09-719-601-5 (1-444) x BQ717429 (1-914)

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REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akizawa, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
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Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hata, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S.,
and Hayashizaki, Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research

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TITLE Group Phase I & II Team.
JOURNAL Analysis of the mouse transcriptome based on functional annotation
REFERENCE of 60,770 full-length cDNAs
AUTHORS Nature 420, 563-573 (2002)
6 (bases 1 to 3129)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hata, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
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QY 415 GlnGlyLysProLeuLeuAlaLeuLeuAspIleAArgSerLeuLysLysSerGly 434
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RESULT 10
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ACCESSION AK090042
VERSION AK090042.1 GI:26105704
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
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Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

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JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 3697)
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/

FEATURES
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 Best Local Similarity: 60.57% Mismatches: 105
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US-09-719-601-5 (1-444) x AK090042 (1-3697)

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 Qy 254 LeuLysTrpLeu-ProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProPhe 273
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DEFINITION	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:DI30069P05 product:DELTA-5 DESATURASE, full insert sequence.		
ACCESSION	AK083959		
VERSION	AK083959.1	GI:26350884	
KEYWORDS	HTC, CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	99279253		
MEDLINE	10349636		
PUBLISHED	1999		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630		
MEDLINE	20499374		
PUBLISHED	2000		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, K., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Sum, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujii, S., Inoue, K., Togawa, Y., Izawa, M., Okara, E., Watanabe, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771		
MEDLINE	20530913		
PUBLISHED	2000		
REFERENCE	4		
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Frieschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stauble, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bjunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Buit, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashina, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. P., Suzuki, H., Tcyo-oka, K., Wang, K. H., Weltz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S. and Hayashizaki, Y.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6921), 685-690		
MEDLINE	21085660		
PUBLISHED	2001		
REFERENCE	5		
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573		
REFERENCE	6		
AUTHORS	Adachi, J., Aizawa, K., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, I., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045 Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp, Tel: 81-45-503-3222, Fax: 81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/		
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DB: 11 Gaps: 3
US-09-719-601-5 (1-444) x AK083959 (1-3318)

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RESULT 12
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DEFINITION library, clone:483423E24 product:unclassified, full insert
sequence.
ACCESSION AK076485
VERSION AK076485.1 GI:26096835
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
93279253
PUBMED 10349636
2
3 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED 11042159
4
5 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Tanaka, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED 11076861
6
7 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, T., Harada, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, I., Nikaido, I., Pecole, G., Suzuki, R.,
Quackenbush, J., Schriml, L.M., Stauber, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,

Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Mazuchioni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schenbach, C., Seva, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyo-oka, K., Wang, K.H., Wetz, C., Whittaker, C., Wilming, L.,
Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kontseki, S.,
and Hayashizaki, Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation

JOURNAL of 60,770 full-length cDNAs

REFERENCE Nature 420, 563-573 (2002)

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ichi, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Niehi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE

JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp).
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.go.jp/>

URL: <http://fantom.gsc.riken.go.jp/>

FEATURES

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US-09-719-601-5 (1-444) x AK076485 (1-2272)

Qy

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Qy 63 TyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheVal 82
Db 578 TATGCTGGCAAGATGCAACCGATGTTTCAGGGCCATGCACCTGGATCGGCATGGTG 637
Qy 83 GlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAsp 102
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Qy 263 HisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGln 282
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ACCESSION BG742318
VERSION    1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 820)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgabbs-remail.nih.gov
           Tissue Procurement: James Cleaver, M.D.
           cDNA Library Preparation: Life Technologies, Inc.
           Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
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               Average insert size 1.5kb. Library constructed by Life
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BASE COUNT 191 a 255 c 180 g 194 t
ORIGIN

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Score:          1449.00      Matches:      265
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US-09-719-601-5 (1-444) x BG742318 (1-820)

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VERSION    BG740873.1
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SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 806)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgabbs-remail.nih.gov
           Tissue Procurement: James Cleaver, M.D.
           cDNA Library Preparation: Life Technologies, Inc.
           Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
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US-09-719-601-5 (1-444) x BG740873 (1-806)

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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 909)
 AUTHORS NTH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaubs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10595 row: g column: 23
 High quality sequence stop: 750.

FEATURES

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 BASE COUNT 207 a 279 c 217 g 206 t
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 Query Match: 57.30% Indels: 6
 DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG674926 (1-909)

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 Db 2 TGGATTCT-ACCTCATCAGGC-TTTGTCTTGTAACTTCAGCCCAAGCTGGATGG 59
 QY 178 -LeuGlnHisAspTyrGlyHisLeuSerValTrrArgLysProLysTrrAsnHisLeuVa 197
 Db 60 GCTGCACATGATTATGGCCACTGTCTGTCTACAGAAACCCCAAGTGAACACCTTGT 119
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Db 360 GATATTCAGTACCAGATCATATGACCATGATGTCCTAAGAACTGGTGGACCTGGC 419
Qy 297 aTrpAlaValSerTyrTyrIleArgPheIleThrTyrIleProPheTyrGlyIleLe 317
Db 420 CTGGGCGGTGAGTACTACATCGGTCTCTTCATCATCCTACATCCCTTTCTACGGCATCCT 479
Qy 317 uGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVa 337
Db 480 GGGAGCCCTCTCTTCTCACTTCTATGAGTTCTTGGAGCCACTGGTT-GTGTGGGT 538
Qy 337 lThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrA-gAspTrpPhe-S 357
Db 539 CACACAGATGAATCATCATGTCATGTCAGATTACACGAGGAGGCTACCGTGACTGGTTCAA 598
Qy 357 eSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerG 377
Db 599 GTAGCCAGCTGACGAGCCACTGCACTGGAGCAGTCTCTTCTCAACGACTGGTTCAGTG 658
Qy 377 lYHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuH 397
Db 659 GACACCTTAATCTCCAGATTGACACCACTCTTCCACC-ATGCCCGCGCACAACTTAC 717
Qy 397 isLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluL 417
Db 718 ACAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCATGTCATGGCATGTAATACCAAGAGA 777
Qy 417 ysProLeuLeuArgAlaLeuLeuAspIleArgSerLeuLysLysSerGly 434
Db 778 GGCAGCTACTGAGGCGCTGTCGACATCATCCGTCCTGAGAGATTGGGA 830

RESULT 16
BG742694 805 bp mRNA linear EST 15-MAY-2001
LOCUS 602632908F1 NCI_CGAP_skn3 Homo sapiens cDNA clone IMAGE:4778329 5',
DEFINITION mRNA sequence.
ACCESSION BG742694
VERSION BG742694.1 GI:14053347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10633 row: 0 column: 02
High quality sequence stop: 798.
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FEATURES
source
Location/Qualifiers
1..805
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4778329"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/note="Osgan: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 194 a 245 c 191 g 175 t
ORIGIN
Alignment Scores: 2.58e-130 Length: 805
Pred. No.: 1379.00 Matches: 254
Score: 1379.00 Conservative: 1
Percent Similarity: 98.84% Mismatches: 1
Best Local Similarity: 98.45% Indels: 1
Query Match: 56.56% Gaps: 0
DB: 10
US-09-719-601-5 (1-444) x BG742694 (1-805)
Qy 189 ArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLys-GlVal 208
Db 1 AGAAACCCCAAGTGGAAACCACTTGTCCACAAATTCGTATTGGCCACTTAAGAGGTGC 60
Qy 208 aSerAlaAsnTrpTrpAsnHis-ArgHisPheGlnHisAlaLysProAsnIlePheH 228
Db 61 CTCTGCCAACTGGTGGAAATCATCGCCACTTCCAGCACCAAGCCCAAGCTTAACATCTTCC 120
Qy 228 isLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleG 248
Db 121 ACAAGGATCCCGATGTGAACATGCTGCAGTGTGTCTCTGGCGCAATGACACCCATCG 180
Qy 248 luTyrGlyLysLysLeuLysLeuLysTyrProTyrAsnHisGlnHisGluTyrPhePheL 268
Db 181 AGTAGCGCAAGAGAGAGCTGAATATCTGCCCTTACAATCACCAGCAGCAATATCTTCTCC 240
Qy 268 eulleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleMetThrMetI 288
Db 241 TGATTGGCGCGCGCTGCTCATCCCATGATTTTCCAGTACCAGATCATCATGACCATGA 300
Qy 288 leValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheI 308
Db 301 TCGTCCATAGAACTGGGTGGACCTGGCTGGCGCGTCACTACTACTACCTCGGTTCCTCA 360
Qy 308 leThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgP 328
Db 361 TCACCTACATCCCTTTCTACGGCATCTCTGGAGCCCTCCCTTTTCCCTCAACTTCATCAGGT 420
Qy 328 heLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleA 348
Db 421 TCCCTGGAGAGCCACTGGTTGTGGGTGCACACAGATGATCATCTCATGAGATTG 480
Qy 348 spGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluG 368
Db 481 ACCAGAGGCGCTACCGTGACTGGTTCACTAGTACCCAGCTGACAGCCACTGCAAGCTGGAGC 540
Qy 368 lnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeuP 388
Db 541 AGTCTCTCTTCAACAGATGGTTCACTAGTGACACCTTAACCTTCCAGATTGAGCACCACTCT 600
Qy 388 heProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysA 408
Db 601 TCCCCACCATGCCCGG-CACAACTTACACAAGATCGCCCGCTGGTGGTGAAGTCTCTATGTG 659
Qy 408 laLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleA 428
Db 660 CCAAGCATGGCATTGAATACCAGGAGAGGCGCTACTGTAGGGGCCCTCTCTGGACATCATCA 719
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QY 428 tGSeLeuLySsSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 720 GTCCTCTGAAGAAGTCTGGAGAGTGTGCTGGAGCGCTACCTTACAAA 769

RESULT 17
AL522956 910 bp mRNA linear EST 22-MAY-2003
LOCUS AL522956 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DB009F18 5-PRIME, mRNA sequence.
ACCESSION AL522956
VERSION AL522956.2 GI:31041219
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 910)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12786449.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DB009DC09QP1&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL : Corporation 1600
http://fulllength.invitrogen.com/ invitrogen
Faraday Avenue Genoscope sequence ID : CS0DB009DC09QP1.
Location/Qualifiers
1..910
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DB009F18"
/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Bclor V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 212 a 263 c 258 g 175 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 3,03e-130 Length: 910
Score: 1379.00 Matches: 252
Percent Similarity: 99.21% Conservative: 0
Best Local Similarity: 99.21% Mismatches: 2
Query Match: 56.56% Indels: 0
DB: 9 Gaps: 0

US-09-719-601-5 (1-444) x AL522956 (1-910)

QY 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20
Db 147 ATGGGGAAGGAGGGAACAGGCGGAGGGGGCGGCGGAGCGGAGGTGTGGTGCCACC 206

QY 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgTrpAspSerGlyLeuValIleAsp 40
Db 207 TTCAGCTGGAGGAGATTCAAAGCATACCTGCGCACCAGCGAGTGTGCTCATTCAC 266

QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
Db 267 CGCAGGTTTACAACATCAACAAATGGTCCATCCAGACCCCGGGGGCGAGCGGTGATC 326

QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
Db 327 GGGCACTAGCTGGAGAAGATGCAACGGATGCTTCCGGCGCTTCCACCTGACCTGGAA 386

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FEATURES

source

RESULT 18

BG742408

LOCUS

DEFINITION

mRNA sequence.

ACCESSION

BG742408

VERSION

BG742408.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 802)

NIH-MGC http://mgc.ncl.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

Sequencing by: Incyte Genomics, Inc.

clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM10639 row: e column: 04

High quality sequence stop: 802.

Location/Qualifiers

1..802

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4780395"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI CGAP Skn3"

/notes="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;


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QY 255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuLeuGlyProProLeuLeu 274
Db 358 AARAAATGCGCTTAAACACARVACGAAWACTTCTTCGTATGGCGCGCTGCTC 417
QY 275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTyrVal 294
Db 418 ATCCCATGATTTCCAGTACCAWACATCAWAGCAGCAWAGCGTCCATARAACATGGGTG 477
QY 295 AspLeuAlaTyrAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314
Db 478 GACCTGGCGCTGGCGCTGAGTAMATATCGGTCTTCAWCACTTAAWCCCTTTCTAC 537
QY 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTyrPhe 334
Db 538 GGCATCTCTGGAGCGCTCTTTCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 597
QY 335 ValTyrValThrGlnMetAsnHisIleValMetGluLeuAspGlnGluAlaTyrArgAsp 354
Db 598 GTGTGGGTCAACACAGATGAATACATGCTCATGAGATTGACAGAGGCGCTACCGTGAC 657
QY 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTyr 374
Db 658 TGGTTCAGTAGCAGCTGACAGCCACCTGCACTGGAGCGAGTCTCTTCTCAGCACTGG 717
QY 375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisIlePheProThrMetProArgHis 394
Db 718 TTCAGTGACACCTTAACCTCCAGATTGAGCACCACCTCTTCCCGCAGCATGCCCGGCAC 777
QY 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
Db 778 AACITACAAWATATCGCCCGCTGGTGAAGTCTCTATGTGCAAGCATGGCATTAATAC 837
QY 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGly 434
Db 838 CAGGAGAGCGCGTACTGAGGCGCGCTGCTGACATCAWAGGTCCCTGAAGAGTCTGGG 897
QY 435 LysLeuTyrLeuAspAlaTyrLeuHisLys 444
Db 898 AAGCTGTGGCTGGAGCGCTACTCTTCAAAA 927

RESULT 20
BX441083
LOCUS
DEFINITION
BX441083 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF014YM11 5-PRIME, mRNA sequence.
ACCESSION
BX441083
VERSION
BX441083.1 GI:30787936
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 952)
Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF014AG06QPI&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF014AG06QPI.
Location/Qualifiers
1 .952
/organism="Homo sapiens"
/mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="CS0DF014YM11"
/tissue_type="FETAL BRAIN"
/dev_stages="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 237 a 280 c 236 g 168 t 31 others
ORIGIN

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Alignment Scores:
Pred. No.: 7,94e-126 Length: 952
Score: 1336.00 Matches: 248
Percent Similarity: 92.94% Conservatives: 2
Best Local Similarity: 92.19% Mismatches: 19
Query Match: 54.80% Indels: 1
DB: 13 Gaps: 0
US-09-719-601-5 (1-444) x BX441083 (1-952)
QY 1 MetGlyLysGlyClyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20
Db 147 ATGGGGAAAGGAGGAAACAGGGCGCAAGCGGCGCAAGCGGCGGCGGCGGCGGCGGCGG 206
QY 21 PheSerTyrGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
Db 207 TTCARCTGGAGGAGAAWTCAAAAGCATACCTGCCGACCGACCAAGKG-CTGTCATTGAM 265
QY 41 ArgLysValTyrAsnIleThrLysTyrPheSerIleGlnHisProGlyGlyGlnArgValIle 60
Db 266 CGCAAGGTTTACAAATACATCACMAAAGGTCCAWCCAGCACCCCGGGGGCGGCGGCGG 325
QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
Db 326 GGGCACTAGCTGGAGAGATCAACGGATGCTTCCAAACAAACACCTGACMTGNA 385
QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100
Db 386 TWCCTGGGCAATTTCTTGAACCCCTGCTGATTGTTGTAACCTGGCCCGGAGGAGCCAGC 445
QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
Db 446 CAGGACACCGCAAGAACTCAAAAACWACTGARGACTTCCGGGGCGCTGAGGAACGGCT 505
QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
Db 506 GARGACATGAACCTGTTCAAAACCAACCAACGACGTTGTTCTTCTCTCTCTGCGCCACATC 565
QY 141 IleAlaLeuGluSerIleAlaThrPheThrValPheTyrPheGlyAsnGlyTyrIlePro 160
Db 566 ATCGCCCTGGAGACATTCGATGGTTTCACTGCTTTTACTTTGGCAATGGCTGGATTCTCT 625
QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTyrLeuGlnHis 180
Db 626 ACCCTCATCAGCGCTTTGTCCTTCTACTCTCAGGCCCAACCTGATGGTGGTCAACAT 685
QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTyrAsnHisLeuValHisLysPhe 200
Db 686 GATTATAGCACCTGCTGCTTACAGAAACCAAGTGGAAACCAACCTTGTCCACAAATTC 745
QY 201 ValIleGlyHisLeuLysGlyValaSerAlaAsnTyrTrpAsnHisArgHisPheGlnHis 220
Db 746 GTCATTTGGCCACTTAAGGGTGGCTCTGCCAATGTTGGTGAATCATCGCACTTCCAGCAC 805
QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
Db 806 CACGCCAAGCCTTACATCTTCCACAAGGATCCGATGTGAACATGCTGACGCTGTTTCTT 865
QY 241 LeuGlyGluTyrProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsn 260

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Db      866 CTGGCGAATGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAAT 925
Qy      261 HisGlnHisGlnTyrPhePhePheLeu 269
Db      926 CACGACGAGATACCTCTTCCTGATT 952

RESULT 21
BG739802
LOCUS   602630527F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4775791 5',
DEFINITION mRNA sequence.
ACCESSION BG739802
VERSION   1
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 745)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Tissue Procurement: James Cleaver, M.D.
          cDNA Library Preparation: Life Technologies, Inc.
          Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L14M10627 row: e column: 08
          High quality sequence stop: 743.
          Location/Qualifiers
            1..745
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:4775791"
              /lab_host="DH10B (TI phage-resistant)"
              /clone_lib="NCI CGAP Skn3"
              /note="Organ: skin; Vector: pCMV-Sport6; Site_1: NotI;
              Site_2: SalI; Cloned unidirectionally. Primer: Oligo dn.
              Average insert size 1.5kb. Library constructed by Life
              Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 172 a 234 C 159 G 180 T
ORIGIN
Alignment Scores:
Pred. No.: 2,99e-125 Length: 745
Score: 1329.00 Matches: 245
Percent Similarity: 98.79% Conservative: 0
Best Local Similarity: 98.79% Mismatches: 3
Query Match: 54.51% Indels: 3
DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG739802 (1-745)

Qy      151 ValPheTyrPheGlyAsnGlyTrrPileProThrLeuIleThrAlaPheValLeuAlaThr 170
Db      3 GTCTTTTACTT-GGCAATGGCTGGATTCTTACCTCATCAGCGCTT-GTCCCTTGCTACC 60
Qy      171 SerGlnAlaGlnAlaGlyTrrPleGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
Db      61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGCCCACTGTCTGTCTACAGAAA 120
Qy      191 ProLysTrrPheAsnHisLeuValHisValPheValIleGlyHisLeuLysGlyAlaSerAla 210
Db      121 CCCAAGTGAACACCTTGTCCCAATTCCTGATTGGCCACATTAAGGGTGGCTCTGCC 180
Qy      211 AsnTrrPheAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
Db      181 AACTGGTGGATCATCGCACTTCCAGCACCACCAAGCTTACATCTTCCACAAGGAT 240

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Qy      231 ProAspValAsnMetLeuHisValPheValLeuGlyLtrPdgInPrOileGluTyrGly 250
Db      241 CCGATGTGAACATGCTGCACCTGTT-GTCTGGGGAATGGCAGCCCATCGATACGGC 239
Qy      251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
Db      300 AAGAAGAAGTGAATACCTGCCTCTACATCACCAGCACGAATACTTCTTCCTGATTGGG 359
Qy      271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
Db      360 CCGCGCTGCTCATCCCATGATTTCAGTACAGATCATCATGACCATGATCGTCCAT 419
Qy      291 LysAsnTrrPheValPheLeuAlaTrrAlaValSerTyrTrrIleArgPhePheIleThrTyr 310
Db      420 AAGAACTGGGTGGACCTGGCGCTGCGCTCAGTACTACATCGGTTCCTTCATCACCTAC 479
Qy      311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
Db      480 ATCCCTTTCTACGGCACTCCGGAGCCCTCTTTCTCAACTTCATCAGGTTCTCTGGAG 539
Qy      331 SerHisTrrPheValTrrValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
Db      540 AGCCACTGGTTTGTGGTTCACACAGATGAATCACATCGTCATGGAGATTGACACGAG 599
Qy      351 AlaTrrArgAspTrrPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
Db      600 GCCTACCGTGACTGGTTCAGTAGCCAGTCAGCCACCTGCAACGTGGAGAGCTCTTC 659
Qy      371 PheAsnAspTrrPheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThr 390
Db      660 TTCAACGACTGGTTCAGTGGACACCTTAACCTCCAGATTGAGCACCACCTCTTCCCCACC 719
Qy      391 MetProArgHisAsnLeuHisLys 398
Db      720 ATGCCCCGGGCACAACTTACACAAG 743

RESULT 22
BG7315881
LOCUS   6018989828F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125342 5',
DEFINITION mRNA sequence.
ACCESSION BG7315881
VERSION   BG7315881.1 GI:11264175
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1091)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
          Plate: LLCW1013 row: g column: 07
          High quality sequence stop: 725.
          Location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:4125342"
              /tissue_type="neuroblastoma"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH_MGC_19"
              /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:

FEATURES
source

```

EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 271 a 317 c 288 g 213 t 2 others
ORIGIN

Alignment Scores:

Pred. No.: 1,268-124 Length: 1091
Score: 1325.00 Matches: 257
Percent Similarity: 93.64% Conservative: 8
Best Local Similarity: 90.81% Mismatches: 13
Query Match: 54.35% Indels: 6
DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BF315881 (1-1091)

Qy 5 GlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGlu 24
Db 1 GGGATCAGGGCGAGGGCGCGCGAGCGAGGTGTGGTGGCCACCTTCAGCTGGAG 60
Qy 25 GluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyr 44
Db 61 GAGATTCAGAACATACCTCGCACCCAGCGAGGTGGTGGTTCATTGACCGCAAGGTTTAC 120
Qy 45 AsnIleThrLysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyrAla 64
Db 121 AACATCACCAGATGTCTTCATCAGACCGGGGGCCAGCGGTTCATCGGCATACGCT 180
Qy 65 GlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLys 84
Db 181 GGAGAAGATGCAACGGATGCTTCGGCGCTTCACCGCTTCACCGCTTCGTTGGGCAAG 240
Qy 85 PheLeuLysProLeuLeuIleGlyLeuAlaProGluGluProSerGlnAspHisGly 104
Db 241 TTTCTGAACCCCTGCTGATGGTGAATGTGCCCGGAGGAGCCAGCCAGCACCGGC 300
Qy 105 LysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsn 124
Db 301 AAGAACTCAAGATCACTCAGGACTTCCGGGCCCTTCAGGAAGAGCGGTGAGGACATGAAC 360
Qy 125 LeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGlu 144
Db 361 CTGTTCAAGACCAACACCGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Qy 145 SerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTyrIleProThrLeuIleThr 164
Db 421 AGCATTCGATGGTTCACGTCTTTTACCTTTGGCAATGGCTGGATTCCTACCTCATCAG 480
Qy 165 AlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHis 184
Db 481 GCCTTTGCTTGTCTTACCTCTCAGGCCCAAGCTGGATGGCTGCAACATGATATGGCCAC 540
Qy 185 LeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHis 204
Db 541 CTGCTGTCTCAGAAAAACCAAGTGAACACCTGTGTCCCAAAATTCGTCATTGGCCAC 600
Qy 205 LeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysPro 224
Db 601 TTAAGGGTGGCTCTGCCAATCTGTGGAAATCATCGCCATTCAGGACCCAGCCAGCCCT 660
Qy 225 AsnIlePheHisLysAsp-ProAspValAsnMetLeu-HisValPhe-ValLeuGlyGlu 243
Db 661 AACATCTTCCACAGGATCCCGATGTGAACATGCTGGCAGCTGTTGATCTGGGGGAA 720
Qy 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLys 263
Db 721 TGGGAGGCCATCGAGTACGGGAGGAAGATG-AAAATTACTTGGGCTATATGACACGAGGC 779
Qy 264 GluTyr-PhePheLeu-IleGlyProProLeuLeuIleProMetTyr-PheGlnTyrGln 282

Db 780 GAATACTTCTCTCTGAGTTGGCCCGGATGGTCCATCCCTGGTTTCCGACCAA 838

RESULT 23
BU845074

LOCUS
DEFINITION
BU845074 932 bp mRNA linear EST 16-OCT-2002
IMAGE:5578608 5', mRNA_sequence.

ACCESSION
BU845074.1 GI:24029515

VERSION
EST.

KEYWORDS
Homo sapiens (human)

SOURCE
Homo sapiens

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 932)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
Unpublished

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2780 row: j column: 16

High quality sequence stop: 768.

Location/Qualifiers

FEATURES

source

1..932

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6578608"

/tissue_type="teratocarcinoma, cell line"

/lab_host="PH10B (phage-resistant)"

/clone_lib="NIH_MGC_109"

/note="Organ: ovary; Vector: pOTB7; Site: 1: EcoRI; Site 2:

XhoI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCACAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

BASE COUNT 204 a 285 c 260 g 178 t 5 others

ORIGIN

Alignment Scores:

Pred. No.: 3,118-123 Length: 932

Score: 1310.50 Matches: 249

Percent Similarity: 91.46% Conservative: 8

Best Local Similarity: 88.61% Mismatches: 15

Query Match: 53.75% Indels: 9

DB: 13 Gaps: 3

US-09-719-601-5 (1-444) x BU845074 (1-932)

Qy 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20

Db 80 ATGGGGAAGAGGAGGAAACAGGGCGAGGGCGCGAGGTGTTCGGTGGCCAC 139

Qy 21 PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40

Db 140 TTCAGTGGAGGAGGAGTTTCAGAGGATATACCTTCGCGCAGCAGGAGGTGTTCATTGAC 199

Qy 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60

Db 200 CGCAAGGTTTACAACATCATCACCAATATGTTCCATCCAGCACCCCGGGGGCGAGGTCATC 259

Qy 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80

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Db      260 GGGCACTACCTGGAGAGATGCAACGAGATGCTTCGCGCTTCACCTGACCTGGAA 319
Qy      81 PheValGlyLysPheLeuLysProLeuLeuLeuGlyGluLeuAlaProGluProSer 100
Db      320 TTCGTGGCAAGTTCATTGAACCCCTGCTGATTGGTGAATGGCCCGGAGAGCCAGC 379
Qy      101 GlnAspHisGlyAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
Db      380 CAGACACGCGAAGAACCTCAAGATCACTGAGGACTTCGCGCCCTGAGGAAGCGGT 439
Qy      121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
Db      440 GAGGACATGAACCTGTTCAAGACCAACACCGTGTCTCTCTCTCTCTCTCTCTCTCT 499
Qy      141 IleAlaLeuGluSerIleAlaThrPheThrValPheThrValPheGlyAsnGlyTrpIlePro 160
Db      500 ATCGCCCTGGAGAGCATGATGCTGCTACAGAAACCCCAAGTGAACACCTTGTCCACAAATTC 559
Qy      161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
Db      560 ACCCTCATCAGGCTTTGCTTGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Qy      181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200
Db      620 GATTATGGCCACCTGCTGTCTACAGAAACCCCAAGTGAACACCTTGTCCACAAATTC 679
Qy      201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
Db      680 GTCATTTGGCCACTTAAGGGTGGCTCTGCCAATGCTGGTGAATCATGCCACCTTCCAGCAC 739
Qy      221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeu---HisValPhe 239
Db      740 CAGCGCAAGCTTAACATCTTCCACAAAGGATCCCGATGTGAACATGTGTCGACGCTTTGT 799
Qy      240 ValLeuGlyGluTrpGln---ProIleGlyTrpGlyLysLysLysLysLysLysTrpLeuProT 259
Db      800 TNCCTGGGCGAATGGCAGCCCATTCGAGTACGGCAAGAAANGAANGCCTGAAATACCT 859
Qy      259 yr-----AsnHisGlnHisGlyTrpPhePheLeu---IleGlyProPro 272
Db      860 GGCNNCCATACATCAACCCAGCAGCAATACCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 918

RESULT 24
LOCUS   B0422100 1246 bp mRNA linear EST 23-MAY-2002
DEFINITION AGENCOURT_7766465 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6021978
5', mRNA sequence.
ACCESSION B0422100
VERSION   B0422100.1 GI:21117415
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1246)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-remail.nih.gov
          Tissue Procurement: DCTD/DTP/Gazdar
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM13228 row: 1 column: 19
          High quality sequence start: 71
          High quality sequence stop: 659.
FEATURES             Location/Qualifiers
     source            1..1246

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6021978"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site: 1; NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 306 a 383 c 281 g 276 t
ORIGIN
Alignment Scores:
Pred. No.: 3,78e-122 Length: 1246
Score: 1301.50 Matches: 269
Percent Similarity: 85.85% Conservative: 10
Best Local Similarity: 82.77% Mismatches: 27
Query Match: 53.38% Indels: 19
DB: 13 Gaps: 8
US-09-719-601-5 (1-444) x B0422100 (1-1246)
Qy 93 GluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAsp 112
Db 58 GAATCGTCGACCCAGCGCTCGTCCAGC-----GTCCGCTCAAGATCACTGAGGAC 108
Qy 113 PheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhe 132
Db 109 TTCGGGCGCTTGAGAAAGCGGTGAGACATGAACTGTTCAAGACCAACCACTGGTTC 168
Qy 133 PheLeuLeuLeuAlaHisIleAlaLeuGluSerIleAlaTrpPheThrValPhe 152
Db 169 TTCCTCTCTCTCTCGCCACATCATCGCTCGAGAGCATTCATCGTGTCTCTCTCTCT 228
Qy 153 TyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGln 172
Db 229 TACTTTTGGCAATGCTGGATTCCTACCTCATCAGCGCTTTGTCTTGTCTCTCTCTCAG 288
Qy 173 AlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLys 192
Db 289 GCCCAAGCTGGATGGCTGCAACATGATTATGGCCACTGTCTGTACAGAAAACCAAG 348
Qy 193 TrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrp 212
Db 349 TGGAAACACCTTGTCCACAAATTCGTCATTGGCCACTTAAAGGGTGCCTCTGCCAACTGG 408
Qy 213 TrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAsp 232
Db 409 TGGAAATCATGCCACATTCACAGCACCCAGCCCAAGCCTAACATCTTCCACAAGGATCCGAT 468
Qy 233 ValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGlyTrpGlyLysLys 252
Db 469 GTGAACATGTGTCACGCTGTTTGTCTGGCGAATGGCAGCCCATCAGATCAGCAGAGAG 528
Qy 253 LysLeuLysTrpLeuProTyrAsnHisGlnHisGlyTrpPhePheLeuIleGlyProPro 272
Db 529 AAGCTGAATACCTGCGCTTACATCACCAGCAGAAATCTTCTCTCTGATTTGGCGCGCG 588
Qy 273 LeuLeuIleProMetTyrPheGlnTrpGlnIleValMetThrMetIleValHisLysAsn 292
Db 589 CTGCTCATCCCATGATTTTCCAGTACCATCATCATGATCATGATGATGATGATGATGATGAT 648
Qy 293 TrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTrpIlePro 312
Db 649 TGGGTGAGCTTGGCGCTGGCGCGTACGACTACTATCATCGGTTCCTTCATCCTACCTACCT 708
Qy 313 PheTyrGlyLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu-SerH 332
Db 709 TTCTACGCGCATCTCTGGAGCGCTCTTTTCTCTCACTTTCATCAGGTTCCTCGAAGAGCC 768
Qy 332 isTrpPheValTrpVal-ThrGlnMetAsnHisIleValMet---GluIleAspGlnGlu 350

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Db      769 ACTGTTGGGTGGTCCCCCGCAGATGAATCACAATCTCTCATGGGAAATTTGACAGGAG 828
Qy      351 AlatyArgAsp-TpPheSer--SerGlnLeuThraLa-ThrCysAsn-ValGluGln 368
Db      829 GCTACCCGGGAAGTGGTTTCACTAGTACCCGCTTGACAGCCCACTGCAACGGGGGAACAG 888
Qy      369 SerPhe---PheAsnAspTTP-PheSerGlyHis---LeuAsnPheGln-----IleG1 384
Db      889 TCCCTTCTTCAACCAACTGGGTTCAGTGGGAACACCTTTAACTTCCAGATTTGAGGAA 948
Qy      384 uHisHisLeuPhe-ProThrMet----ProArgHisAsnLeuHis---LysIlealaPro 401
Db      949 CCACCTCTTTTCCCAACAATGGCCCGGGATACAACTTTAAACCAAAAATTTGCCCCC 1007

RESULT 25
LOCUS   BG741484
DEFINITION BG741484 829 bp mRNA Homo sapiens linear EST 15-MAY-2001
VERSION   BG741484
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL     National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1CM2884 row: n column: 21
            High quality sequence start: 25

FEATURES
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            /mol_type="mRNA"
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            /clone="IMAGE:4777317"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NCI CGAP Skn3"
            /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 1.5kb. Library constructed by Life
            Technologies. Note: this is a NCI-CGAP Library."
BASE COUNT 187 a 247 c 237 g 158 t
ORIGIN
Alignment Scores:
Pred. No.: 8-5e-121 Length: 829
Score: 1286.00 Matches: 242
Percent Similarity: 96.85% Conservatives: 4
Best Local Similarity: 95.28% Mismatches: 6
Query Match: 52.75% Indels: 3
DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG741484 (1-829)
Qy      1 MetGlyValGlyGlyAsnGln-GlyGluGlyAlaAlaGluArgGluValSerValProTh 20
Db      72 ATGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 131
Qy      20 rPheSerTTPGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAs 40

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Db      132 CTTCACTGGGAGGAGATT'CAGAAGCATAACTCGCCACCGACAGGTGGCTGGTCATTGA 191
Qy      40 pArgLysValTyrAsnIleThrLysTTPSerIleGlnHisProGlyGlyGlnArgValIrl 60
Db      192 CCACAAGGTTTACACATCACAATATGGTTCATCCAGCACCCGGGGGCGGAGGGGTAT 251
Qy      60 eGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuG1 80
Db      252 CGGGCACTACGCTGGAGAAGATGCAACGATGCTTCGCGGCTTCACCTGACCTGACCTGGA 311
Qy      80 uPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSe 100
Db      312 ATTCTGGGGCAAGTTCTTGAACCCCTGCTGATGGTGAACCTGGCCCGGAGAGGCCAG 371
Qy      100 rGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAl 120
Db      372 CCAGGACCCAGGCAAGAACTCAAGATCACTGAGGACTTCGCGGCTTCGAGGAAGACGGC 431
Qy      120 aGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIrl 140
Db      432 TGAGGACATGAACCTGTTCAAGACCAACCAACCGTGTTCCTCTCTCTCTCTCTCTCTCT 491
Qy      140 eIleAlaLeuGluSerIleAlaTTPPheThrValPheTyrPheGlyAsnGlyTTPlePr 160
Db      492 CATCGCCCTGGAGAGCATTCGATGGTTCACGTCTTTTACTTTGGCAATGGCTGGATTCC 551
Qy      160 oThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTTPleuGlnHi 180
Db      552 TACCCTCATCAGCGCCTTTGCTCTGCTACCTCTCAGGCCCAAGCTGGATGCTGCAACA 611
Qy      180 sAspTyrGlyHis-LeuSerValTyrArgLysProLysTTPAsnHisLeuValHisLysP 200
Db      612 TGATTATGGCCACCACTGCTGCTACGAACCCCAAGTGGACCACTTGTCCCAAT 671
Qy      200 heValIleGlyHisLeuLysGlyAlaSerAlaAsnTTPTrpAsnHisArgHisPheGlnH 220
Db      672 TCGTCATTGGCCACTTAAAGGTGCTCTGCAACCTGGTGAATCATCGCCACTTCGACG 731
Qy      220 iHisAlaLysProAsnIlePheHisLysAspProAspValLenMetLeuHisValPheV 240
Db      732 ACCAGCCCAAGCTTAACATCTTCCAGAGGATCCGATGTGAACATGTCACGTGTATT 791
Qy      240 alLeuGlyGluTTPGlnProIleGluTyrGlyLysLys 252
Db      792 GTCTGGGCGAATGGCAGCATC-GAGTACGGCAGAAGA 828

RESULT 26
LOCUS   BU856567
DEFINITION AGENCOURT_10472773 NIH_MGC_109 Homo sapiens cDNA clone
            IMAGE:6646293 5', mRNA sequence.
ACCESSION BU856567
VERSION    BU856567.1 GI:24041557
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 938)
            NTH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1CM2884 row: n column: 21
            High quality sequence start: 25

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High quality sequence stop: 567.

FEATURES

Location/Qualifiers

source

1..938
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6646293"
 /tissue_type="teratocarcinoma, cell line"
 /lab_host="PH108 (phage-resistant)"
 /clone_lib="NIH_MGC_109"
 /note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 BASE COUNT 219 a 293 c 204 g 219 t 3 others
 ORIGIN

Alignment Scores:

Pred. No.: 9,996-121 Length: 938
 Score: 1266.00 Matches: 262
 Percent Similarity: 88.63% Conservative: 3
 Best Local Similarity: 87.63% Mismatches: 19
 Query Match: 52.75% Indels: 16
 DB: 13 Gaps: 5

US-09-719-601-5 (1-444) x BU856567 (1-938)

QY 118 LysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeu 137
 DB 34 AAGACGGCTGAGACATGAACTGTTCAAGACCAACACCGTGTCTTCTCTCTCTCTG 93
 QY 138 AlaHisIleAlaLeuGluSerIleAlaTppPheThrValPheTyrPheGlyAsnGly 157
 DB 94 GCCCC-ATCATGCCCTCGAGGACATGATGTTTACATGCTTTTACTTGGCAATGGC 152
 QY 158 TrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrp 177
 DB 153 TGGATTCTCACTACCTCATCGCCCTTGTCCCTGTACCTCTCAGGCCCAAGCTGGATGG 212
 QY 178 LeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTyrAsnHisLeuVal 197
 DB 213 CTCACACATGATTATGCCACCTGTCTGTCTACAGAAACCCCAAGTGGACCACTTGTCT 272
 QY 198 HisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHis 217
 DB 273 CACAAATTCGTCTATTGCCCACTTAAAGGGTGCCTCTGCCAACTGTGTGAATCATGCCAC 332
 QY 218 PheGlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHis 237
 DB 333 TTCACACACACCCCAAGCCTACATCTTCCACAGATCCCGATGTGAACTGTGTGAC 392
 QY 238 ValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLysTyrLeu 257
 DB 393 GTCTTTGTCTGGCGAATGGCAGCCCATCGAGTACGCCAAGAAGCTGAATACCTG 452
 QY 258 ProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProLeuLeuIleProMet 277
 DB 453 CCTTCAATCACCAGACCAATACTTCTCTGATTGGGCGCGCTGTCTATCCCCATG 512
 QY 278 TyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAla 297
 DB 513 TATTTCAGTACCATCATCATGATCATGATGATGATGATGATGATGATGATGATGATGATG 572
 QY 298 TrpAlaValSerTyrTrpIleArgPhePheIleThrTyrIle-PropPheTyrGlyIle 317
 DB 573 TGNCGCGTACGTACATACATCCCGTCTCTATCACCCTATACCTCTCTACGGATCCT 632
 QY 317 uGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVa 337

DB 633 GNGAGCCCTCTTTTCTCACTCATCAGTTCTCTGGAGAGCACTGGTTTGTGGGT 692
 QY 337 lThrGlnMetAsnHisIleValMetGluLeuAspGlnGluAla-TyrArgAspTrpPhe 357
 DB 693 CACACAGATGAATCATCGTATGAGATTGACAGGAGGCCCTACCTGACTGNTCA 752
 QY 357 erSer-GlnLeuThrAla-ThrCysAsnValGluGlnSer---Phe-PheAsnAspTrp 375
 DB 753 ATAGCCAGCTGACAGCCCACTGCAAGTGTGGAGCAGTCCCTCTTCAAGACTGG 812
 QY 375 heSerGly---His--LeuAsnPheGln---lleGluHisHisLeuPhe-----Pr 389
 DB 813 GTTCAGGGGAACACCTTTAACTTCAGGATTGGAGCAACACCTTCTTCCCCAAC 872
 QY 389 oThrMetProArgHisAsnLeu-----HisLysIleAlaPro 401
 DB 873 ATTGGCCCGGGGAACAACTTAAACACACAAAATCCCCCCC 915
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 LOCUS 602273891F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4361855 5',
 DEFINITION mRNA sequence.
 ACCESSION BF970711
 VERSION BF970711.1 GI:12337926
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 802)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM10005 row: e column: 24
 High quality sequence stop: 712.
 Location/Qualifiers
 1..802
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4361855"
 /tissue_type="adrenal cortex carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_84"
 /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site 1:
 NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT
 primed. Average insert size 1.229 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH MGC Library."
 BASE COUNT 193 a 241 c 187 g 181 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,856-120 Length: 802
 Score: 1282.50 Matches: 245
 Percent Similarity: 96.09% Conservative: 1
 Best Local Similarity: 95.70% Mismatches: 6
 Query Match: 52.60% Indels: 6
 DB: 10 Gaps: 1
 US-09-719-601-5 (1-444) x BF970711 (1-802)
 QY 190 LysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSer 209

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Db      3  AAACCAAGTGGACCACTTGTGCACAAATGGTCATTTGAGGGTGCCTCT 62
Qy      210 AlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLys 229
Db      63  GCCAACTGGTGAATCATCGGCATTCAGACACACCCAGCCAGCTTAATCTTCCCAAG 122
Qy      230 AspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyr 249
Db      123 GATCCGATGGAACATGCTGCACGTGTTGTCTGGGGAATGGCAGCCATCGAGTAC 182
Qy      250 GlyLysLysLysLeuLysTyrLeuProTyrAsnHisGln---HisGluTyrPhePheLeu 268
Db      183 GGCAGAGAAAGCTGAATACCTCCCTACAAATCACCAGCCAGCAAAATTAATCTTCTCTG 242
Qy      269 IleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIle 288
Db      243 ATTGGCCGCGCTGCTCATCCCATGTAATTCAGTACGATCATCATGACCATGATC 302
Qy      289 ValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg-PhePheI 308
Db      303 GTCCATAGAACTGGGTGGACCTGGCCCTGGCCCTGAGCTACTACATCCGGGTCTTTCAT 362
Qy      308 eThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeuAsnPheIleArgPh 328
Db      363 CACCTACATCCCTTTCAGGCATCTGGGAGCCCTCTCTTCTCACTTCATCAGTT 422
Qy      328 eLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAs 348
Db      423 CCTGAGAGCCACTGTTTGTGGTGCACACAGATGAATCACAATCATCGTATGGAGATTGA 482
Qy      348 pGluGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluI 368
Db      483 CCAGAGCCCTACCGTGAATGAGTGGTGGAGCCCTGACAGCCACCTGCAACGTGGAGCA 542
Qy      368 nSerPheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPh 388
Db      543 GTCCTTCTCAACGACTGGTTCAGTGGACACTTAACTTCCAGATTGAGCACCACCTCTT 602
Qy      398 eProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAl 408
Db      603 CCCACCATGCCCCGGGCAACTTACACAGAGAACCGTA-CTGAGGGCCCTCTGACCATCATC 661
Qy      408 aLysHis-GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp-IleIle 427
Db      662 CAACATGGGCAATGAATACACAGAGAACCGTA-CTGAGGGCCCTCTGACCATCATC 720
Qy      428 ArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyr 441
Db      721 AGGTCCCTGAAAAATTTTGGAAACTGTGGTTGAAGCTTAC 762

RESULT 28
LOCUS   BG741398
DEFINITION BG741398 764 bp mRNA linear EST 15-MAY-2001
          mRNA sequence.
ACCESSION BG741398
VERSION   BG741398.1 GI:14052051
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL  NTH-MGC http://mgi.nci.nih.gov/.
COMMENT  National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished
          Contact: Robert Straubers, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: James Cleaver, M.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
          Sequencing by: Incyte Genomics, Inc.

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM10830 row: n column: 13

High quality sequence stop: 764.

Location/Qualifiers

source
1. .764

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4777164"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 179 a 232 c 184 g 169 t

ORIGIN

Alignment Scores:

Prod. No.: 4.46e-120 Length: 764

Score: 1278.50 Matches: 236

Percent Similarity: 97.52% Conservative: 0

Best Local Similarity: 97.52% Mismatches: 5

Query Match: 52.44% Indels: 2

DB: 10 Gaps: 1

US-09-719-601-5 (1-444) x BG741398 (1-764)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLys 223

Db 3 CACTTAAAGGGTGGCTCTGCCAACTGGTGGAAATATCGCCACTTCCAGCACCCCAAG 62

Qy 224 ProAsnIlePheHis---LysAspProAspValAsnMetLeuHisValPheValLeuGly 242

Db 63 CCTAACATCTTCCACTAAGGATCCCTGATGTGAACATGCTGCACGTGTTGTTCTGGGC 122

Qy 243 GluTrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLys 262

Db 123 GAATGGAGCCCATCGAGTACGGCAAGAGAGTGAATACCTGCCCTTACATCACCAG 182

Qy 263 HisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGln 282

Db 183 CACGAATATCTTCTCTGATTTGGGCGCGCTGCTCATCCCATGATATTCCAGTACCAG 242

Qy 283 IleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyr 302

Db 243 ATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGGCGCTCAGCTAC 302

Qy 303 TyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPhe 322

Db 303 TACATCCGGTCTTCTCATCACCTACATCCCTTTTACGGCATCTCTGGAGCCCTCTTTTC 362

Qy 323 LeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHis 342

Db 363 CTCAACTTTCATCAGGTCTCTGAGAGCCACTGGTTGTGGTGCACACAGATGAATCAC 422

Qy 343 IleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAla 362

Db 423 ATCGTCATGGAGATTGACAGAGGCCCTACCGTGAATGTTTCACTAGTACGAGTACGCC 482

Qy 363 ThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisIleAsnPheGln 382

Db 483 ACCTGCAACGTGGAGCAGTCTCTTCTTCAACGACTGGTTCAGTGGAGCCCTTAACTCCAG 542

Qy 383 IleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeu 402

Db 543 ATTAGCACCACCTCTTCCCAACCATGCCCCGGGCAACTTACACAAATCGC-CCGCTG 601

Qy 403 VallySerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAla 422

Db 602 GTGAAGTCTATGTGCCAAGCATGGCATTTGAATACACAGGAGAGCCGCTACTGAGGCC 661

QY 423 LeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeu 442
 Db 662 CTGCTGGACATCATCAGGACTGAGAAAGTCTGGAGAGCTGGCTGACCCCTACCTT 721

QY 443 HisLys 444
 Db 722 CACAAA 727

RESULT 29
 BG696305 832 bp mRNA linear EST 07-MAY-2001
 DEFINITION 602659454F1 NCI_CGAP_skn3 Homo sapiens cDNA clone IMAGE:4802820 5',
 mRNA sequence.
 ACCESSION BG696305
 VERSION 1 (bases 1 to 832)
 KEYWORDS BG696305.1 GI:13961310
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 832)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LHAM10697 row: k column: 13
 High quality sequence stop: 787.

FEATURES
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 1..832
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4802820"
 /lab_host="PH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Skn3"
 /notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 185 a 250 c 238 g 159 t
 ORIGIN

Alignment Scores:
 Pred. No.: 7.09e-120 Length: 832
 Score: 1277.00 Matches: 242
 Percent Similarity: 96.09% Conservative: 4
 Best Local Similarity: 94.53% Mismatches: 6
 Query Match: 52.38% Indels: 4
 DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG696305 (1-832)

QY 1 MetGlySerGlyValSerGlnGlyGluValAlaGluArgGluValSerValProThr 20
 Db 72 ATGGGAAGAGGGAGAACCAAGTCGAGGGGGCGCGGAGCGAGGTGCGGTGCCACC 131
 QY 21 PheSerTrpGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
 Db 132 TTCAGCTGGGAGGAGATTACAGACATAACCTCGCACCGACAGCGGTGGTCAATTGAC 191
 QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
 Db 192 CGCAAGGTTTACAAACATCACCAAAATGGTCATCCAGCACCCCGGGGGCCAGCGGGTCATC 251

QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
 Db 252 GGGCACTACCTCGAGAGAGATGCAACGGATGCTTCCGGGCTTCCACCTGCACCTGGAA 311
 QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100
 Db 312 TTCGTGGCAAGTTCTTGAACCCCTGCTGATTGGTGAATGGCCCCGGAGAGCCGAGC 371
 QY 101 GluAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
 Db 372 CAGGACCAACGGCAAGAACTCAAGATCACTGAGGACTTCGGGGCCCTGAGGAGACGGCT 431
 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
 Db 432 GAGGACATGAACCTGTTCAAGACCAACACGCTGCTTCTCTCTCTCTCTCTCTCTCTCT 491
 QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160
 Db 492 ATGCGCTGGAGAGCATTCGATGGTTCACTGCTCTTTTACTTTGGCAATGGCTGGATTCT 551
 QY 161 ThrIleuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
 Db 552 ACCCTCATCACGGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 611
 QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200
 Db 612 GATTATGGCCACCTGCTGCTACAGAAACCCAGTGGACCACTTGTCCAAATTC 671
 QY 201 ValIleGlyHis-LeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
 Db 672 GTCATTTGGCCACTTAAAGGGTGGCTCTGCAACTGGTGAATCATCGGCACATCCAGCA 731
 QY 220 sHisAlaLysProAsnIlePheHis-LysAspProAspValAsnMetLeuHisValPheV 240
 Db 732 CCAGCCCAAGCCTAACATCTTCCACCAAGGATCCGATGACCATGTCACGTGTCAGCTGT 791
 QY 240 alleuGlyGlu-TrpGlnProIleGlu-TyrGlyLysLys 252
 Db 792 GTCTGGGGGACTTGGGAGCCCATCGAAGTACGGACCAAGA 831

RESULT 30
 BG698232
 LOCUS 602660143F1 NCI_CGAP_skn3 Homo sapiens cDNA clone IMAGE:4803082 5',
 DEFINITION mRNA sequence.
 ACCESSION BG698232
 VERSION BG698232.1 GI:13965316
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 689)
 AUTHORS NTH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LHAM10698 row: f column: 11
 High quality sequence stop: 687.

FEATURES
 source
 1..689
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4803082"

/lab host="DH10B (T1 phage-resistant)"

/clone lib="NCI CGAP_Skn3"

Note: Organ: sKin; Vector: PCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 167 a 214 c 148 g 160 t

ORIGIN

Alignment Scores:
Pred. No.: 2,39e-118 Length: 689
Score: 1261.00 Matches: 225
Percent Similarity: 99.12% Conservative: 1
Best Local Similarity: 98.68% Mismatches: 2
Query Match: 51.72% Indels: 1
DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG696235 (1-689)

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QY 171 SerGlnAlaGlnAlaGlyTTPLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
Db 5 TCTCAGGCCCAAGCTGGATGCTGCAACATGATTATGCCACCTGTCTGTCTACAGAAA 64
QY 191 ProlysTTPAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
Db 65 CCCAAGTGGAAACCACTTGTCCAAATTCGTATTGGCCCACTTAAAGGGTGCCTCTGCC 124
QY 211 AsnTTPAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
Db 125 AACTGGTGGATCATCGCCACTTCCAGCACCAAGCCCAAGCTTAAACATCTTCCACAGGAT 184
QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTTPGlnProIleGluTyrGly 250
Db 185 CCCGATGTGAACATGCTCAGCTGTGTTCTTGGCGAATGCGACCCATCGAGTACGGC 244
QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
Db 245 AAGAAGAGCTGAATATCTCCCTACATCACCAGCACGATATCTTCTCTGATTGGG 304
QY 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
Db 305 CGCCGCTGCTCATCCCATGTATTTCAGTACCATCATCATCATCATCATCATCATCATCAT 364
QY 291 LysAsnTTPValAspLeuAlaTTPAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
Db 365 AAGAAGTGGTGGACCTGGCCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
Db 425 ATCCCTTTCTACGGCATCTGGGAGCCCTCTTTCTCTCAACTTCATCAGGTTCCTGGAG 484
QY 331 SerHisTTPPheValTTPValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
Db 485 AGCCACTGGTT-GTGTGGGTACACAGATGAATCATCATCGTATGGAGATGACAGGAG 543
QY 351 AlaTyrArgAspTTPPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
Db 544 GCCTACCGTACTGCTTTCAGTAGCAGCTGACAGCCACCTCAAGCTGGAGACGCTCTTC 603
QY 371 PheAsnAspTTPPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThr 390
Db 604 TTCACGACTGGTTTCAGTGGACACCTTAATTCAGATTGAGCCACCTCTTCCCAAC 663
QY 391 MetProArgHisAsnLeuHisLys 398
Db 664 ATGCCCCCGAACAACCTTACACAG 687
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RESULT 31

BG696235

LOCUS

DEFINITION

602659366F1 NCI CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802272 5', mRNA sequence.

ACCESSION

BG696235

VERSION BG696235.1 GI:13961176

KEYWORDS

EST. Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 697)

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Invitrogen, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10696 row: d column: 17
High quality sequence stop: 695.

FEATURES

source

1..697
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4802272"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_Skn3"
/note="Organ: sKin; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 166 a 214 c 170 g 147 t

ORIGIN

Alignment Scores:

Pred. No.: 2,55e-117 Length: 697
Score: 1251.00 Matches: 229
Percent Similarity: 98.71% Conservative: 0
Best Local Similarity: 98.71% Mismatches: 2
Query Match: 51.31% Indels: 1
DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG696235 (1-697)

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QY 34 AppSerGlyLeuValIleAspArgLysValTyrAsnIleThrLysTTPSerIleGlnHis 53
Db 2 GACAGTGGCTGGTCTATTGCCGCAAGTTTACAACATCACCAATGGTCCATCCAGCAC 61
QY 54 ProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArg 73
Db 62 CCGGGGGGCGACGGGTCTATCGGGCACTACGCTGGAGAGATGCAACGATGCTTCCG 121
QY 74 AlaPheHisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGlu 93
Db 122 GCCTTCCACCTGACCTGGAATTCGTGGCAAGTCTTGAACCCCTGCTGATGGTGA 181
QY 94 LeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPhe 113
Db 182 CTGGCCCCGAGAGAGCCAGCCAGGACGAGGAGCACTCAAGATCACTGAGGACTTC 241
QY 114 ArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePhe 133
Db 242 CGGGCCCTGAGGAAGACGGCTGAGGACATGAACCTGTTCAAGACCAACACCGTGTCTTC 301
QY 134 LeuLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTTPPheThrValPheTyr 153
Db 302 CTCCTCTCTGCGCCACATCATCGCCCTGGAGAGCAITGCAATGGTTCCTGCTTTTAC 361
QY 154 PheGlyAsnGlyTTPileProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAla 173
Db 362 TTTGGCAATGGCTGGATTCTACCTCATACGGCCTTGTCTTGTCTTGTCTCTCAGGCC 421
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QY 174 GlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrAcLysProLysTrp 193
Db 422 CAAAGTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAAACCCAGTGG 481
QY 194 AsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrp 213
Db 482 AACCACTTGTCCACAAATTCCTATTGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGG 541
QY 214 AsnHisAspHisPheGlnHisAlaLysProAsnIlePheHisLysAspProAspVal 233
Db 542 ATATCATGGCCACTTCAGACACCAAGCCCAAGCTTAACATCTTCCAAAGATCCCGATGTG 601
QY 234 AsnMetLeuHisValPhe-ValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLY 253
Db 602 AACATGCTGACGTGTTGGTCTGGGCGAATGGCAGCCATCGAGTACGGCAAGAA 661
QY 253 IleuLysTyrLeuProTyrAsnHisGlnHisGlu 264
Db 662 GCTGAAATACCTGCCTCAATCACACGACGAA 695

RESULT 32
BG740017 796 bp mRNA linear EST 15-MAY-2001
LOCUS 602630980F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776427 5',
DEFINITION mRNA sequence.
ACCESSION BG740017
VERSION BG740017.1 GI:14050670
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 796)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10628 row: 0 column: 20
High quality sequence stop: 737.
FEATURES
source Location/Qualifiers
1..796
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4776427"
/lab_host="DHIOB (T1 phage-resistant)"
/clone_lib="NCI CGAP_Skn3"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI CGAP Library."
BASE COUNT 184 a 244 c 174 g 193 t
ORIGIN
Alignment Scores:
Pred. No.: 6,14e-117 Length: 796
Score: 1248.00 Matches: 252
Percent Similarity: 93.38% Conservative: 2
Best Local Similarity: 92.65% Mismatches: 7
Query Match: 51.19% Indels: 13
DB: 10 Gaps: 2

US-09-719-601-5 (1-444) x BG740017 (1-796)

```

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QY 152 PheTyrPheGlyVasnglyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSer 171
Db 2 TTTTACTTTGGCAATGGCTGGATTCTACCTCATCCAGGC-ITTTGCTCTTCTACCTCT 60
QY 172 GlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysPro 191
Db 61 CAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAAACCC 120
QY 192 LysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsn 211
Db 121 AAGTGGACCACTTGTCCACAAATTCGTCAITGGCCACTTAAAGGGTGCCTCTGCCAAC 180
QY 212 TrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePheHisLysAspPro 231
Db 181 TGTGTGAATCATGCCACTTCCAGCACCAAGCCCAAGCTTAACATCTTCCAAAGGATCCC 240
QY 232 AspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLys 251
Db 241 GATGTGAACATGCTGCACGTGTTGTTCTGGGCGAATGGCAGCCATCGAGTACGGCAAG 300
QY 252 LysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyPro 271
Db 301 AAGAAGCTGAATACCTGCCTACAATCACACGACCAAGCTTAACATCTTCCAAAGGATCCC 360
QY 272 ProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLys 291
Db 361 CCGCTGCTCATCCCATGTATNTCCAGTACCAGATCATCATGACCATGATCGTCCATAG 420
QY 292 AsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIle 311
Db 421 AACTGGGTGGACCTGGCGCTGGCGCTGAGTACTACATCCGGTCTTCTCATCACTCAATC 480
QY 312 ProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSer 331
Db 481 CCTTTCTACCGGACTCTGGGAGCCCTCTTTCTCACTTCACTGTTCCCTGGAGAGC 540
QY 332 HisTrpPheValTrpValThr-GlnMetAsnHisIleValMetGluIleAspGlnGluAl 351
Db 541 CACTGGTTTGTGGGTCAACACAGATGAATCATCATCGTATGGAGATTGACCAAGAGGC 600
QY 351 aTyrArgAspTrp-PheSerSerGlnLeuThrAla-ThrCysAsnValGluGlnSer-Ph 370
Db 601 CTACCGGTGACTGGGTTTCAAGTACGAGCTGACAGCCACCTGCAACGTTCCCTGGAGAGC 660
QY 370 ePheAsnAsp-TrpPhe-SerGlyHisLeuAsnPheGlnIleGluHisHis-LeuPhePr 389
Db 661 CTTCACGACTTGGTTTCAAGTGGACACCTTAA-TTCCAGATAGAGCACCACTCTT---CC 716
QY 389 oThrMetProArgHisAsnLeuHis---LysIleAlaProLeuValLysSer-LeuCysA 408
Db 717 CACCATGCCCGGAACAACTTACACCAAGAAATTGCCCGCTGGGTGAAGTCTCTTATGTG 776
QY 408 laLys-HisGlyIleGlu 413
Db 777 CCAAGGCATGSCATTGAA 794

RESULT 33
BG7401667 963 bp mRNA linear EST 12-SEP-2002
LOCUS AGENCOURT 8868718 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6341523
DEFINITION 5', mRNA sequence.
ACCESSION BG7401667
VERSION BG7401667.1 GI:22804803
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 963)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCGM2539 row: 1 column: 04
High quality sequence start: 12
High quality sequence stop: 493.
Location/Qualifiers
1. 963
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6341523"
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/clone_lib="NIH MGC 47"
/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 230 a 296 c 229 g 208 t
ORIGIN
Alignment Scores:
Pred. No.: 9,97e-117 Length: 963
Score: 1247.00 Matches: 233
Percent Similarity: 96.71% Conservative: 2
Best Local Similarity: 95.88% Mismatches: 5
Query Match: 51.15% Indels: 3
DB: 13 Gaps: 0
US-09-719-601-5 (1-444) x BU501667 (1-963)
Qy 62 HisTyrAla-GlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPh 81
Db 3 CACTACGCATGAGAGATGCAACGGATGCCTTCGGCGCTTCACCGCTGCACCTGGAAAT 62
Qy 81 eValGlyLysPheLeuLysProLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 101
Db 63 CGTGGGCAAGTTCTTGAAACCCCTGCTGATTGGTGAATGGCCCCGGAGGAGGCCAGCCA 122
Qy 101 nAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArg-LysThrAlaG 121
Db 123 GGACACACGGCAAGAACTCAAGATCACTGAGGACTTCGGGGCCCTGAGGGAAGACGGCTG 182
Qy 121 LuAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuLeuLeuLeuLeu 141
Db 183 AGGACATGAACCTGTTCAAGACCAACACCGTGTCTTCCTCCTCTCTCGGCCCAATCA 242
Qy 141 lEAlaLeuGluSerIleAlaTppPheThrValPheTyrPheGlyAsnGlyTrpIleProT 161
Db 243 TCGCCCTGGAGAGCATTCGATGGTTCACTGCTCTTTACTTTTGGCAATGGCTGGATTCCTA 302
Qy 161 hrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 181
Db 303 CCTCATCATCGGCCTTGTGCTTGTGTACTCTCTCAGGCCAAACCTGGATGGCTGCACATG 362
Qy 181 spTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPheV 201
Db 363 ATTATGGCACTGTCGTCTACAGAAACCCAGTGGAAACCACTTGTGCCAATAATCG 422
Qy 201 alrleGlyHisLeuLysGlyAlaSerAlaAsnTppTrpAsnHisArgHisPheGlnHis 221
Db 423 TCATTGGGCACCTAAAGGGTGCTCTGGCAACTGGTGGATCATCGCACTTCCACACACC 482

QY 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20
 Db 68 ATGGGGAGAGGAGGAGAACCGAGGGGAGGGGGGGCGGAGCGGAGAGGTGTGGTGCCAC 127
 QY 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValleAsp 40
 Db 128 TTCAGCTGGGAGGAGATTTCAGAGCATACCTCGCCAGCCAGCAGAGTGGTGCATTCAC 187
 QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValle 60
 Db 188 CGCAGGTTTACAAATACCAAAATGTCATCCAGACCCCGGGGGGCGAGCGGTATC 247
 QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
 Db 248 GGGCACTAGCGTGGAGAGATGCAACGAGTGCCTTCGGCGCTTCACACCTGACCTGAA 307
 QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluProSer 100
 Db 308 TTGCTGGGCAAGTTCCTTGAACCCCTGCTGATGTGTGAATGCTGGCCCGGAGGCCAGC 367
 QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
 Db 368 CAGGACACCGCAAGAACTCAAGATCACTGAGGACTTCGGGGCTTCGAGGAAGCGCT 427
 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
 Db 428 GAGGACATGAACCTGTTCAGACCAACACCGTGTCTTCCTCTCTCTCTCTCTCTCTCT 487
 QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160
 Db 488 ATCGCCCTGGAGAGCATTCATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 547
 QY 161 ThrLeuIleThrAlaPheValleuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
 Db 548 ACCCTCATCAGCGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 607
 QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200
 Db 608 GATTATGGCCACCTGTCTGTCTACAGAAACCCNAGTGGACCACTTGTCCACAAATC 667
 QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
 Db 668 GTCAATGGCCACTTAAGGGTGCCTCTGCAATGGTGGAAATCATCGCCACTTCCAGCAA 727
 QY 221 HisAlaLysProAsnIlePheHisLysAspProAspVal 233
 Db 728 CCAGCCACGCTTAACATCTTCCACAGGATCCGATGTG 766

RESULT 35

BI752239
 LOCUS 60302433F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192744 5',
 DEFINITION mRNA sequence.

ACCESSION BI752239.1 GI:15743817

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE EST.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NIH-MGC http://mgi.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11482 row: b column: 09
 High quality sequence stop: 759.
 Location/Qualifiers
 source

1..759

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5192744"

/lab_host="DH10B"

/clone_lib="NIH_MGC_114"

/notes="Organ: Brain; Vector: pCMV-SPORT6; Site: 1. NotI;

Site 2: EcoRV (destroyed); RNA source anonymous pool of 6

male brains, age range 23-27 yo. Library is oligo-dT

primed and directionally cloned (EcoRV site is destroyed

upon cloning). Average insert size 1.5 kb, insert size

range 1-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 019. Note:

this is a NIH MGC library."

BASE COUNT 168 a 233 c 213 g 145 t

ORIGIN

Alignment Scores:

Pred. No.: 1-87e-116 Length: 759

Score: 1243.00 Matches: 228

Percent Similarity: 98.70% Conservatives: 0

Best Local Similarity: 98.70% Mismatches: 3

Query Match: 50.98% Indels: 0

DB: 12 Gaps: 0

US-09-719-601-5 (1-444) x BI752239 (1-759)

QY 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20

Db 67 ATGGGGAGGAGGAGAACCGAGGGGAGGGGGCGGAGCGGAGGTGTGGTGCCAC 126

QY 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValleAsp 40

Db 127 TTCAGCTGGGAGGAGATTTCAGAGCATACCTCGCCAGCCAGCAGGTGGTGTGCATTCAC 186

QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValle 60

Db 187 CGCAAGGTTTACAAATACCAAAATGTCATCCAGCACCCGGGGGGCGAGCGGGTGCATC 246

QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80

Db 247 GGGCACTACCTGGAGAGATGCAACGAGTGCCTTCGGCGCTTCCACCTGACCTGGAA 306

QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluProSer 100

Db 307 TTCGTGGGCAAGTTCCTTGAACCCCTGCTGATGGTGAACCTGGCCCGGAGGAGCCACG 366

QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120

Db 367 CAGGACACCGCAGAGACTCAAGATCACTGAGACTTCCGGGCCCTCGAGGAAGCGCT 426

QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140

Db 427 GAGGACATGAACCTGTTCAGAGCAACCAACCGTGTCTTCCTCTCTCTCTCTCTCTCT 486

QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160

Db 487 ATCCCTCTGGAGAGCATTCATGCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 546

QY 161 ThrLeuIleThrAlaPheValleuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180

Db 547 ACCCTCATCAGCGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 606

QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200

Db 607 GATTATGGCCACCTGTCTGTCTACAGAAACCCCAAGTGGAACCTTGTGCCAAATTC 666

QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220

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Db      667 GTCAATGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGGATCATGCCACTTCCAGCAC 726
QY      221 HisAlaLysProAsnIlePheHisLysAspPro 231
Db      727 CACGCCAAGCCTAAACATCTTCCACAAGATCCC 759

RESULT 36
BG743597
LOCUS   602633951F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778892 5',
DEFINITION mRNA sequence.
ACCESSION BG743597
VERSION   BG743597.1 GI:14054250
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 799)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10635 row: f column: 13
High quality sequence stop: 795.
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4778892"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NCI_CGAP_Skn3"
            /note="Organ: skin; Vector: pCMV-Sport6; Site:1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 1.5kb. Library constructed by Life
            Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 182 a 236 c 205 g 176 t
ORIGIN
Alignment Scores:
Pred. No.: 5,13e-116 Length: 799
Score: 1239.00 Matches: 224
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.82% Indels: 0
Gaps: 10
US-09-719-601-5 (1-444) x BG743597 (1-799)

QY      221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
Db      2 CACGCCAAGCCTAACATCTTCCACAAGATGCCAGTGGATCATGCCACTTCCAGCAC 61
QY      241 LeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsn 260
Db      62 CTGGCGCAATGGCAGCCCATCGAGTACGCGCAAGAAGAGCTGAATACCTGCCCTACAAT 121
QY      261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
Db      122 CACCAAGCAGCAATATCTTCTGATTTGGCGCGCTGCTATCCCATGATTTCCAG 181
QY      281 TyrGlnIleLeuMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300

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Db      182 TACCAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGGCCGCTC 241
QY      301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db      242 AGCTACTCATCCGGTTCCTCATCACCTACATCCCTCTTACGGCATCTCGAGGCCCTC 301
QY      321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTyrPheValTrpValThrGlnMet 340
Db      302 CTTTTCCTCAACTTCATCAGGTTCCTGGAGAGCCACTGGTTGTGTGGTCCACAGATG 361
QY      341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
Db      362 AATCACATCGTCATGAGATTACCAAGAGGCTACCGTACTGGTTTCAGTAGCCAGCTG 421
QY      361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
Db      422 ACAGCCACCTGCAACGCTGGAGCAGTCTCTTCAACGACTGGTTTCAGTGGACACCTTAAC 481
QY      381 PheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
Db      482 TTCCAGATTGACGACCACTCTTCCCACTGCTCCCGGACACTTACACAAAGATCGCC 541
QY      401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db      542 CGCTGGTGAAGTCTCTATGTCACAGCATGGCATTGAATACCAAGAGCGGCTACTG 601
QY      421 ArgAlaLeuLeuAspIleIleArgSerLeuLysSerGlyLysLeuTrpLeuAspAla 440
Db      602 AGGGCCCTCTCGACATCATCAGGTCCCTGAAGAAGTCTGGGAAGCTGTGGCTGGACGCC 661
QY      441 TyrLeuHisLys 444
Db      662 TACCTTCACAAA 673

RESULT 37
BQ071205
LOCUS   1022 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT 6853101 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5927574
5', mRNA sequence.
ACCESSION BQ071205
VERSION   BQ071205.1 GI:19900251
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1022)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2102 row: 1 column: 07
High quality sequence stop: 656.
FEATURES
    Location/Qualifiers
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            /mol_type="mRNA"
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            /clone="IMAGE:5927574"
            /tissue_type="neuroblastoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_47"
            /note="Organ: brain; Vector: pOTB7; Site:1: XhoI; Site:2:
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'

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adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by King Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 224 a 313 c 283 g 202 t
ORIGIN

Alignment Scores:
Pred. No.: 3,67e-115 Length: 1022
Score: 1232.00 Matches: 244
Percent Similarity: 83.28% Conservative: 10
Best Local Similarity: 80.00% Mismatches: 22
Query Match: 50.53% Indels: 30
DB: 13 Gaps: 5

US-09-719-601-5 (1-444) x BQ071205 (1-1022)

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Qy 1 MetGlyLeuGlyAsnGlnGlyGluAlaGluArgGluValserValProThr 20
Db 80 ATGGGAAGGGAGGAACAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 139
Qy 21 PheSerTrpGluLeuGlnGlyHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
Db 140 TTCAGCTGGAGGAGATTGAGAAGCATAACTCGCCACGACAGGTGGCTGTCTATTGAC 199
Qy 41 ArgLeuValIleAsnLeuThrTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
Db 200 CGCAAGGTTTACAAATCATCAACCAATGGTCCATCCAGCACCGGGGGGGGGGGGGTCA 259
Qy 61 GlyHisValAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
Db 260 GGGCACTACCTCGAGGAAGATGAACGATGCGCTCCCGCTTCACCTGACCTGGAA 319
Qy 81 PheValGlyLeuPheLeuLeuProLeuLeuLeuGlyGluLeuAlaProGluProSer 100
Db 320 TTCGTGGGCAAGTTCCTGAACCCCTGCTGATTGGTGAATGGCCCGGAGGAGCCAGC 379
Qy 101 GlnAspHisGlyLeuAsnSerIleThrGluAspPheArgAlaLeuArgIleThrAla 120
Db 380 CAGGACACGCGCAAGAACTCAAGATGACTGAGGACTTCGGGGCCCTGAGGAAGCGGCT 439
Qy 121 GluAspMetAsnLeuPheLeuThrAsnHisValPhePheLeuLeuLeuLeuAlaHisIle 140
Db 440 GAGGACATGAACCTGTTCAAGACCAACCGAGTGTCTTCTCTCTCTCTCTCTCTCTCT 499
Qy 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTrpPheGlyAsnGlyTrpIlePro 160
Db 500 ATCGCCCTGGAGAGCATTCGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 559
Qy 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
Db 560 ACCCTCATACGCGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGT 619
Qy 181 AspTrpGlyHisLeuSerValIleArgLeuProGlyTrpAsnHisLeuValHisLeuPhe 200
Db 620 GATTATGGCCACCTGTCTGTCTACAGAAACCCCAAGTGAACCACTTGTCTCCACAA-TTC 678
Qy 201 ValIleGlyHisLeuLeuGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
Db 679 GTCAATGGCCACTTTAAAGGTGCTCTGCAACTGTTGGTAATCATGCCACTTCCAGCAC 738
Qy 221 HisAlaLeuProAsnIle-PheHisLeuAspProAspValAsnMetLeuHisVal----- 238
Db 739 CACGCCAAGCCTTAACATCTTCCACAGATCCCGGAGGGAACATGCTGCACGTGGTTTG 798
Qy 239 -----PheValLeuGlyGluTrpGlnProIleGluTrpGlyLeuValLeuLeuLeu----- 255
Db 799 TTTCTGGGCGAAGGGCAGCCCATCCA---AGTACGGGCAAGAGAACTGAATATAC 855
Qy 256 -----TyrLeuPro-----Ty 899

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Db 856 CTGGCCCTAAATTCGCCGCCGGAATAAATTCCTTCCTGAAATGGGGGGCGCCGCTT 915
Qy 259 rAsnHisGlnHisGluTrpPhePhe-----LeuIleGlyProProLe 273
Db 916 GCTTCATTCCTCCCATGTAATATTCCTTACCCAAATCTCTCTTGGACCCCTGTT 975
Qy 273 uLeuIleProMet 277
Db 976 ATCCGTCCCGCTT 988

RESULT 38
LOCUS BG743135
DEFINITION 602634281F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779189 5', mRNA sequence.
ACCESSION BG743135
VERSION BG743135.1 GI:14053788
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (Bases 1 to 755)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMI0636 row: b column: 22
High quality sequence stop: 751.
FEATURES
Location/Qualifiers
1..755
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:4779189"
/lab_host="DH10B (TI phase-resistant)"
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/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.5kb Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 166 a 233 c 212 g 144 t
ORIGIN

Alignment Scores:
Pred. No.: 1.28e-114 Length: 755
Score: 1225.00 Matches: 225
Percent Similarity: 98.68% Conservative: 0
Best Local Similarity: 98.68% Mismatches: 3
Query Match: 50.25% Indels: 0
DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG743135 (1-755)
Qy 1 MetGlyLeuGlyGlyAsnGlnGlyGluGlyAlaGluArgGluValserValProThr 20
Db 72 ATGGGAAGGGAGGAACAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 131
Qy 21 PheSerTrpGluGluIleGlnHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
Db 132 TTCAGCTGGAGGAGATTGAGAAGCATAACTCGCCACGACAGGTGGCTGGTCAATTGAC 191
Qy 41 ArgLeuValIleAsnIleThrTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
Db 192 CGCAAGGTTTACAAATCATCAACCAATGGTTCATCCAGCACCGGGGGGGGGGGTCA 251

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QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
 Db 252 GGGCACTACGCTGGAGAGATGCACGATGCTTCCTCGGCGCTTCACCTGACCTGGAA 311
 QY 81 PheValGlyLysPheLeuLysProLeuLeuGlyGluLeuAlaProGluGluProSer 100
 Db 312 TTCGTGGGCAAGTCTTCAAAACCTGCTGATGTTGTAACCTGGCCCGGAGGAGCCAGC 371
 QY 101 GlnAspHisGlyLysAsnSerLysLeuThrGluAspPheArgAlaLeuArgLysThrAla 120
 Db 372 CAGGACCAAGGAGAGACTCAAGATCACTGAGGACTTCGCGGCTTCGAGGAGACGGCT 431
 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
 Db 432 CAGGACATGAACCTGTTCAAGACCAACACGCTGTTCTTCCTCTCTCTCGGCGCACATC 491
 QY 141 IleAlaLeuGluSerIleAlaThrPheThrValPheTyrPheGlyAsnGlyTyrIlePro 160
 Db 492 ATCGCCCTGGAGAGATTCGATGGTTCACCTGCTCTTTTACTTTGGCAATGGCTGGATTCCT 551
 QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTyrLeuGlnHis 180
 Db 552 ACCCTCATCAGGCTTGTCTGCTTACCTCTCAGGCCCAAGCTGGATGGCTGCAACAT 611
 QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTyrAsnHisLeuValHisLysPhe 200
 Db 612 GATTATGGCCACCTGCTGTCTACAGAAACCCCAAGTGAACCACTGTGTCACAAATTC 671
 QY 201 ValIleGlyHisLeuLysGlyValAsnSerAlaAsnTyrTyrAsnHisArgHisPheGlnHis 220
 Db 672 GTCATTTGCCACTTAAGGGTGCCTTCGCAACTGGTGGATCATCGCCACTTCCAGCAC 731
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 ACCESSION CA488711
 VERSION CA488711.1 GI:24951219
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 971)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contract: Robert Strausberg, Ph.D.
 Email: c9abbs-remail.nih.gov
 Tissue Procurement: Kristi A. Eglund, Ira Pastan
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM14281 row: b column: 23
 High quality sequence start: 25
 High quality sequence stop: 562.
 Location/Qualifiers
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 /clone="IMAGE:6720887"
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 LNCaP"

FEATURES
 source

BASE COUNT 228 a 291 c 236 g 216 t
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 Alignment Scores:
 Pred. No.: 2,378-113 Length: 971
 Score: 1214.00 Matches: 215
 Percent Similarity: 98.17% Conservative: 0
 Best Local Similarity: 98.17% Mismatches: 4
 Query Match: 49.79% Indels: 0
 DB: 14 Gaps: 0

US-09-719-601-5 (1-444) x CA488711 (1-971)
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 QY 187 ValTyrArgLysProLysTyrAsnHisLeuValHisLysPheValIleGlyHisLeuLys 206
 Db 70 GTCTACAGAAACCCCAAGTGAACCACTGTGCCAAATTCCTCATTTGGCCACCTTAAAG 129
 QY 207 GlyAlaSerAlaAsnTyrTyrAsnHisArgHisPheGlnHisHisAlaLysProAsnIle 226
 Db 130 GGTGCTCTGCGCAACTGGTGGAAATCATGCCACTTCCAGCACACGCGCAAGCTTACATC 189
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 QY 247 IleGluTyrGlyLysLysLysLysLysTyrLeuProTyrAsnHisGlnHisGluTyrPhe 266
 Db 250 ATCGATACGGCAAGAGAGAGCTGAAATACCTGCGCTTCAATCACAGCACGCAATACTTTC 309
 QY 267 PheLeuIleGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIleIleMetThr 286
 Db 310 TTCTCATTTGGCGCGCGCTGCTCATCCCATGTATTTCCAGTACCATCATCATGACC 369
 QY 287 MetIleValHisLysAsnTyrValAspLeuAlaTyrAlaValSerTyrTyrIleArgPhe 306
 Db 370 ATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGGCGCTGAGTACTACATCCGGTTC 429
 QY 307 PheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIle 326
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 QY 327 ArgPheLeuGluSerHisTyrPheValTyrValThrGlnMetAsnHisIleValMetGlu 346
 Db 490 AGGTTCTCTGGAGAGCCACTGGTTGTGTGGGTGCACACAGATGAATCACAATCGCTATGGAG 549
 QY 347 IleAspGlnGluAlaTyrArgAspTyrPheSerSerGlnLeuThrAlaThrCysAsnVal 366
 Db 550 ATTGACCAAGAGGCTTACCGTACTGTTTCACTAGTACAGCTGACAGCCACCTTGCACCGTG 609
 QY 367 GluGlnSerPhePheAsnAspTyrPheSerGlyHisLeuAsnPheGlnIleGluHis 385
 Db 610 GAGCAGTCTCTTCTTCAACGACTGGTTTCACTGGACACCTTAACCTTCCAGAATGAGCAC 666

RESULT 40
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 mRNA sequence.
 ACCESSION BG422898

EST 14-MAR-2001
 linear
 753 bp
 mRNA
 Homo sapiens cDNA clone IMAGE:4586387 5',
 mRNA sequence.
 BG422898

/lab host="EMDH10B"
 /clone lib="MAPcL"
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 Directionally cloned. Priming method: oligo-dT. Average
 insert size: 1800 bp. Library amplification: 26,000 fold.
 Kristi A. Eglund, James J. Vincent, Robert Strausberg,
 Bungkook Lee & Ira Pastan: Discovery of new breast
 cancer genes encoding membrane and secreted proteins.
 Manuscript submitted."

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VERSION      BG422898.1  GI:13329404
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 753)
JOURNAL      NIH-MGC http://mgi.nci.nih.gov/
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: gspbs-remail.nih.gov
            Tissue Procurement: DCTD/DTF
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LCM320 row: d column: 20
            High quality sequence stop: 677.
FEATURES     Location/Qualifiers
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                /clone="IMAGE:4588387"
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                /clone_lib="NIH_MGC_14"
                /notes="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
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                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
            BASE COUNT  175 a  224 c  190 g  164 t
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            Pred. No.:      2,72e-113      Length:      753
            Score:          1212.00      Matches:      223
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            Best Local Similarity: 99.55%      Mismatches: 1
            Query Match:      49.71%      Indels:      1
            DB:                10      Gaps:          0
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            Db      2 TTCAGGACCAAGCCAGCCAGCTACATCTCCACAGGATCCCGATGGAACATGTCGCAC 61
            QY      238 ValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLysTyrLeu 257
            Db      62 GTGTT-GTTCTGGCGAATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAATACCTG 120
            QY      258 ProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMet 277
            Db      121 CCTTACCAATCCAGACAGCAATCTCTCTGATTTGGCGCCGCTGCTCATTCCTCATG 180
            QY      278 TyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAla 297
            Db      181 TATTTCCAGTACCAAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCC 240
            QY      298 TrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeu 317
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            QY      318 GlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVal 337

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QY      338 ThrGlnMetAsnHisIleValMetClnIleAspGlnIleAlaTyrArgAspTrpPheSer 357
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QY      378 HisLeuAsnPheGlnIleGlnHisHisIleuPhePheThrMetProArgHisAsnLeuHis 397
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Db      541 AAGATCGCCCGCTGTGTGAAGTCTCTATGTGCCAAGCATGTCATTGAATACAGGAGAAG 600
QY      418 ProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGlyLysLeuTrp 437
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QY      438 LeuAspAlaTyr 441
Db      661 CTGGAGCGCTAC 672

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Search completed: December 10, 2003, 20:05:52
Job time : 1981 secs

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2	1830.4	57.5	1843	15	US-10-191-513A-7	Sequence 7, Appli
3	1675	52.6	1686	15	US-10-191-513A-6	Sequence 6, Appli
4	1383.2	43.4	1474	15	US-10-102-806-232	Sequence 232, App
5	697.8	21.9	1717	15	US-10-262-617-2	Sequence 2, Appli
6	608.2	19.1	1928	15	US-10-262-617-4	Sequence 4, Appli
7	608.2	19.1	1972	9	US-09-822-849A-485	Sequence 485, App
8	608.2	19.1	4213	13	US-10-133-937-7	Sequence 7, Appli
9	602.8	19.9	1335	15	US-10-191-513A-1	Sequence 1, Appli
10	565.8	17.8	1478	10	US-09-981-876-63	Sequence 63, Appli
11	565.8	17.8	1478	11	US-09-148-545-63	Sequence 63, Appli
12	443.6	13.9	456	9	US-09-604-287A-313	Sequence 313, App
13	443.6	13.9	456	10	US-09-339-338-313	Sequence 313, App
14	443.6	13.9	456	11	US-09-551-621-313	Sequence 313, App
15	443.6	13.9	456	13	US-10-134-805-313	Sequence 313, App

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Db	15	GCGTACTTCACCTGGACAGAGTGGCCCGCTCAGGGTGCAGAGGCGGTGGCTAGT		74	
Qy	293	CATTGACCGCAAGGTTTACAAACAT	CCCAATGGTCCATCCAGCACCCCGGGGGGCCACGC	352	

Db 75 GATCGACCGTAAAGGTGTACAAATCAGCGAGTTACCCCGCGGATCAGCGGGGCTCCCG 134
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Db 135 GGTCACTACGCACTACGCGCGGAGGATGCCAGGATCCCTTTGTGGCTTCCACATCAA 194
QY 413 CTGTGAATTCGTGGGCAAGTCTTGAACCCCTGCTGATGTTGTAACCTGGGCCCGGAGGA 472
Db 195 CAAGGCGCTTGTGAAGAATATGAATCTCTCTCTGATTGGAATCTCTCCAGAGCA 254
QY 473 GCCACGACGAGCAGCAGGCAAGAACTCAAGATCACTAGGACTTCGGGCCCTGAGGAA 532
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QY 533 GAGGGTGAAGCATGAACCTGTTCAAGAACCAACACGTTGTTCTCTCTCTCTCTCTCTGGC 592
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QY 593 CCACATCATCGCCCTGGAGAGCAATGTCATGTTGATGTTCTCTCTCTCTCTCTCTCTCTG 652
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QY 653 GATTCCTACCTCATC- - -ACGGCCCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 709
Db 435 TTTCGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 494
QY 710 GCTGCAACATGATTATGGCCACTCTGCTCTACAGAAACCCAGTGGACCACTCTGT 769
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QY 770 CCAAAATTCGTCAATGGCCACTTAAAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 829
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RESULT 2

US-10-191-513A-7
; Sequence 7, Application US/0191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-7

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Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy	690	TCTCAGCCCAAGCTGGATGCTGCACATGATTATGGCCACCTGCTGTCTACAGAAA	749
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Qy	750	CCCAAGTGGAAACCACTTGTCCAAATTCGTATTGGCCACCTAAAGGCTGCTCTGCC	809
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Qy	810	AACCTGGTGGATCATCCGCACTCCAGCACCGCCAGCCTAACATCTTCCACAGGAT	869
Db	181	AACCTGGTGGATCATCCGCACTCCAGCACCGCCAGCCTAACATCTTCCACAGGAT	240
Qy	870	CCCGATGTGAACATGCTGCACGTGTTTGTCTGGCGGAATGGCAGCCCATCGAGTACGGC	929
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Qy	930	AAGAAGAGCTGAATACCTGCCCTACAAATCAGCACCGCAAGCAATCTTCTCTGATGGG	989
Db	301	AAGAAGAGCTGAATACCTGCCCTACAAATCAGCACCGCAAGCAATCTTCTCTGATGGG	360
Qy	990	CCGCGGTGCTCATCCGCCATGATTTTCCAGTACAGATCATCATGACCATGATCGTCCAT	1049
Db	361	CCGCGGTGCTCATCCGCCATGATTTTCCAGTACAGATCATCATGACCATGATCGTCCAT	420
Qy	1050	AAGAAGCTGGTGGACCTGGCGTGGCGTACGCTACATATCCGGTTCCTTCATCACCTAC	1109
Db	421	AAGAAGCTGGTGGACCTGGCGTGGCGTACGCTACATATCCGGTTCCTTCATCACCTAC	480
Qy	1110	ATCCCTTTCTACGGCATCTCCGGAGCCCTCTTTCTCAACTTCATCAGGTTCCCTGGAG	1169
Db	481	ATCCCTTTCTACGGCATCTCCGGAGCCCTCTTTCTCAACTTCATCAGGTTCCCTGGAG	540
Qy	1170	AGCCACTGGTTGTGTGGGTCAACAGATGAATCAATGCTATGAGATGACAGGAG	1229
Db	541	AGCCACTGGTTGTGTGGGTCAACAGATGAATCAATGCTATGAGATGACAGGAG	600

Qy	1230	GCCTACCGTGACTGGTTCACTAGCCAGCTGACAGCCACCTGCAACCTGGAGCAGTCTTCT	1289
Db	601	GCCTACCGTGACTGGTTCACTAGCCAGCTGACAGCCACCTGCAACCTGGAGCAGTCTTCT	660
Qy	1290	TTCAACGACTGGTTCACTAGCAGCCTTAACTTCCAGATTGAGCAGCAGCTTCTTCCACC	1349
Db	661	TTCAACGACTGGTTCACTAGCAGCAGCTTAACTTCCAGATTGAGCAGCAGCTTCTTCCACC	720
Qy	1350	ATGCCCGGACAACTTACCAAGATCGCCCGCTGCTGCTGAAGTCTCTATGTGCCAAGCAT	1409
Db	721	ATGCCCGGACAACTTACCAAGATCGCCCGCTGCTGCTGAAGTCTCTATGTGCCAAGCAT	780
Qy	1410	GGCATTGAATACAGAGAGAGCCCTACTAGGGCCCTGCTGGACATCATCAGTCTCCTG	1469
Db	781	GGCATTGAATACAGAGAGAGCCCTACTAGGGCCCTGCTGGACATCATCAGTCTCCTG	840
Qy	1470	AAGAAGTCTGGGAAAGCTGTGGCTGGAGCCCTTACCTTCACAAAATGAAGCCACAGCCCGG	1529
Db	841	AAGAAGTCTGGGAAAGCTGTGGCTGGAGCCCTTACCTTCACAAAATGAAGCCACAGCCCGG	900
Qy	1530	CACACCGTGGGAAAGGGGTGAGTGGGGTATGGCCAGAGGAATGATGGCTTTTGTTC	1589
Db	901	CACACCGTGGGAAAGGGGTGAGTGGGGTATGGCCAGAGGAATGATGGCTTTTGTTC	960
Qy	1590	TGAGGGGTGTCGAGAGAGCTGCTGTATGCACTGTCTACGGACCCCATGTTTGGATCTTCT	1649
Db	961	TGAGGGGTGTCGAGAGAGCTGCTGTATGCACTGTCTACGGACCCCATGTTTGGATCTTCT	1020
Qy	1650	CCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1709
Db	1021	CCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1080
Qy	1710	CTGCCCTCCCTCAGCGTCAGCCATCAGCCATGAGCCCTCCAGAGCTCTCCCTAGCCCTTC	1769
Db	1081	CTGCCCTCCCTCAGCGTCAGCCATCAGCCATGAGCCCTCCAGAGCTCTCCCTAGCCCTTC	1140
Qy	1770	TTCCAAGGAGCAGAGAGTGGCCACCGGGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1829
Db	1141	TTCCAAGGAGCAGAGAGTGGCCACCGGGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1200
Qy	1830	CTAAGATGGGAGGAGCAGCGGTCCATGGGTCTGGCTGTGGCTGTGGCTGTGGCTGTGGCT	1889
Db	1201	CTAAGATGGGAGGAGCAGCGGTCCATGGGTCTGGCTGTGGCTGTGGCTGTGGCTGTGGCT	1260
Qy	1890	TGGTCACTAGGCATCACCCCGCTTTTGGTTCTTTCAGATGCTCTTGGGGTTCATAGGGCA	1949
Db	1261	TGGTCACTAGGCATCACCCCGCTTTTGGTTCTTTCAGATGCTCTTGGGGTTCATAGGGCA	1320
Qy	1950	GGTCTAGTCCGGCAGGCGCCCTGACCTCCGGGCTGGCTTCACTCTCCCTGACGGCTG	2009
Db	1321	GGTCTAGTCCGGCAGGCGCCCTGACCTCCGGGCTGGCTTCACTCTCCCTGACGGCTG	1380
Qy	2010	CCATTGGTCCACCCCTTTTCATAGAGAGGCTGCTTTTGTACAAAGCTCGGGTCTCCCTCT	2069
Db	1381	CCATTGGTCCACCCCTTTTCATAGAGAGGCTGCTTTTGTACAAAGCTCGGGTCTCCCTCT	1440
Qy	2070	GCAGTCTGGTTAAGTACCCGAGGCTCTCTTAAAGTGTCCAGGGCCCGCAGCCCGGGC	2129
Db	1441	GCAGTCTGGTTAAGTACCCGAGGCTCTCTTAAAGTGTCCAGGGCCCGCAGCCCGGGC	1500
Qy	2130	ACAGCCAGCCCAAACTTTGGGCGCTGGAGAGTCTCTCCACCCCATCATCTAGAGTCTCTG	2189
Db	1501	ACAGCCAGCCCAAACTTTGGGCGCTGGAGAGTCTCTCCACCCCATCATCTAGAGTCTCTG	1560
Qy	2190	ACCTTGGGCTTTCACGGGCGCCCATTCACCGCTCCCCCACTTGGAGCTGTGACCTTGGG	2249
Db	1561	ACCTTGGGCTTTCACGGGCGCCCATTCACCGCTCCCCCACTTGGAGCTGTGACCTTGGG	1620
Qy	2250	ACCAAGGGGAGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2309
Db	1621	ACCAAGGGGAGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1680
Qy	2310	GGGGCGGGCTGGCGGTGAGGCTCAGCCCAACCCCTCAGCTTTTCTCAGGGTGTCTGAGG	2369

Db	1681	GGGGCCGGCTGGCTGGAGGCTCAGCCACCCCTCCAGCTTTTCTCCTCAGGGTCTCCTGAGG	1740
Qy	2370	TCCAAGATTCTGAGCAACTGACCCCTTCTCCAAAGGCTCTGTATTACGCTGGCAGTGCC	2429
Db	1741	TCCAAGATTCTGAGCAACTGACCCCTTCTCCAAAGGCTCTGTATTACGCTGGCAGTGCC	1800
Qy	2430	CAGCAATCCTCGCCATTTGGCCCCCAGGGGAGCTGGGCCCTG	2473
Db	1801	CAGCAATCCTCGCCATTTGGCCCCA-GGGGAGCTGGGCCCTG	1843
RESULT 3			
US-10-191-513A-6			
; Sequence 6, Application US/10191513A			
; Publication No. US20030104596A1			
; GENERAL INFORMATION:			
; APPLICANT: Abbott Laboratories			
; APPLICANT: Mukerji, Pardeep			
; APPLICANT: Leonard, Amanda E.			
; APPLICANT: Huang, Yung-Sheng			
; APPLICANT: Tapas, Das			
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF			
; FILE REFERENCE: 6295.US.D3			
; CURRENT APPLICATION NUMBER: US/10/191,513A			
; CURRENT FILING DATE: 2002-09-25			
; PRIOR APPLICATION NUMBER: US 09/227,613			
; PRIOR FILING DATE: 1999-01-08			
; PRIOR APPLICATION NUMBER: PCT/US98/07422			
; PRIOR FILING DATE: 1998-04-10			
; PRIOR APPLICATION NUMBER: US 08/833,610			
; PRIOR FILING DATE: 1997-04-11			
; NUMBER OF SEQ ID NOS: 54			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 6			
; LENGTH: 1686			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-191-513A-6			
Query Match 52.6%; Score 1675; DB 15; Length 1686;			
Best Local Similarity 99.9%; Pred: No. 0;			
Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;			
Qy	787	GCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATATCGCCACTTCAGCACCACGCCA	846
Db	1	GCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATATCGCCACTTCAGCACCACGCCA	60
Qy	847	AGCCTAAACATCTTCACAGAGATCCCGATGTGACATGCTGCAGTGTTTCTCTGGCG	906
Db	61	AGCCTAAACATCTTCACAGAGATCCCGATGTGACATGCTGCAGTGTTTCTCTGGCG	120
Qy	907	AATGGCAGCCCATCGAGTACGGCAAGAAAGAGTGAATACTGCCCTACAAATCACCAGC	966
Db	121	AATGGCAGCCCATCGAGTACGGCAAGAAAGAGTGAATACTGCCCTACAAATCACCAGC	180
Qy	967	AGCAATATCTTCTGATTGGGCGCGCTGCTCATCCCATGATTTCCAGTACCAGA	1026
Db	181	AGCAATATCTTCTGATTGGGCGCGCTGCTCATCCCATGATTTCCAGTACCAGA	240
Qy	1027	TCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGGCGCTCAGTACT	1086
Db	241	TCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGGCGCTCAGTACT	300
Qy	1087	ACATCGGTTCTTCAATCACTACCTTTCTACGGCACTCTGGAGCCCTCTTTTCC	1146
Db	301	ACATCGGTTCTTCAATCACTACCTTTCTACGGCACTCTGGAGCCCTCTTTTCC	360
Qy	1147	TCAACTTCATCAGTTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATACA	1206
Db	361	TCAACTTCATCAGTTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATACA	420
Qy	1207	TCGTCAATGAGATATGACCAAGGAGCCCTACCGTGACTGGTTCAGTACCGAGTGCAGCCA	1266

Db 1501 GAGCAGTGGCCACCGTTTCAGGAGGGGGCGGCTGGGCTGGAGGCTCAGCCCAACCCCTCCAG 1560
QY 2347 CTTTCTCCTCAGGGTGCTCAGGTCAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGG 2406
Db 1561 CTTTCTCCTCAGGGTGCTCAGGTCAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGG 1620
QY 2407 CTTCTGTTATCAGTGGGAGTGCGCAGCCAAATCCCTGGCCATTGGCCCCCAGGGGACGTG 2466
Db 1621 CTTCTGTTATCAGTGGGAGTGCGCAGCCAAATCCCTGGCCATTGGCCCCCA-GGGGACGTG 1679
QY 2467 GGGCCCTG 2473
Db 1680 GGGCCCTG 1686

RESULT 4
US-10-102-806-232
; Sequence 232, Application US/10102806
; Publication No. US2003005421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 232
; LENGTH: 1474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1337)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1355)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1377)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-232

Query Match 43.4%; Score 1383.2; DB 15; Length 1474;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1433; Conservative 4; Mismatches 35; Indels 3; Gaps 3;

QY 652 GGATTCTACCTCATCAGCGCCCTTGTCTGTCTACCTCTCAGGCCCAAGCTGGATGGC 711
Db 1 GGATTCTACCTCATCAGCGCCCTTGTCTGTCTACCTCTCAGGCCCAAGCTGGATGGC 60
QY 712 TGCACATGATATGGCACTGTCTGTCTACAGAAACCCAAAGTGGAACCACTTGTC 771
Db 61 TGCACATGATATGGCACTGTCTGTCTACAGAAACCCAAAGTGGAACCACTTGTC 120
QY 772 ACAATTCGTCATGGCCACTTAAAGGTGCTCTGCGCAACTGTGGAATCATGCCACT 831
Db 121 ACAATTCGTCATGGCCACTTAAAGGTGCTCTGCGCAACTGTGGAATCATGCCACT 180
QY 832 TCCAGCACCAAGCCCAAGCTTAACATCTTCCAAAGGATCCGATGTGAACATGTCGACG 891
Db 181 TCCAGCACCAAGCCCAAGCTTAACATCTTCCAAAGGATCCGATGTGAACATGTCGACG 240
QY 892 TGTGTTCTGGCGAATGGGCGCCATCGAGTACGCGCAAGAAAGCTGAATACCTGC 951
Db 241 TGTGTTCTGGCGAATGGGCGCCATCGAGTACGCGCAAGAAAGCTGAATACCTGC 300

QY 952 CCTACAAATCAGCAGCAAGAAATACCTTCTTCTGATTGGGCGCGCGCTGCTCATCCCATGT 1011
Db 301 CCTACAAATCAGCAGCAAGAAATACCTTCTTCTGATTGGGCGCGCGCTGCTCATCCCATGT 360
QY 1012 ATTTCCAGTACCAAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCT 1071
Db 361 ATTTCCAGTACCAAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCT 420
QY 1072 GGGCCGTCACTACTACATCCGGTTCCTCATCACTTACATCCCTTCTTCTAGGATCCTGG 1131
Db 421 GGGCCGTCACTACTACATCCGGTTCCTCATCACTTACATCCCTTCTTCTAGGATCCTGG 480
QY 1132 GAGCCCTCTTTTCTCACTTCACTAGGTTCCTTGAGAGCCCACTGTTTGTGTGGTCA 1191
Db 481 GAGCCCTCTTTTCTCACTTCACTAGGTTCCTTGAGAGCCCACTGTTTGTGTGGTCA 540
QY 1192 CACAGATGAATCAGATCGTCAATGAGATGACCAAGAGGCTACCGTACTGTTCACTA 1251
Db 541 CACAGATGAATCAGATCGTCAATGAGATGACCAAGAGGCTACCGTACTGTTCACTA 600
QY 1252 GCCAGCTGAGAGCCCACTGCAAGCTGGAGCAGTCTTCTTCAACGACTGGTTCAGTGGAC 1311
Db 601 GCCAGCTGAGAGCCCACTGCAAGCTGGAGCAGTCTTCTTCAACGACTGGTTCAGTGGAC 660
QY 1312 ACCTTAACTTCCAGATTGAGCAACCACTTCTTCCCACTGCCCCGCGCACACTTACACA 1371
Db 661 ACCTTAACTTCCAGATTGAGCAACCACTTCTTCCCACTGCCCCGCGCACACTTACACA 720
QY 1372 AGATCGCCCGCTGCTGAGTCTCTATGTCGAGCAGTGGCATTTGAATACAGGAGAGC 1431
Db 721 AGATCGCCCGCTGCTGAGTCTCTATGTCGAGCAGTGGCATTTGAATACAGGAGAGC 780
QY 1432 CGTACTGAGGGCCCTGCTGAGCATCATCAGTCTTCTTGAAGAGTCTGGGAAGCTGTGGC 1491
Db 781 CGTACTGAGGGCCCTGCTGAGCATCATCAGTCTTCTTGAAGAGTCTGGGAAGCTGTGGC 840
QY 1492 TGGAGCCCTACTTTCACAAATGAAGCCAGCCCGCGGACACCGTGGGAGGGTGGCA 1551
Db 841 TGGAGCCCTACTTTCACAAATGAAGCCAGCCCGCGGACACCGTGGGAGGGTGGCA 900
QY 1552 GGTGGGGTGATGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGTGG 1611
Db 901 GGTGGGGTGATGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGTGG 960
QY 1612 TGTATGCACTGCTACGAGCCCACTGTTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1671
Db 961 TGTATGCACTGCTACGAGCCCACTGTTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
QY 1672 CTTCACTCTCCCCATAGCACCCCTGCTCATGAGGACCTGCCCTCCCTCAGCCGTGAGC 1731
Db 1021 CTTCACTCTCCCCATAGCACCCCTGCTCATGAGGACCTGCCCTCCCTCAGCCGTGAGC 1080
QY 1732 CATCAGCATGGCCCTCCAGTGCTCTAGCCCTTCTTCCAAAGGACAGAGAGGTGGC 1791
Db 1081 CATCAGCATGGCCCTCCAGTGCTCTAGCCCTTCTTCCAAAGGACAGAGAGGTGGC 1140
QY 1792 CACCGGGGTGGCTGTCTGCTTACCTTCCACTCTCTGCCCCCTAAAGATGGGAGAGACCAGC 1851
Db 1141 CACCGGGGTGGCTGTCTGCTTACCTTCCACTCTCTGCCCCCTAAAGATGGGAGAGACCAGC 1200
QY 1852 GGTTCATGGGTGGCCCTGTGAGTCTCCCTTTGAGCCTGTGCTCCTAGGATCAGCCCGC 1911
Db 1201 GGTTCATGGGTGGCCCTGTGAGTCTCCCTTTGAGCCTGTGCTCCTAGGATCAGCCCGC 1260
QY 1912 CTTTGGTTCCTCAGATGCTCTTGGGTTTCATAGGGCAGGTCTAGTCTGCGAGGGGCC 1970
Db 1261 CTTTGGTTCCTCAGATGCTCTTGGGTTTCATAGGGCAGGTCTAGTCTGCGAGGGGCC 1320
QY 1971 CTGACCCCTCCCGCCCTGGCTTCACTCTCCCTG-AGGGCTGCAATTTGTTCCACCTTTTCA 2029
Db 1321 CTGACCCCTCCCGCCCTGGCTTCACTCTCCCTGAAACGTTNGCAATTTGTTCCACCTTTTCA 1380
QY 2030 AGAGAGGCCCTGTTTGTGTACAAAGCTCGGGTCTCCCTCTGAGCTCGGTAAAGTACCGG 2089

Db 1381 AAAAAGGCTGCTGTGTACAAAGTTCGGGTTTTCCTTCTCTGACCTCGGTAA-FAACCG 1439
Qy 2090 AGCCCTCTCTTAAGATGTCAGGCGCCCGAGGCCG 2124
Db 1440 AAGGCTCTCTTAAGATGTTTCAAGGCGCCCAAGGCCG 1474

RESULT 5
US-10-262-617-2
; Sequence 2, Application US/10262617
; Publication No. US2003007747A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
; FILE REFERENCE: PF-0494-1 DIV
; CURRENT APPLICATION NUMBER: US/10/262,617
; PRIOR FILING DATE: 2002-09-30
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CB1
US-10-262-617-2

Query Match 21.9%; Score 697.8; DB 15; Length 1717;
Best Local Similarity 70.7%; Pred. No. 8.2e-190;
Matches 943; Conservative 0; Mismatches 387; Indels 3; Gaps 1;

Qy 198 CAGGCGAGGGGGCGCGGAGCGGAGTGTCGGTGCCTCCACCTTCAGCTGGAGGAGATT 257
Db 99 CCGGGGAGGAGACCGCGCGACGAGTGGCTGTGCATCGAGCGCGCGTCTACGACATC 158
Qy 258 CAGAAGCATAACCTGCGCACCGACAGTGGGTGTGTATTGATACCGCAAGGTTTACAAATC 317
Db 159 CGCGCGACGACCGCGCGGCGACAAAGTGGCTGTGCATCGAGCGCGCGTCTACGACATC 218
Qy 318 ACCAAATGTTCCATCCAGACCCCGGCGGCGAGGGGTCTATCGGCACTACGCTGGAGAA 377
Db 219 AGCCCGTGGGCACAGCGGACCCAGGGGGAGCGCCCTTCATCGGCCACCGCGCTGAG 278
Qy 378 GATGCAACGGGATGCTTCCGGGCGCTTCCACCTGTACCTGGAATTCGTGGCAAGTTCTTG 437
Db 279 GAGCGACGGATGCTTCCGGTCCCTTCCATCAAGATCTCAATTTGTGCGCAAGTTCTTA 338
Qy 438 AAACCCCTGCTGATTTGGTGAAGTCCCGGAGGAGCCAGCGGCACTACGCTGGAGAA 497
Db 339 CAGCCCGCTGTTGATTTGAGAGTGGCTCGGAAGAACCCAGCGAGATGAGACCCCTGAT 398
Qy 498 TCAAGATCACTGAGGACTTCCGGGCGCTTCCGAGAGAGCGGTGAGGACATGAACCTGTTC 557
Db 399 GCGGAGCTGCTGAGGACTTCCGAGCGCTTCCAGCGGCTGACACGAGCGAGGACATGAAGTGT 458
Qy 558 AAGACCAACCAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 617
Db 459 GATGCCAGTCCCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 518
Qy 618 GATGTTTCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 677
Db 519 GCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 578
Qy 678 GTCTTTGTACCTCTCTCAGGCCCAAGTGGATGGGTGCAACATGATTAAGCCACCTGTCT 737
Db 579 ATCTGGCCATCTCTCTCAGGCTCAGTCTCTGTGTCTGTGACATGACCTGGGCCATCCCTCC 638

Qy 738 GTCTACAGAAAAACCAAGTGGAAACCACTTGTTCACAAATTCGTCATTTGGCCACTTAAAG 797
Db 639 ATCTTCAAGAAGTCTCTGGTGAACCACTGTCGCCAGAAAGTTCGTGATGGGCGAGCTAAAG 698
Qy 798 GGTGCTCTCTGCAACTGTTGGAATCATCGCCACTTCCAGCACCAAGCCCAAGCCTTAACATC 857
Db 699 GGCTTCTCCGCCCACTGTTGGAATCTTCCGCCACTTCCAGCACCAAGCCCAAGCCTTAACATC 758
Qy 858 TTCCACAAGGATCCCGATGTGAACATCTGCAAGTGTTCCTTGGGCGAATGGCAGCCC 917
Db 759 TTCCACAAGGATCCCGATGTGAACATCTGCAAGTGTTCCTTGGGCGAATGGCAGCCC 815
Qy 918 ATCAGTACGCAAGAGAGTGAATTAATCTGCTGCTTACCAATCAGCAGCAGCAATCTTC 977
Db 816 GTCAGTATGCAAGAGAGAGTGAATTAATCTGCTGCTTACCAATCAGCAGCAGCAATCTTC 875
Qy 978 TTCTGATTTGGCGCGCGCTGCTCATCCCATGTAATTTCCAGTACCAAGATCATCATGCC 1037
Db 876 TTCTGATTCGCGCGCGCTGCTCATCCCATGTAATTTCCAGTACCAAGATCATCATGCC 935
Qy 1038 ATGATCGTCCATAAGAACTGGTGGAGCTGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCT 1097
Db 936 ATGCTGTGTGCATGCAAGTGGCGGAGTTGCTCTGGGCGCGGAGTTGCTGCTGCTGCTGCT 995
Qy 1098 TTCTACCTACATCCCTTTCTAGCGCATCTCTGGGAGCCCTCTCTTTTCTCAACTTCATC 1157
Db 996 TTCTATCTTACCTCCCTTCTACCGGCTGCTCTGGGTGCTGCTCTCTTTGTTGCTGTC 1055
Qy 1158 AGTTTCTGGAGAGCACTGTTTGTGGGTGTCACAGATGAATCAGATGATCATGTCATGGAG 1217
Db 1056 AGGTCCTTGGAAAGCACTGTTTGTGGGTGTCACAGATGAATGAACCAATCCCCAAGAG 1115
Qy 1218 ATTGACCAAGGAGGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1277
Db 1116 ATCGGCGCAGAGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1175
Qy 1278 GAGCAGTCTCTTCAACGACTGTTTGTGGGTGTCACAGTGAATTAATCTTCCAGATGAGCACC 1337
Db 1176 GAGCCTCTCACTTTTCAACCACTGTTTGTGGGTGTCACAGTGAATGAACCAATCCCCAAGAG 1235
Qy 1338 CTCTTCCCAACCATCCCGCGGCACTTACAAAGATCGCCGCTGCTGCTGCTGCTGCTGCTG 1397
Db 1236 CTCTTCCCAACCATCCCGCGGCACTTACAAAGATCGCCGCTGCTGCTGCTGCTGCTGCTG 1295
Qy 1398 TGTGCAAGCATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1457
Db 1296 TGTGCAAGCATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1355
Qy 1458 ATCAGTCTCTTCAAGAGTCTGGAAGTGTGGTGGAGCGCTTACCTTCACTTCACTTCACTT 1517
Db 1356 GTGAGTCTCTTCAAGAGTCTGGAAGTGTGGTGGAGCGCTTACCTTCACTTCACTTCACTT 1415
Qy 1518 CACAGCCCGCGG 1530
Db 1416 CAACACCCAGGCG 1428

RESULT 6
US-10-262-617-4
; Sequence 4, Application US/10262617
; Publication No. US2003007747A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
; FILE REFERENCE: PF-0494-1 DIV
; CURRENT APPLICATION NUMBER: US/10/262,617
; PRIOR FILING DATE: 2002-09-30
; PRIOR FILING DATE: 1998-03-26

```
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1928
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US2003007747A1 2056310CB1
US-10-262-617-4

Query Match      19.1%; Score 608.2; DB 15; Length 1928;
Best Local Similarity 66.0%; Pred. No. 5.1e-164; Indels 3; Gaps 1;
Matches 896; Conservative 0; Mismatches 458;

QY 200 GGGCGAGGGGGCGCGAGCGGAGGTGTCGGTGCCTCCACCTTACGCTGGAGGAGATCA 259
DB 101 GGGCGCGAGAGCGGGGCTCAGGACCTACCCCGGCTACTTACCTGGGAGGAGTGGC 160
QY 260 GAAGCATACCTGCGACCGACAGTAGTGGGTGCTCATTTGACCGCAAGGTTTACACATCAC 319
DB 161 CCAGCCCTCAGGTCGGAGGAGCGGTGCTAGTATGATCGACCCGTAAGGTGTACACATCAG 220
QY 320 CAAATGGTCCATCCAGCACCCCGGGGGCCAGCGGGGTTCATCGGCGCATACGCTGGAGAAGA 379
DB 221 CGAGTTCAACCGCGGATCCAGGGGGCTCCCGGGTTCATCAGCCATCAGCCCGGCGAGA 280
QY 380 TGCAACGAGATGCTTCGGGCGCTTCCACCGTACCTGAGTAATTCGTGGGCAAGTTCTTGA 439
DB 281 TGGCCAGGATCCCTTTGTGGCCCTTCCACATCAACAAGGGCCCTTGTGAAGAATATATGAA 340
QY 440 ACCCTGCTGATGGTGAATCTGCCCGGAGGAGCCAGCCAGGACCCGCAAGAACTC 499
DB 341 CTCTCTCTGATGGAGACTGTCTCCAGAGAGCCCGAGCTTTGAGCCCAACCAAGATTA 400
QY 500 AAAGATCACTAGGACTTCGGGCGCTCGAGAGAGAGCGGTGAGGACATGAACCTGTTCAA 559
DB 401 AGAGCTGACAGATGAGTTCGGGAGGTGCGGGCCACAGTGGAGCGGATGGGCTCATGAA 460
QY 560 GACCAACCACTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
DB 461 GGGCAACCATGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 520
QY 620 ATGCTTCACTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679
DB 521 CTGCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 580
QY 680 CTTGCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 739
DB 581 GCTCAGTGCAGTTCAGGCGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 740 CTACAGAAAACCCAGTGGAAACCACTTGTCCAAATTCGTCAATTTGGCCACTTAAAGG 799
DB 641 CTTTCAAGACCTCAAGTGGAAACCACTTGTCTACATCTATTTTGTATTTGGCCACTTAAAG 700
QY 800 TGCCTCTGCACTGTTGGAAATCATCCGCACTTCCAGCACCGCCCAAGCTTAACATCTT 859
DB 701 GGGCCCCCGCAGTGGTGGAAACCACTGCACTTCCAGCACCATGCGCAAGCCCAAGCTTCT 760
QY 860 CCACAAGGATCCCGATGTGAACATGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 916
DB 761 CCGCAAGACCCAGACATCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 820
QY 917 CATCGATGACGGCAAGAGAGTGAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 976
DB 821 TGTGGAGCTTGGGAAACAGAGAAATAATATATGCGGTACCAACCCAGCAACCAATACCTT 880
QY 977 CTTCTGATTTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1036
DB 881 CTTCTGATTTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 940
QY 1037 CATGATCGTCCATGAAGACTGGGTGAGCTGGCTGGCGGTCTGAGTCTACATTCGGTT 1096
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RESULT 7

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US-09-822-849A-485/C
; Sequence 485, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 485
; LENGTH: 1972
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-485

Query Match      19.1%; Score 608.2; DB 9; Length 1972;
Best Local Similarity 66.0%; Pred. No. 5.2e-164;
Matches 896; Conservative 0; Mismatches 458; Indels 3; Gaps 1;

QY 200 GGGCGAGGGGGCGCGAGCGGAGGTGCTGGTGCCTACCTTACGCTGGAGGAGATCA 259
DB 1865 GGGCGCGAGAGCGGGGCTCAGGGACCTACCCCGGCTACTTACCTGGGAGGAGTGC 1806
QY 260 GAAGCATACCTGCGCACCGGACAGTGGGCTGGTCTATTGACCGCAAGGTTTACACATCAC 319
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Db 1305 CCAGCGCTCAGGTCGAGGAGCGGTGGCTAGTGTATCGACCGTAAGGTGTACACATCAG 1746
Qy 320 CAAATGTTCCATCAGCACCCGGGGGCGGACCGGTCATCGGSCACTACGCTGGAGAAGA 379
Db 1745 CGAGTTCAACCGCGGCGCATCCAGGGGCTCCCGGGTCATCAGCCACTACGCGGGCAGGA 1686
Qy 380 TGCACGGATGCTTCCGCGCTTCCACCTGACCTGGAATTCGTGGCAAGTCTTTGAA 439
Db 1685 TGCACGGATGCTTCCGCGCTTCCACATCAACAGGGGCTTGTGAAGATGATATGAA 1626
Qy 440 ACCCGCTGATGTTGTTGAACTGGCCCGGAGGAGCCGACGACGACCAAGCAAGAACTC 499
Db 1625 CTCTCTCTGATGAGAACTGTCTCCAGAGAGCCGAGCTTTGAGCCACCAAGAAATA 1566
Qy 500 AAAGATCACTAGAGACTTCGGGCGCTGAGAGAGCGCTGAGACATGAACCTGTTCAA 559
Db 1565 AGAGCTGACATGAGTTCGGGAGCTCGGGCCACAGTGGAGCGGATGGGCTCATGAA 1506
Qy 560 GACCAACACATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Db 1505 GGCCACCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1446
Qy 620 ATGTTTACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679
Db 1445 CTGGCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1386
Qy 680 CTTGCTACCTCTCAGGCGCAAGCTGGATGCTGCAATGATATGAGCCACCTGCTGT 739
Db 1385 GCTCAGTCAGTTCAGGCGCAGGCTGGCTGACTGACGACATGACTTTGGCACCTGTCGT 1326
Qy 740 CTACAGAAACCCAGTGGAAACCACTTGTCCCAAAATGTCATTCGTCATTCAGGAGG 799
Db 1325 CTTACGACCTCAAGTGGAAACCACTTGTCTACATCATTTTGTGATGGCCACCTGAAAGG 1266
Qy 800 TGCCTCTGCACTGCTGGTGAATCATCGGCATCTCCAGCACCAAGCCGCAAGCTAACATCTT 859
Db 1265 GCGCCCGCGGCTTGGTGGAAACCACTGCACTTCAGCACCACTGCAAGCCCACTGCTT 1206
Qy 860 CCACAGGATCCGATGTAACATGCTGC---AGTGTGTTGTTGGCGAATGGCAGCC 916
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Qy 917 CATCAGTACGCAAGAGAGAGCTCAATATCTGCTCTCAATCACCAGCAGCAATACTT 976
Db 1145 TGTGAGCTTGGAAACAGAGAAATATATGCGTACACCAACCAAGCAACATACTT 1086
Qy 977 CTTCTGATTTGGCGCGCTGCTCATCCCAATGATTTCCAGTACCAAGATCATCATGAC 1036
Db 1085 CTTCTTAATTTGGCGCGCGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1026
Qy 1037 CATGATCGTCCATAAGACTGGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1096
Db 1025 TGTATCCAGCGAAAGAGTGGTGGAGCTTGGCGCTGGATGATTAACCTTCTAGCTCGCT 966
Qy 1097 CTTTCATCACTACATCCCTTTCTACGCGATCCCTGGAGCCCTCTCTCTCTCTCTCTCT 1156
Db 965 CTTCTCTCACTTATGTGCCACTATTTGGGCTGAAAGCTTCTCTGGGCTCTCTCTCTCT 906
Qy 1157 CAGGTTCTTGAGAGCCACTGTTTGTGGGTGACACAGATGATCATCATGCTCATGGA 1216
Db 905 CAGGTTCTTGAGAGCAACTGTTTGTGGGTGACACAGATGATCATCATGCTCATGGA 846
Qy 1217 GATTGACAGGAGGCTTACCTGACTGTTTCACTAGTACGAGCTGACAGCACTGCAAGT 1276
Db 845 CATTGATCATGACCGGAACATGACTGGTTCACCCAGCTCCAGGCGACATGCAATGT 786
Qy 1277 GAGAGAGCTCTCTCTCAAGACTGTTTCACTGAGACACTTACTTCCAGATGAGCACA 1336
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Qy 1337 CTTCTTCCCACTGCGCGGACCAACTTACAGAGATCGCGCGCTGGTGAAGTCTCT 1396
Db 725 TCTTTTCCACGATGCTTCGACACAAATACCAAGTGGCTCCCTCTGCTGCTGCTCTCT 666

Qy 1397 ATGTGCCAGCATGGCTTGAATACAGGAGAGCCGCTACTAGGCGCCCTGCTGGACAT 1456
Db 665 GTGTGCCAAGCATGGCTTGAATACAGGAGAGCCGCTACTAGGCGCCCTGCTGGACAT 606
Qy 1457 CATCAGGTCCCTGAGAAAGTCTGGAAAGCTGTGGCTGGAGCCCTACCTTCAAAATGAAG 1516
Db 605 CATCCACTCACTAAAGGAGTCAAGGCGAGCTCTGGCTAGATGCTTCTTCCCAATAACA 546
Qy 1517 CCACAGCCCGGAGCACCGGTGGGGAAGGGGTGCAGG 1553
Db 545 ACAGCCACCTGCGCCAGTCTCTGMAAGAGAGGAGGAAG 509

RESULT 8
US-10-133-937-7
; Sequence 7, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-7

Query Match 19.1%; Score 608.2; DB 13; Length 4213;
Best Local Similarity 66.0%; Pred. No. 7.3e-164;
Matches 896; Conservative 0; Mismatches 458; Indels 3; Gaps 1;

Qy 200 GGGCGAGGGGGCGCGGAGCGGAGGTGCTGGTGGCCACCTTCAGCTGGAGGAGATTCA 259
Db 98 GGGCGCGAGAGCGCGGCTCAGGAGACCTTACCCGCGCTACTTCACCTGGAGCAGGTGGC 157
Qy 260 GAAGATAACCTGGCACCGACAGTGGGCTGGTGTATTGACCGCAAGGTTTACAAATCAC 319
Db 158 CAGCGCTCAGGCTGCGAGAGCGGTGGCTAGTATCGACCGTAAAGTGTACAAATCAG 217
Qy 320 CAAATGGTCCATCAGACACCGGGGGCGAGCGGGTTCATCGGCTACGCGCTGGAGAAGA 379
Db 218 CGAGTTTCAACCGCGCATCCAGGGGGCTCCCGGGTTCATCAGCCACTACCGCGGCGAGA 277
Qy 380 TGCAACGGATGCTTCCGCGCTTCCACCGCTGACCTGGAATTCGTGGGCAAGTCTTTGAA 439
Db 278 TGCAAGGATCCCTTTGTGGCTTCCACATCAACAGGGCTTGTGAAGATGATATGAA 337
Qy 440 ACCCTGCTGATTTGGTGAATCTGCCCGCGGAGGAGCCAGCAGGACCAAGCAAGAACTC 499
Db 338 CTCTCTCTGATTTGGAATCTGTCTCAGAGCAGCCGCTTTGAGCCCAAGAAATAA 397
Qy 500 AAAGATCACTAGGAGCTTCCGCGCTGAGGAAGAGCGCTGAGGACATGAACCTGTTCAA 559
Db 398 AGAGCTGACAGATGATTTCCGAGAGCTGCGGGCCACAGTGGAGCGGATGGGCTCATGAA 457
Qy 560 GACCAACACAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Db 458 GGGCAACCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 517
Qy 620 ATGTTTCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679
Db 518 CTGCTCACCTTTGGGTCTTTGGAGCTCTTTTGGCGCTTCTCTCTCTCTCTCTCTCTCT 577

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QY 680 CTTTGCTACCTCTCAGGCCCAAGCTGGATGGCTGCAAAATGATATGGCCACTGCTGTGT 739
Db 578 GCTCAGTGCAGTTTCAGGCCCAAGCTGGCTGGCTGCAAGATGATATGGCCACTGCTGTGT 637
QY 740 CTACAGAAACCAAGTGGAAACCACTGTGCACAAATTCGTCATTTGGCCACTTAAAGG 799
Db 638 CTTACAGCACTCAAGTGGAAACCACTGTGCACAAATTCGTCATTTGGCCACTTAAAGG 697
QY 800 TGCCTCTGCAATCTGTGGAAATCATCGGCATCTTCCAGCACCGCCCAAGCCCTAAACATCTT 859
Db 698 GGCCTCCGCGCAGTTGTGGAAACCACTGTGCACAAATTCGTCATTTGGCCACTTAAAGG 757
QY 860 CCACAGGATCCGATGTGAACATGTGC---ACGTGTTTGTCTGGGGAATGGCAGCC 916
Db 758 CCGCAAGACCCAGACATCAACATGATCCCTCTCTTTGCTTGGGAAATGCTCTC 817
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Db 818 TGTGGAGCTTGGGAACAGAAATAATATATGCGGTACCAACCAAGCCAGCAAAATCTT 877
QY 977 CTTCTGATTTGGCCCGCCAGCTTGTGCTCTCTACTTCCAGTGTATATTTCTATTT 937
Db 1037 CATGATCGTCCATAAGAACTGGGTGGACCTGGCTGGCGCTCAGCTACTACATCGGTT 1096
QY 938 TGTATCCAGCGAAAGAGTGGTGGACTTGGCTGGATGATTACCTTCTACGTCGCTT 997
QY 1097 CTTTCACTACATCTCCCTTTTACGGCATCTGGGAGCCCTCTTTTCTCACTTAT 1156
Db 998 CTTCTCTCACTATGTGCGCATATGGGGCTGAAAGCCTTCCCTGGGCTTTTCTTCACT 1057
QY 1157 CAGTTTCTGGAGAGCCACTGGTTTGTGGGTGCACACAGATGAATCAATCTCATGGA 1216
Db 1058 CAGTTTCTGGAAAGCACTGGTTTGTGGGTGCACACAGATGAATCAATCTCATGGA 1117
QY 1217 GATTGACAGAGGCCCTACCGTGTACTGTTGAGTGGCTGACAGCTGACAGCCCTGCAAGT 1276
Db 1118 CATTGATCATGACCGGAACATGGAAGTGGCTTCCACCCAGCTCCAGGCCCATGCAATGT 1177
QY 1277 GGAGCAGTCTCTTCTTCAAGCACTGGTTTCACTGGACACTTAACTTCCAGATTCAGACCA 1336
Db 1178 CCACAGTCTGCTTCAATGACTGTTTCACTGGACACTTAACTTCCAGATTCAGACCA 1237
QY 1337 CTTCTTCCCAACCATGCCCCGCACTTACACAGATTCGCCCCGCTGTGAGTCTCT 1396
Db 1238 TCTTTTCCCAACCATGCCCCGCACTTACACAGATTCGCCCCGCTGTGAGTCTCT 1297
QY 1397 ATGTGCAAGCATGCTGATTAATACAGGAGAGCCGCTTACTGAGGCCCTGCTGGACAT 1456
Db 1298 GTTGGCAAGCATGCTGATTAATACAGGAGAGCCGCTTACTGAGGCCCTGCTGGACAT 1357
QY 1457 CATCAGTCTCTGAGAGTCTGGAAAGCTGTGCTGGAGCCCTTACCTTCAAAATGAAG 1516
Db 1358 CATCACTCACTAAAGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 1417
QY 1517 CCACAGCCCGGACACCTGGGAGGAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 1553
Db 1418 ACAGCCACCTGCGCCAGTCTGGAAGAGAGAGGAGGAG 1454

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RESULT 9
US-10-191-513A-1
; Sequence 1, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3

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; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-191-513A-1

Query Match      18.9%; Score 602.8; DB 15; Length 1335;
Best Local Similarity 66.6%; Pred. No. 1.6e-162;
Matches 878; Conservative 0; Mismatches 437; Indels 3; Gaps 1;

QY 200 GGGCGAGGGGGCCCGCAGCGCGAGGTGTGGTCCCACTTTCAGCTGGGAGGAGATTCA 259
Db 18 GCGCGCGAGACCGGGCTCAGGACCTACCCCGGCTACTTCACTGGGAGCGAGGTGGC 77
QY 260 GAAGCATAACTGCGCCAGCAGACTGGGTGTGATTCAGCGCAAGGTTTACACATCAC 319
Db 78 CCAGCGCTCAGGTCGCGAGGAGCGGTGTGTAGTCGACCGTAAGGTGTACACATCAG 137
QY 320 CAATATGTCCTCAGACACCCCGGGGGCAGCGGTGTATCGGCACTACGCTGGAGAGA 379
Db 138 CGAGTTCACTCCCGCGCATCCAGGGGGCTCCCGGGCTCATCAGCCACTACGCGGGCAGGA 197
QY 380 TGCAACGATGCTTCCCGGCTTCCACCTGACCTGGAATTCGTGGCAAGTCTTGAA 439
Db 198 TGCCACGATGCTTGTGGGCTTCCACATCAACAGGGGCTTGTGAAGATGATATGAA 257
QY 440 ACCCTGTGATGTTGGTAACCTGGCCCGGAGAGCCAGCCAGGACCAAGCAAGCACTC 499
Db 258 CTCTCTCTGTGATGAGAACTGTCTCCAGAGCAGCCAGCTTGTGAGCCCAAGATAA 317
QY 500 AAAGATCACTGAGGACTTCCCGGCTTGAAGAGACCGCTGAGGACATGAACCTGTTCAA 559
Db 318 AGAGTGCAGATGATGTTCCCGGAGCTCGGGGCCACAGTGAGCGGATGGGGCTCATGAA 377
QY 560 GACCAACACAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Db 378 GCGCAACCACTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 437
QY 620 ATGGTTCACTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679
Db 438 CTGGCTCACTCTTGGGTCTTGGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 497
QY 680 CTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 739
Db 498 GCTCAGTCAGTTCAGGCGCCAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 557
QY 740 CTACAGAAACCCCAAGTGGAAACCACTTGTGCACAAATTCGTCATTTGGCCACTTAAAGG 799
Db 558 CTTTACAGCACTCAAGTGGAAACCACTTGTGCATCATTTTGTGATTTGGCCACTTAAAGG 617
QY 800 TGCCTCTGCAATCTGTGGAAATCATCGGCATCTTCCAGCACCGCCCAAGCCCTAAACATCTT 859
Db 618 GGCCTCCGCGCAGTTGTGGAAACCACTTCCAGCACCGCCCAAGCCCTAAACATCTT 677
QY 860 CCACAGGATCCGATGTGAACATGCTGC---ACGTGTTTGTCTGGGGAATGGCAGCC 916
Db 678 CCGCAAGACCCAGACATCAACATGATCCCTCTCTCTTCTTGGCTTGGGAAATGCTCTC 737
QY 917 CATCGAGTACGGAAGAGCTGAAATACCTGCGCTTACAAATCAACAGCAGGAGATCTT 976
Db 738 TGTGGAGCTTGGGAACAGAAATAATATATGCGGTACCAACCAAGCCAGCAAAATCTT 797
QY 977 CTTCTGATTTGGCCCGCCAGCTGCTCATCCCATGATTTTCCAGTACCATCATCATGAC 1036

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Db 798 CTTCCTAATGGGCCCCAGCCTTGCTGCTCTCTACTTCCAGTGGTATATTTCTATTT 857
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Db 858 TGTATTCAGGGAAGAGTGGGTGGACCTTGCGCTGGATGATACCTTCTACGTCGCTT 917
Qy 1097 CTTTCATCACTTACATCCCTTTCTACGGCATCTCTGGGAGCCCTCTCTTTTCTCAACTTCAT 1156
Db 918 CTTCTCTCACTTATGTGCCACTATTGGGCTGAAAGCCTTCTCTGGGCTCTTTCTTCTCATAGT 977
Qy 1157 CAGTTCCTGAGAGCCACTGTTTGTGGTGCACACAGATGAATCATCATCTCATGGA 1216
Db 978 CAGTTCCTGAGAGCACTGTTTGTGGTGCACACAGATGAATCATCATCTCATGGA 1037
Qy 1217 GATTGACAGAGCCCTTACCGTGACTGGTTTCAGTAGCCAGCTGACAGCCACCTGCAACGT 1276
Db 1038 CATTGATCATGACCGAATGGAATGGTGTTCACCCAGCTCTCTGGCCACATGCAATGT 1097
Qy 1277 GGAGCAGTCTTCTTCAAGCACTGGTTTCAGTGGACACCTTAACCTTCCAGATTGAGCACCA 1336
Db 1098 CCACAAGTCTGCTTCAATGATGCTGTTTCAGTGGACACCTCAACTTCCAGATTGAGCACCA 1157
Qy 1337 CTTCTTCCCAACCATGCCCCGGGCACTTACACAAGATCCCGCTGGTGAAGTCTCT 1396
Db 1158 TCTTTTCCACGATGCTTCGACACATTTACCAACAAGTGGCTCCCTGGTGGAGTCTT 1217
Qy 1397 ATGTCCCAAGCATGTCATTAATACCGAGAGAGCGCTACTGAGGCGCTTGGTGGACAT 1456
Db 1218 GTGTCCCAAGCGTGGCATAGATACCACTCAAGCCCTCTGTGACGCTTTCGCGGACAT 1277
Qy 1457 CATCAGGTCCCTGAAGAAGTGTGGAACTGTGGCTGGAGCCCTACCTTCAACAATGA 1514
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RESULT 10

US-09-981-876-63
; Sequence 63, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633

; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,669
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,312
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,313
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,672
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,877
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,889
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,893
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,630
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,878
; PRIOR FILING DATE: 1997-08-22

Db 730 ATCTACCTCCCTTCTACGGGTCCTCGGGTGTCTCTCTTTGTTGCTGTGAGGGT 789
QY 1163 CTTGGAGAGCCACTGTTTGTGGGTACACAGATGAATCATCCTGTCATGGAGATTGA 1222
Db 790 CTTGGAAGCCACTGTTTGTGGGTACACAGATGAATCATCCTGTCATGGAGATTGA 849
QY 1223 CCAGGAGGCTACCGTGACTGTTTCAAGTACAGGAGGAGGAGGAGGAGGAGGAGG 1282
Db 850 CCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 909
QY 1283 GTCTTCTTCAACGACTGTTTCAAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1342
Db 910 CTCACTTTTCAACGACTGTTTCAAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 969
QY 1343 CCCACCATCCCGGACACAACTTACACAGATGCGCCCGCTGGTGAATCTCTATGTGC 1402
Db 970 CCCAGGATCCGAGACACAACTTACACAGATGCGCCCGCTGGTGAATCTCTATGTGC 1029
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Db 1030 CAAGCAGGCTCAGCTACGAG-ATGAAGGCGCTTCCCTCAGCGGCTGGTGAATCTCTATGTGC 1088
QY 1463 GTCCCTGAAGAGTCTGGTGAATCTCTATGTGC-ATGAAGGCGCTTCCCTCAGCGGCTGGTGAATCTCTATGTGC 1522
Db 1089 GTCCCTGAAGAGTCTGGTGAATCTCTATGTGC-ATGAAGGCGCTTCCCTCAGCGGCTGGTGAATCTCTATGTGC 1148
QY 1523 CCCCGGGG 1530
Db 1149 CCCAGGCG 1156

RESULT 11

US-09-148-545-63
; Sequence 63, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22

Db 790 CTGGAAGCCACTGGTTCGTGTGGATCACAGATGAACACATCCCCAGGAGATCGG 849
QY 1223 CCAGGAGGCTACCGTGTAGTGTTCAGTAGCCAGCTGACAGCCACCTGCAACGTTGGAGCA 1282
Db 850 CCACGAGAGCACCAGGAGTGGTTCAGTCTCAGCTGGCAGCCACCTTGCACGTTGGAGCC 909
QY 1283 GTCTCTTTCACAGTGTGTTTCAGTGGACACCTTAACTTCAGATTCAGACACCTCTTT 1342
Db 910 CTCACCTTTTTCACCACTGGTTCAGGGGACCTCAACTTCAGATTCAGACACCACTCTTT 969
QY 1343 CCCCACCATGCCCGGCAACCTTACACAAGATGCCCGGCTGGTGAAGTCTCTATGTGC 1402
Db 970 CCCCAGGATGCCAGACACAACCTACAGCGGGTGGCCCGCTGGTCAAGTCTGTGTGC 1029
QY 1403 CAGCATGCTATGATACCAAGGAGCCCTACTAGGCGCCCTGCTGCACATCATCAG 1462
Db 1030 CAGGACGCGCTCAGCTAGCA-ATGAAGCCCTTCTCACCAGCTGGTGGACATCGTCAG 1088
QY 1463 GTCCCTGAAGAACTCTGGGAAGCTGTGGCTGGAGCGCTTACCTTCACAAATGAAGCCACAG 1522
Db 1089 GTCCCTGAAGAACTCTGGTGACATCTGGCTGGAGCGCTTACCTTCATCAGTGAAGCAACA 1148
QY 1523 CCCCCGGG 1530
Db 1149 CCGAGCG 1156

RESULT 12
US-09-604-287A-313
; Sequence 313, Application US/09604287A
; Patent No. US2002006487A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-313

Query Match 13.9%; Score 443.6; DB 9; Length 456;
Best Local Similarity 99.1%; Pred. No. 6.1e-117;
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACCTAAAGGCTGCTGCAACTGGTGAATCATCGCCACTCCAGCACCACGCCAA 847
Db 2 CCACCTAAAGGCTGCTGCAACTGGTGAATCATCGCCACTCCAGCACCACGCCAA 61
QY 848 GCCTAACATCTTCCACAAGATCCCGATGTGAACATGCTGCACTGTGTTCTTGGCGCA 907
Db 62 GCCTAACATCTTCCACAAGATCCCGATGTGAACATGCTGCACTGTGTTCTTGGCGCA 121
QY 908 ATGGCAGCCATCGAGTACGCAAGAAAGCTGAATACCTGCCCTACATCACCAGCA 967
Db 122 ATGGCAGCCATCGAGTACGCAAGAAAGCTGAATACCTGCCCTACATCACCAGCA 181
QY 968 CGAATACTTCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 1027
Db 182 CGAATACTTCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 241
QY 1028 CATCATGACCATGATGTCATTAAGAACTGGTGGAGCTGGCCCTGGCGCTGAGCTACTA 1087
Db 242 CATCATGACCATGATGTCATTAAGAACTGGTGGAGCTGGCCCTGGCGCTGAGCTACTA 301
QY 1088 CATCCGGTCTTTCATCATCCTACCTCCCTTCTACGGCATCCTGGGAGCCCTCTCTTTTCT 1147
Db 302 CATCCGGTCTTTCATCATCCTACCTCCCTTCTACGGCATCCTGGGAGCCCTCTCTTTTCT 361
QY 1148 CAACCTTCATCAGTTCCTGGAGAGCCACTGGTGTGTGGGTACACAGATGAATCAGAT 1207
Db 362 CAACCTTCATCAGTTCCTGGAGAGCCACTGGTGTGTGGGTACACAGATGAATCAGAT 421
QY 1208 CGTATGAGATTCACCAAGGAGGCTTACCG 1237
Db 422 CGTATGAGATTCACCAAGGAGGACCTCGG 451

Db 242 CATCATGACCATGATGTCATTAAGAACTGGTGGAGCTGGCCCTGAGCTACTA 301
QY 1088 CATCCGGTCTTTCATCATCCTACCTCCCTTCTACGGCATCCTGGGAGCCCTCTCTTTTCT 1147
Db 302 CATCCGGTCTTTCATCATCCTACCTCCCTTCTACGGCATCCTGGGAGCCCTCTCTTTTCT 361
QY 1148 CAACCTTCATCAGTTCCTGGAGAGCCACTGGTGTGTGGGTACACAGATGAATCAGAT 1207
Db 362 CAACCTTCATCAGTTCCTGGAGAGCCACTGGTGTGTGGGTACACAGATGAATCAGAT 421
QY 1208 CGTATGAGATTCACCAAGGAGGCTTACCG 1237
Db 422 CGTATGAGATTCACCAAGGAGGACCTCGG 451

RESULT 13
US-09-338-313
; Sequence 313, Application US/0933838A
; Patent No. US20020102602A1
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-338-313

Query Match 13.9%; Score 443.6; DB 10; Length 456;
Best Local Similarity 99.1%; Pred. No. 6.1e-117;
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACCTAAAGGCTGCTGCAACTGGTGAATCATCGCCACTTCAGCACCACGCCAA 847
Db 2 CCACCTAAAGGCTGCTGCAACTGGTGAATCATCGCCACTTCAGCACCACGCCAA 61
QY 848 GCCTAACATCTTCCACAAGATCCCGATGTGAACATGCTGCACTGTGTTCTTGGCGCA 907
Db 62 GCCTAACATCTTCCACAAGATCCCGATGTGAACATGCTGCACTGTGTTCTTGGCGCA 121
QY 908 ATGGCAGCCATCGAGTACGCAAGAAAGCTGAATACCTGCCCTACATCACCAGCA 967
Db 122 ATGGCAGCCATCGAGTACGCAAGAAAGCTGAATACCTGCCCTACATCACCAGCA 181
QY 968 CGAATACTTCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 1027
Db 182 CGAATACTTCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 241
QY 1028 CATCATGACCATGATGTCATTAAGAACTGGTGGAGCTGGCCCTGGCGCTGAGCTACTA 1087
Db 242 CATCATGACCATGATGTCATTAAGAACTGGTGGAGCTGGCCCTGGCGCTGAGCTACTA 301
QY 1088 CATCCGGTCTTTCATCATCCTACCTCCCTTCTACGGCATCCTGGGAGCCCTCTCTTTTCT 1147
Db 302 CATCCGGTCTTTCATCATCCTACCTCCCTTCTACGGCATCCTGGGAGCCCTCTCTTTTCT 361
QY 1148 CAACCTTCATCAGTTCCTGGAGAGCCACTGGTGTGTGGGTACACAGATGAATCAGAT 1207
Db 362 CAACCTTCATCAGTTCCTGGAGAGCCACTGGTGTGTGGGTACACAGATGAATCAGAT 421
QY 1208 CGTATGAGATTCACCAAGGAGGCTTACCG 1237
Db 422 CGTATGAGATTCACCAAGGAGGACCTCGG 451

Thu Dec 11 15:18:13 2003

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RESULT 14
US-09-551-621-313
; Sequence 313, Application US/09551621
; Publication No. US20030104366A1
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C5
; CURRENT APPLICATION NUMBER: US/09/551,621
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-621-313

Query Match      13.9%; Score 443.6; DB 11; Length 456;
Best Local Similarity 99.1%; Pred. No. 6.1e-117;
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACTTAAAGGGTGCCTCTGCCAAGGATCCCGATGGAACATGCTGCACTGTTGTTTCTGGGGA 847
DB 2 CCACTTAAAGGGTGCCTCTGCCAAGGATCCCGATGGAACATGCTGCACTGTTGTTTCTGGGGA 61

QY 848 GCCTAACATCTTCCACAAGGATCCCGATGGAACATGCTGCACTGTTGTTTCTGGGGA 907
DB 62 GCCTAACATCTTCCACAAGGATCCCGATGGAACATGCTGCACTGTTGTTTCTGGGGA 121

QY 908 ATGGCAGCCCATCGAGTACGGCAAGAGCTGGAATACCTGCCATCTTCCAGTACCAGAT 967
DB 122 ATGGCAGCCCATCGAGTACGGCAAGAGCTGGAATACCTGCCATCTTCCAGTACCAGAT 181

QY 968 CGAATACCTTCTCTGATTTGGCGCGCTGCTCATCCCCCATGTAATTCAGTACCAGAT 1027
DB 182 CGAATACCTTCTCTGATTTGGCGCGCTGCTCATCCCCCATGTAATTCAGTACCAGAT 241

QY 1028 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGAGCTACTA 1087
DB 242 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGAGCTACTA 301

QY 1088 CATCCGGTTCTTATCATCACTTATCCCTTTTACGGCATCTGGAGCCCTCCTTTTCT 1147
DB 302 CATCCGGTTCTTATCATCACTTATCCCTTTTACGGCATCTGGAGCCCTCCTTTTCT 361

QY 1148 CAATTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGGGTGCACAGATGAATCAGAT 1207
DB 362 CAATTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGGGTGCACAGATGAATCAGAT 421

QY 1208 CGTCATGAGATTGACAGGAGGCTACCG 1237
DB 422 CGTCATGAGATTGACAGGAGGCTACCG 451

RESULT 15
US-10-124-805-313
; Sequence 313, Application US/10124805
; Publication No. US2003016602A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
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; CURRENT APPLICATION NUMBER: US/10/124,805
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-313

Query Match      13.9%; Score 443.6; DB 13; Length 456;
Best Local Similarity 99.1%; Pred. No. 6.1e-117;
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACTTAAAGGGTGCCTCTGCCAAGGATCCCGATGGAACATGCTGCACTGTTGTTTCTGGGGA 847
DB 2 CCACTTAAAGGGTGCCTCTGCCAAGGATCCCGATGGAACATGCTGCACTGTTGTTTCTGGGGA 61

QY 848 GCCTAACATCTTCCACAAGGATCCCGATGGAACATGCTGCACTGTTGTTTCTGGGGA 907
DB 62 GCCTAACATCTTCCACAAGGATCCCGATGGAACATGCTGCACTGTTGTTTCTGGGGA 121

QY 908 ATGGCAGCCCATCGAGTACGGCAAGAGCTGGAATACCTGCCATCTTCCAGTACCAGCA 967
DB 122 ATGGCAGCCCATCGAGTACGGCAAGAGCTGGAATACCTGCCATCTTCCAGTACCAGCA 181

QY 968 CGAATACCTTCTCTGATTTGGCGCGCTGCTCATCCCCCATGTAATTCAGTACCAGAT 1027
DB 182 CGAATACCTTCTCTGATTTGGCGCGCTGCTCATCCCCCATGTAATTCAGTACCAGAT 241

QY 1028 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGAGCTACTA 1087
DB 242 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGAGCTACTA 301

QY 1088 CATCCGGTTCTTATCATCACTTATCCCTTTTACGGCATCTGGAGCCCTCCTTTTCT 1147
DB 302 CATCCGGTTCTTATCATCACTTATCCCTTTTACGGCATCTGGAGCCCTCCTTTTCT 361

QY 1148 CAATTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGGGTGCACAGATGAATCAGAT 1207
DB 362 CAATTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGGGTGCACAGATGAATCAGAT 421

QY 1208 CGTCATGAGATTGACAGGAGGCTACCG 1237
DB 422 CGTCATGAGATTGACAGGAGGCTACCG 451

RESULT 16
US-10-007-805-313
; Sequence 313, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-007-805-313

Query Match      13.9%; Score 443.6; DB 14; Length 456;
Best Local Similarity 99.1%; Pred. No. 6.1e-117;
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATGCCACTTCCAGCACCGCAA 847
Db 2 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATGCCACTTCCAGCACCGCAA 61

QY 848 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCAAGCTGTTGTCGGCGCA 907
Db 62 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCAAGCTGTTGTCGGCGCA 121

QY 908 ATGGCAGCCCATCGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 967
Db 122 ATGGCAGCCCATCGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 181

QY 968 CGAATACCTTCTTCCATGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 1027
Db 182 CGAATACCTTCTTCCATGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 181

QY 1028 CATCATGACCATGATCGTCCATTAAGAACTGGGTGGACCTGGCCCTGGCCCTGAGCTACTA 1087
Db 242 CATCATGACCATGATCGTCCATTAAGAACTGGGTGGACCTGGCCCTGAGCTACTA 301

QY 1088 CATCGGTTCTTATCATCACTACATCCCTTCTACGGCATCTCGGAGCCCTGCTTTTCT 1147
Db 302 CATCGGTTCTTATCATCACTACATCCCTTCTACGGCATCTCGGAGCCCTGCTTTTCT 361

QY 1148 CAATTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGTGGGTACACAGATGAATCAGAT 1207
Db 362 CAATTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGTGGGTACACAGATGAATCAGAT 421

QY 1208 CGTCATGGAGATTGACAGGAGCCCTACCG 1237
Db 422 CGTCATGGAGATTGACAGGAGCCCTCGG 451

RESULT 17
US-10-076-622-313
; Sequence 313, Application US/10076622
; Publication No. US2003023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-313

Query Match      13.9%; Score 443.6; DB 15; Length 456;
Best Local Similarity 99.1%; Pred. No. 6.1e-117;
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATGCCACTTCCAGCACCGCAA 847
Db 2 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATGCCACTTCCAGCACCGCAA 61

QY 848 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCAAGCTGTTGTCGGCGCA 907
Db 62 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCAAGCTGTTGTCGGCGCA 121

QY 908 ATGGCAGCCCATCGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 967
Db 122 ATGGCAGCCCATCGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 181

QY 968 CGAATACCTTCTTCCATGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 1027
Db 182 CGAATACCTTCTTCCATGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 241

QY 1028 CATCATGACCATGATCGTCCATTAAGAACTGGGTGGACCTGGCCCTGGCCCTGAGCTACTA 1087
Db 242 CATCATGACCATGATCGTCCATTAAGAACTGGGTGGACCTGGCCCTGAGCTACTA 300

; ORGANISM: Homo sapiens
US-09-604-287A-425
; Sequence 425, Application US/09604287A
; Patent No. US20020064872A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-425

Query Match      13.9%; Score 443.4; DB 9; Length 446;
Best Local Similarity 99.8%; Pred. No. 6.8e-117;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATGCCACTTCCAGCACCGCAA 847
Db 1 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATGCCACTTCCAGCACCGCAA 60

QY 848 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCAAGCTGTTGTCGGCGCA 907
Db 61 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCAAGCTGTTGTCGGCGCA 120

QY 908 ATGGCAGCCCATCGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 967
Db 121 ATGGCAGCCCATCGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 180

QY 968 CGAATACCTTCTTCCATGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 1027
Db 181 CGAATACCTTCTTCCATGAGTACGGCAAGAAGCTGAAATACCTTGCCTTACATCAACAGCA 240

QY 1028 CATCATGACCATGATCGTCCATTAAGAACTGGGTGGACCTGGCCCTGGCCCTGAGCTACTA 1087
Db 241 CATCATGACCATGATCGTCCATTAAGAACTGGGTGGACCTGGCCCTGAGCTACTA 300
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1088 CATCCGGTCTTTCATCACTACATCCCTTTCTACGGCATCCTGGAGCCCTCCTTTTCCT 1147
Db CATCCGGTCTTTCATCACTACATCCCTTTCTACGGCATCCTGGAGCCCTCCTTTTCCT 360
1148 CAATTCATCAGTTCTTGGAGCCACTGGTTGTGTGGGTACACAGATGAATCAGAT 1207
Db CAATTCATCAGTTCTTGGAGCCACTGGTTGTGTGGGTACACAGATGAATCAGAT 420
1208 COTCATGGAGATTGACAGGAGGCC 1232
Db CGTCATGGAGATTGACAGGAGGAC 445

RESULT 19
US-09-551-621-425
; Sequence 425, Application US/09551621
; Publication No. US20030104366A1
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C5
; CURRENT FILING DATE: 2000-04-17
; CURRENT APPLICATION NUMBER: US/09/551,621
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-621-425

Query Match 13.9%; Score 443.4; DB 11; Length 446;
Best Local Similarity 99.8%; Pred. No. 6.8e-117;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

788 CCACCTTAAGGGTGCCTCTGCCAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 847
Db 1 CCACCTTAAGGGTGCCTCTGCCAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 60
848 GCCTAACATCTTCCACAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 907
Db 61 GCCTAACATCTTCCACAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 120
908 ATGCGAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAAATCACCAGCA 967
Db 121 ATGCGAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAAATCACCAGCA 180
968 CGAATATCTTCTCTGATTGGGCGCGCTGCTCATCCCATATATTTCCAGTACCAGAT 1027
Db 181 CGAATATCTTCTCTGATTGGGCGCGCTGCTCATCCCATATATTTCCAGTACCAGAT 240
1028 CATCATGACCATGATCTCCATAGAACTGGGTGGACCTGGCCCTGAGCTACTA 1087
Db 241 CATCATGACCATGATCTCCATAGAACTGGGTGGACCTGGCCCTGAGCTACTA 300
1088 CATCCGGTCTTTCATCACTACATCCCTTTCTACGGCATCCTGGAGCCCTCCTTTTCCT 1147
Db 301 CATCCGGTCTTTCATCACTACATCCCTTTCTACGGCATCCTGGAGCCCTCCTTTTCCT 360
1148 CAATTCATCAGTTCTTGGAGCCACTGGTTGTGTGGGTACACAGATGAATCAGAT 1207
Db 361 CAATTCATCAGTTCTTGGAGCCACTGGTTGTGTGGGTACACAGATGAATCAGAT 420
1208 CGTCATGGAGATTGACAGGAGGCC 1232
Db 421 CGTCATGGAGATTGACAGGAGGAC 445

Query Match 13.9%; Score 443.4; DB 11; Length 446;
Best Local Similarity 99.8%; Pred. No. 6.8e-117;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 20
US-10-124-805-425
; Sequence 425, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124,805
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-425

Query Match 13.9%; Score 443.4; DB 13; Length 446;
Best Local Similarity 99.8%; Pred. No. 6.8e-117;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

788 CCACCTTAAGGGTGCCTCTGCCAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 847
Db 1 CCACCTTAAGGGTGCCTCTGCCAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 60
848 GCCTAACATCTTCCACAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 907
Db 61 GCCTAACATCTTCCACAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 120
908 ATGCGAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAAATCACCAGCA 967
Db 121 ATGCGAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAAATCACCAGCA 180
968 CGAATATCTTCTCTGATTGGGCGCGCTGCTCATCCCATATATTTCCAGTACCAGAT 1027
Db 181 CGAATATCTTCTCTGATTGGGCGCGCTGCTCATCCCATATATTTCCAGTACCAGAT 240
1028 CATCATGACCATGATCTCCATAGAACTGGGTGGACCTGGCCCTGAGCTACTA 1087
Db 241 CATCATGACCATGATCTCCATAGAACTGGGTGGACCTGGCCCTGAGCTACTA 300
1088 CATCCGGTCTTTCATCACTACATCCCTTTCTACGGCATCCTGGAGCCCTCCTTTTCCT 1147
Db 301 CATCCGGTCTTTCATCACTACATCCCTTTCTACGGCATCCTGGAGCCCTCCTTTTCCT 360
1148 CAATTCATCAGTTCTTGGAGCCACTGGTTGTGTGGGTACACAGATGAATCAGAT 1207
Db 361 CAATTCATCAGTTCTTGGAGCCACTGGTTGTGTGGGTACACAGATGAATCAGAT 420
1208 CGTCATGGAGATTGACAGGAGGCC 1232
Db 421 CGTCATGGAGATTGACAGGAGGAC 445

Query Match 13.9%; Score 443.4; DB 13; Length 446;
Best Local Similarity 99.8%; Pred. No. 6.8e-117;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 21
US-10-007-805-425
; Sequence 425, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: McNeill, Patricia D.

APPLICANT: Durham, Margarita
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.470C10
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 593
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 425
LENGTH: 446
TYPE: DNA
ORGANISM: Homo sapiens
US-10-007-805-425

Query Match 13.9%; Score 443.4; DB 14; Length 446;
Best Local Similarity 99.8%; Pred. No. 6.8e-117;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTTAAAGGGTGCCTCTGCGCAACTGGTGGATCATCGCCACTTCCAGCACCCAGGCCAA 847
Db 1 CCACCTTAAAGGGTGCCTCTGCGCAACTGGTGGATCATCGCCACTTCCAGCACCCAGGCCAA 60
QY 848 GCCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTTGTTGTTCTGGGCGA 907
Db 61 GCCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTTGTTGTTCTGGGCGA 120
QY 908 ATGGCAGCCCATCGAGTACGGCAAGAGAGTGAATACCTGCCCTACATCACACGCA 967
Db 121 ATGGCAGCCCATCGAGTACGGCAAGAGAGTGAATACCTGCCCTACATCACACGCA 180
QY 968 CGAATACCTTCTCTGATTTGGCCCGCTGCTCATCCCATGTTATTTCCAGTACACGAT 1027
Db 181 CGAATACCTTCTCTGATTTGGCCCGCTGCTCATCCCATGTTATTTCCAGTACACGAT 240
QY 1028 CATCATGACCATGATCGTCCATAAGACTGGTGGACCTGGCTGGGCGCTCAGCTACTA 1087
Db 241 CATCATGACCATGATCGTCCATAAGACTGGTGGACCTGGCTGGGCGCTCAGCTACTA 300
QY 1088 CATCGGTTCTTCACTACCTATCCCTTTCTACGGCATCTCGGAGCCCTCCTTTTCT 1147
Db 301 CATCGGTTCTTCACTACCTATCCCTTTCTACGGCATCTCGGAGCCCTCCTTTTCT 360
QY 1148 CCACTTCATCAGTCTCTGGAGCCACTGGTTTGTGGTGCACAGATGATACAT 1207
Db 361 CCACTTCATCAGTCTCTGGAGCCACTGGTTTGTGGTGCACAGATGATACAT 420
QY 1208 CGTCATGGAGATTGACCCAGGAGCC 1232
Db 421 CGTCATGGAGATTGACCCAGGAGCC 445

RESULT 22

US-10-076-622-425
Sequence 425, Application US/10076622
Publication No. US2003023036A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Persing, David H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.470C11
CURRENT FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 627
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 425
LENGTH: 446
TYPE: DNA
ORGANISM: Homo sapiens
US-10-076-622-425

Query Match 13.9%; Score 443.4; DB 15; Length 446;

Best Local Similarity 99.8%; Pred. No. 6.8e-117;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTTAAAGGGTGCCTCTGCGCAACTGGTGGATCATCGCCACTTCCAGCACCCAGGCCAA 847
Db 1 CCACCTTAAAGGGTGCCTCTGCGCAACTGGTGGATCATCGCCACTTCCAGCACCCAGGCCAA 60
QY 848 GCCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTTGTTGTTCTGGGCGA 907
Db 61 GCCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTTGTTGTTCTGGGCGA 120
QY 908 ATGGCAGCCCATCGAGTACGGCAAGAGAGTGAATACCTGCCCTACATCACACGCA 967
Db 121 ATGGCAGCCCATCGAGTACGGCAAGAGAGTGAATACCTGCCCTACATCACACGCA 180
QY 968 CGAATACCTTCTCTGATTTGGCCCGCTGCTCATCCCATGTTATTTCCAGTACACGAT 1027
Db 181 CGAATACCTTCTCTGATTTGGCCCGCTGCTCATCCCATGTTATTTCCAGTACACGAT 240
QY 1028 CATCATGACCATGATCGTCCATAAGACTGGTGGACCTGGCTGGGCGCTCAGCTACTA 1087
Db 241 CATCATGACCATGATCGTCCATAAGACTGGTGGACCTGGCTGGGCGCTCAGCTACTA 300
QY 1088 CATCGGTTCTTCACTACCTATCCCTTTCTACGGCATCTCGGAGCCCTCCTTTTCT 1147
Db 301 CATCGGTTCTTCACTACCTATCCCTTTCTACGGCATCTCGGAGCCCTCCTTTTCT 360
QY 1148 CCACTTCATCAGTCTCTGGAGCCACTGGTTTGTGGTGCACAGATGATACAT 1207
Db 361 CCACTTCATCAGTCTCTGGAGCCACTGGTTTGTGGTGCACAGATGATACAT 420
QY 1208 CGTCATGGAGATTGACCCAGGAGCC 1232
Db 421 CGTCATGGAGATTGACCCAGGAGCC 445

RESULT 23

US-10-191-513A-13
Sequence 13, Application US/10191513A
Publication No. US20030104596A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardeep
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.D3
CURRENT FILING DATE: 2002-09-25
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1998-04-10
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 864
TYPE: DNA
ORGANISM: Homo sapiens
US-10-191-513A-13

Query Match 13.2%; Score 421.6; DB 15; Length 864;
Best Local Similarity 69.9%; Pred. No. 1.7e-110;
Matches 584; Conservative 0; Mismatches 249; Indels 3; Gaps 1;

QY 682 TTGCTACTCTCAGGCCCGGAGTGGCTGCGTGAACATGATATGCGCACCTGCTGCT 741
Db 29 TTGCGGCGAGTTTCAGGCCCGGAGTGGCTGCGTGAACATGATATGCGCACCTGCTGCT 88
QY 742 ACAGAAAACCAAGTGGAAACACCTTGTCCAAAATTCGTTCATTTGGGCCACTTAAAGGGTG 801

Db 89 TCAGCAGCTCAAAGTGAACCACTGCTACATCAATTTGTGATGGCCACCTGAAGGGG 148
QY 802 CTTCTGCCAACTGGTGGATCATCGCACTTCCAGCACCAGCCCAAGCTAACTCTTCC 861
Db 149 CCCCCGCCAGTTGGTGGAAACCATGCACTTTCAGCACCACATGCGCAAGCCCACTCTTCC 208
QY 862 ACAAGATCCCGATGTGAACATCTGTC---ACGTGTTTGTGCGGGAATGGCAGCCCA 918
Db 209 GCAAGACCCAGACATCAACATGATCTCTCTTTGCTTGGGGAAGATCTCTCTG 268
QY 919 TCAGTACGCCAAGAGAGCTGAATACCTGCTTACATCACCAGCAGCAATACTTCT 978
Db 269 TGGAGCTTGGAAACAGAAATAATATGCGGTACAAACACACAGCAAAATCTTCT 328
QY 979 TCCGTGATGGCGCGCGCTGCTCATCCCATGATTTCCAGTACCAAGATCATGACCA 1038
Db 329 TCCATATGGCCCCCAGCGCTTCTGCTCTCTTACCTTCCAGTGGTATATTTCTATT 388
QY 1039 TGATGTCCTAAGAACTGGGTGGAGCTGCGCTGGCGCTGAGCTACTACATCGGTTCT 1098
Db 389 TTATCCAGCGAAAGTGGGTGGAGCTTGGCGCTGGAGATTAACCTTCTACGTCGCTCT 448
QY 1099 TCATCAGCTACATCCCTTTCTAGGCACTCTGGGAGCGCTCTTTTCTCAACTTCATCA 1158
Db 449 TCCCTACTATGTCCACTATTGGGCTGAAGCTTCTGGGCTTTTCTTTCATAGTCA 508
QY 1159 GGTTCCTGGAGAGCACTGTTGTGTGGTTCACAGATGAATCATCGTCAATGAGA 1218
Db 509 GGTTCCTGGAAAGCACTGTTGTGTGGTTCACAGATGAATCATTTCCCATGACA 568
QY 1219 TTGACAGGAGGCTACCGTGACTGTTTCAGTAGCCAGCTGACAGCCACCTGCAAGCTGG 1278
Db 569 TTGATCATGACCGAAATGAGCTGGTTTCCACCCAGCTCCAGGCCACATGCAATGTC 628
QY 1279 AGCAGTCTTCTTCAACAGCTGTTTCAGTGGAGCACTTAACTTCCAGATGAGCAGCC 1338
Db 629 ACAAGTCTGCTTCAATGACTGTTTCAGTGGAGCACTTCAACTTCCAGATGAGCAGCATC 688
QY 1339 TCTTCCCAACATGCGCGGACCAACTTACAGAGATGCGCGCTGGTGAAGTCTCTAT 1398
Db 689 TTTTTCACAGATGCTGACACAAATACACAAATGCTGCTGCTGCTGCTGCTGCTGCT 748
QY 1399 GTGCCAAGCATGGCATTTGAATACAGGAGAGCGCTTACTGAGGCGCTCTGCGACATCA 1458
Db 749 GTGCCAAGCATGGCATAGATGACAGTCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 808
QY 1459 TCAGTCTCTCAAGAGCTGCGGAGCTGTGCTGGAGCGCTACTCTTCAAAATGA 1514
Db 809 TCCACTCAAGAGAGTCAAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 864

RESULT 24
US-09-918-995-29095
; Sequence 29095, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT FILING DATE: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29095
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1)...(453)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-29095
Query Match 12.1%; Score 384.4; DB 11; Length 453;
Best Local Similarity 95.6%; Pred. No. 6.5e-100;
Matches 394; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 440 ACCCTCTGATGGTGAATGCGCGGAGGAGCCAGCCAGGACCCAGGACCCAGGCAAGATC 499
Db 42 ATCAGTACAGNGCGGNGGAATTCCTCGGCTCGAGGCCAGCCAGGACCCAGGCAAGATC 101
QY 500 AAAGATCACTGAGGACTTCGGGCGCTTGAGGAAGACGGCTGAGGACATGAACCTGTCAA 559
Db 102 AAAGATCACTGAGGACTTCGGGCGCTTGAGGAAGACGGCTGAGGACATGAACCTGTCAA 161
QY 560 GACCAACACGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Db 162 GACCAACACGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 221
QY 620 ATGCTTCACTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 679
Db 222 ATGCTTCACTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 281
QY 680 CTTTCTACCTCTCAGGCCCAAGCTGGATGGCTGCAACATGATTTATGCGCACCTGTCTGT 739
Db 282 CTTTCTACCTCTCAGGCCCAAGCTGGATGGCTGCAACATGATTTATGCGCACCTGTCTGT 341
QY 740 CTACAGAAAACCCAAAGTGGACCACTTGTCCAAAATTTGTCATTGGCCACTTAAAGGG 799
Db 342 CTACAGAAAACCCAAAGTGGACCACTTGTCCAAAATTTGTCATTGGCCACTTAAAGGG 401
QY 800 TGCCTCTCCAACTGGTGAATCATGCGCACTTCCAGACCCAGCCAGCT 851
Db 402 TGCCTCTCCAACTGGTGAATCATGCGCACTTCCAGACCCAGCCAGCT 453

RESULT 25
US-10-191-513A-35
; Sequence 35, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-35

Query Match 11.6%; Score 370.4; DB 15; Length 960;
Best Local Similarity 64.5%; Pred. No. 9.6e-96;
Matches 570; Conservative 0; Mismatches 311; Indels 3; Gaps 1;
QY 200 GGGCGAGGGGGCGCGGAGCGGAGGTGTGCTGCGCCACCTTCAGCTGGAGGATTC 259
Db 48 GGGCGGAGAGCGCGGCTCAGGACCTACCCCGGCTACTTCACCTGGGACGAGGTGC 107

260 GAAGCAATACCTCGCCACCGACAGTGGCTGTGTTGACCGCAAGGTTTACAACATCAC 319
 108 CACGCGCTCAGGCTGCGAGGCGGTGGCTAGTATGATCGACCGTAAAGTGTACACATCAG 167
 320 CAAATGGTCATCCAGCACCCGGGGGGCCAGCGGTGATCGGCGTACATCGGCTAGAGAGA 379
 168 CGAGTTTCAACCGCGCGCATCCAGGGGGGCTCCCGGGTATCAGCCACTACGCGCGGCGGA 227
 380 TGCAACGGATGCTTCCGGCGCTTCCACCGCTACCTGGAATTCGTGGGCAAGTTCTTGAA 439
 228 TGCCACGGATCCCTTTGTGGCTTCCACATCAACAGGGCTTGTGAAGATATATGAA 287
 440 ACCCTGCTGATGTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 499
 288 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 347
 500 AAAGATCACTGAGGACTTCCGGGCGCTGAGGAGAGCGGTGAGGACATGAACCTGTTCAA 559
 348 AGAGCTGACAGATGAGTTCCGGGAGCTGCGGCCACAGTGGAGCGGATGGGCTCATGAA 407
 560 GACCAACCAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
 408 GGGCAACCAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 467
 620 ATGGTTCACTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679
 468 CTGGCTCACCTTTGGGTCTTTGGGAGCTCTTTTGGCTCTCTCTCTCTCTCTCTCTCT 527
 580 CTTGTGTACTCTCAGGCGGAGCTGATGGTGTGCTGCAATGATGATGATGATGATGATG 739
 528 GCTCAGTGAGTTTCAAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 587
 740 CTACAGAAACCAAGTGGAAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
 588 CTTGAGCACTCAAGTGGAAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647
 800 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859
 648 GGGCGCGCGAGTTGTTGGAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 707
 860 CCAAGAGTCCCGATGTTGAACATGCTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 916
 708 CCGCAAGAGCCAGACATCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 767
 917 CATCGAGTCCGCAAGAGCTGAAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 976
 768 TGTGAGCTTGGAAACAGAGAAATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 827
 977 CTTCTGATGTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1036
 828 CTTCTGATGTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 887
 1037 CATGATCGTCCATGAAAGCTGGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 888 TGTATCCAGGAAAGAGTGGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931

RESULT 26
 US-10-191-513A-5
 ; Sequence 5, Application US/10191513A
 ; Publication No. US20030104596A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pardeep
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Tapas, Das
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295 US D3
 ; CURRENT APPLICATION NUMBER: US/10/191,513A
 ; CURRENT FILING DATE: 2002-09-25
 ; PRIOR APPLICATION NUMBER: US 05/227,613
 ; PRIOR FILING DATE: 1999-01-08

; PRIOR APPLICATION NUMBER: PCT/US98/07422
 ; PRIOR FILING DATE: 1998-04-10
 ; PRIOR APPLICATION NUMBER: US 08/833,610
 ; PRIOR FILING DATE: 1997-04-11
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 918
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (755)...(755)
 ; OTHER INFORMATION: r = g or a at position 755
 ; US-10-191-513A-5

Query Match 11.5%; Score 367.4; DB 15; Length 918;
 Best Local Similarity 65.2%; Pred. No. 6.9e-95;

Matches 555; Conservative 1; Mismatches 292; Indels 3; Gaps 1;
 QY 233 GCCACCTTCAGCTGGGAGGATTCAGAGCATACCAATGGTCCATCAGCACCGGGGGCGCAGCG 292
 Db 15 GCGCTACTTCACTGGGACGAGGTGGCCAGCGCTCAGGGTGGGAGGCGGTGGGTAGT 74
 QY 293 CATTCACCGCAAGTTTACAAATCACCACATCAAAATGGTCCATCAGCACCGGGGGCGCAGCG 352
 Db 75 GATCAGCGTAAAGTGTACACATCAGGAGTTCACCGCGCGCATCCAGGGGGCTCCCG 134
 QY 353 GGTCTCGGGCACTACGCTGGAGAGATGCAAGGATGCTTCGGGCGCTTCACCGCTGA 412
 Db 135 GGTCTACGACACTACCGCGGGCAGGATGCCAGGATCCCTTTGTGGCTTCCACATCAA 194
 QY 413 CTTGAAATTCGTGGGCAAGTTCTTGAACCCCTCTCTGATTGGTGAATCTGCCCGCGGAGGA 472
 Db 195 CAAGGGCTTGTGAAGAGTATATGAACTCTCTCTGATTGGAGAACTGTCTCCAGAGCA 254
 QY 473 GCCAGCCAGACACCGCAGAACTCAAGATCACTAGAGACTTCGGGCGCTTGAGGAA 532
 Db 255 GCCAGCTTGAAGCCCAACAAAGAGCTCAGAGTGGTCCGGGAGCTGGGGC 314
 QY 533 GACGGCTGAGGACATGAACCTGTTCAAGACCAACCAAGCTGTTCTTCTCTCTCTCTCTGGC 592
 Db 315 CACAGTGGAGCGGATGGGGCTCATGAAGGCCAACCATGTCTTCTCTCTGCTGTACCTGCT 374
 QY 593 CCAGATCATCGCTCGGAGAGCATGATGGTTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTG 652
 Db 375 GCACATCTGTCTGGATGGTGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 434
 QY 653 GATTCCTACCTCATCAGCGCTTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
 Db 435 TTTGGCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494
 QY 713 GCAGATGATTATGGCCACCTGCTGCTACAGAAACCCAGTGGAGAACCACTTGTCCA 772
 Db 495 GCAGATGACTTTGGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 554
 QY 773 CAAATTCGTTCATGGCCACTTTAAAGGGTGGCTTTCGCAACTGCTGCTGCTGCTGCTGCTGCT 832
 Db 555 TCAATTTTGTGATGGCCACTTGAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 614
 QY 833 CCAGCACCAACCGCAGCTTACATCTTCCACAGGATCCCGATGCTGCTGCTGCTGCTGCTGCTGCT 889
 Db 615 CCAGCACCAATGCCAAGCCCAACTGCTTCCGAAAGACCCAGACATCAATGATGCTGCTGCT 674
 QY 890 CGTGTGTTGTTGGGCGAATGGCAGCCCATCGAGTACGGCAAGAGAGTGAATACCT 949
 Db 675 CTTCTTGGCTTGGGAGAGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
 QY 950 GCGCTACATCACCAGCAGCAATATCTTCTCTGATTGGGCGCGCTGCTGCTGCTGCTGCTGCT 1009
 Db 735 GCGCTACAAACCCAGACATATCTTCTCTGATTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCT 794
 QY 1010 GTATTTCAGTACCAGATCATCATGATGATGCTCCATGAAGAACTGGGTGGAGCTGGC 1069

Db 795 CTACTCCAGTGGTATATTTCTATTGTTATCCAGCAAGAGTGGTGGACTTGGC 854
QY 1070 CTGGGCGGTCA 1080
Db 855 CTGGATCAGCA 865

RESULT 27

US-10-191-513A-34
; Sequence 34, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295, US, D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-34

Query Match 11.0%; Score 351.8; DB 15; Length 990;
Best Local Similarity 64.7%; Pred. No. 2.2e-90;
Matches 540; Conservative 0; Mismatches 292; Indels 3; Gaps 1;

QY 200 GGGCGAGGGGGCCCGAGCGGAGGTCGGTCCCACTTCAGTGGAGGAGATTC 259
Db 18 GGGCGGAGAGCCGGCTCAGGAGCACTACCCCGCTACTTCCCTGGAGAGGTGGC 77
QY 260 GAAGCATAACTGGCAGCCAGACAGTGGCTGTCATTGACCGCAAGTTTACAACTAC 319
Db 78 CCAGCGTCAAGTGGCAGGAGCGGTGGCTAGTATCGACCGTAAGTGTACAACTAG 137
QY 320 CAAATGTTCCATCAGCACCCCGGGGGCCAGCGGGTCCATCGGCACCTACGCTGGAAGA 379
Db 138 CGAGTTCCACCCCGCGCATCCAGGGGGCTCCCGGGTCCATCAGCCACTACGCGGGCAGGA 197
QY 380 TGCAACGAGTGCCTTCGGCGCTTCCACCTGACCTGGAATTCGTGGGCAAGTTCTTGAA 439
Db 198 TGCCACGATCCCTTTGTGGCTTCCATCAACAGGGCTTGTGAGAGATATAGAA 257
QY 440 ACCCTCTGATGGTGAATGGCCCGAGAGGCCAGCCAGGACCAAGGAAAGTCC 499
Db 258 CTCTCTCTGATTGGAGAGTGTCTCCAGAGCAGCCAGCTTTGAGCCCAAGAAATAA 317
QY 500 AAGATCACTGAGACTTCGGGGCCCTGAGAGAGCGCTGAGACATGAACCTGTTC 559
Db 318 AGAGCTGACATGAGTTTCGGGAGCTTCGGGGCCACAGTGAGCGGATGGGCTCATGAA 377
QY 560 GACCAACCACTGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Db 378 GGCCAAACCATGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 437
QY 620 ATGGTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679
Db 438 CTGGCTACCCCTTTGGGTCTTTGGAGCTCTCTTTTGGCTCTCTCTCTCTCTCTCTCTCT 497
QY 680 CTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 739

Db 498 GCTCAGTGGAGTTCAGGCCAGGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 557
QY 740 CTACAGAAAAACCAAGTGGAAACCACTTGTCCACAAATTCGTCATTTGGCCACTTAAGGG 799
Db 558 CTTTCAGCACCTCAAAGTGGAAACCACTTGTCTACATCATTTTGTGATTTGGCCACTTAAGGG 617
QY 800 TGCTCTGCCAACTGGTGGAAATCATCGCCACTTCCAGCACCAGGCCAAGCCTTAACATCTT 859
Db 618 GGCCCCCGCCAGTGGTGGAAACCACTTGTCTACATCATTTTGTGATTTGGCCACTTAAGGG 677
QY 860 CCACAAGGATCCCGATGTGAACATGTCTGCG---ACGTGTTTGTCTGGGGAATGGCAGCC 916
Db 678 CCGCAAGACCCAGACATCAACATGTCATCCCTTCTTTTGGCTTGGGGAAGATCCTCTC 737
QY 917 CATCGAGTACGCAAGAGAGCTGAATACCTGCTCCCTCAATCACCAGCAGCAATACTT 976
Db 738 TGTGGAGCTTTGGGAACAGAAATAATATATGCGGTACCAACCAACGACCAAAATACTT 797
QY 977 CTTCTCTGATTGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAATCATC 1031
Db 798 CTTCTCTGATTGGCGCGCGCTGCTCATCCCATGTATTTCCAGTACCAATCATC 852

RESULT 28

US-09-981-876-119
; Sequence 119, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581

[illegible]

RESULT 29
US-09-148-545-119
; Sequence 119, Application US/09148545
; Publication No. US20030027132A1

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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23

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; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 2016

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Query Match      10.1%; Score 321.8; DB 11; Length 2016;
Best Local Similarity 66.5%; Fred. No. 1.3e-81;
Matches 533; Conservative 1; Mismatches 261; Indels 7; Gaps 5;

Qy 361 GGCACCTAGCTGGAGAGATGCAAGGATGCTTCCGGCTTCCACCTGGAAT 420
Db 135 GCGAGGGGCTGCGGGANCCCAACAGGATGCTTCCGTCCTCCATCAAGATCTCAAT 194
Qy 421 TCGTGGGCAAGTCTTGAACCCCTGCTGATGTGGAAGTGGCCCGGAGAGCCAGCC 480
Db 195 TTGTGGGCAA-TTCCTACAGCCCTTGTGATGGAGAGCTGGCTCCGAGAGACCCAGCC 253
Qy 481 AGGACACGCGCAAGAACTCAAGATCACTGAGGACTTCCGGGCTTCCGAGAGAGCGCTG 540
Db 254 AKGATGGACCCCTGGAATGC--GCATGTGAGGAGCTTCCGAGGCTTCCAGGAGCCG 311
Qy 541 AGGACATGACCTGTTCAAGACCCAGGACCGTGTCTTCTCTCTCTCTCTCTCTCTCT 600
Db 312 AGGACATGAGCTGTTTGTATGTCAGTCCACCTTCTTGTCTTCTTCTTCTTCTTCT 371

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QY 601 TGGCCCTGGAGAGCAATGTCATGTTTCACTGTCTTCTACTTTGGCAATGGCTGGATTCTTA 660
Db 372 TGGCCATGAGGTGCTGGCTGGCTCTTATCTACCTCTCTGGTCTCTGGCTGGCTGGCTGG 431
QY 661 -CCCTCATCAGCGCTTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 719
Db 432 GTGCGCTGNGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 491
QY 720 GATTATGGCCACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 779
Db 492 GACCTGGGCA-TGCTCCATCTTCAAGAGTCTCTGGTGAACCACTGGTGGCCCGAGATTC 550
QY 780 GTCAATGGCCACTTAAAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 839
Db 551 GTGATGGGCACTTAAAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 610
QY 840 CAGCCCAAGCCTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 899
Db 611 CAGCCCAAGCCTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 670
QY 900 CTGGGCGAATGGAGCCCATCGAGTACGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959
Db 671 CTGGGCGA--GTCACTCGTGAATGATGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728
QY 960 CAGCAGCAGATACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1019
Db 729 CAGCAGCAGTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 788
QY 1020 TACCAGATCATGATGACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1079
Db 789 GTGGAATAATCGCGTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 848
QY 1080 AGTACTACATCGGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1139
Db 849 AGTCTTATCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 908
QY 1140 CTTTCTCTCACTTCATCAGGT 1161
Db 909 CTCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 930
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RESULT 30

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US-10-191-513A-4
; Sequence 4, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-4
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Query Match          9.5%; Score 302.4; DB 15; Length 304;
Best Local Similarity 99.7%; Pred. No. 2.1e-76;
Matches 303; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 630 GTCTTCTACTTTGGCAATGGCTGGATTCTTACCTCATCAGCGCTTTCTCTTGGCTTACC 689
Db 1 GTCTTTTACTTTTGGCAATGGCTGGATTCTTACCTCATCAGCGCTTTGTCTTGTCTTACC 60
QY 690 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 749
Db 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 120
QY 750 CCAAGTGGAAACACCTTGTCTCAAAATTTGTCATTTGGCCACTTAAAGGGTGCCTCTGCC 809
Db 121 CCAAGTGGAAACACCTTGTCTCAAAATTTGTCATTTGGCCACTTAAAGGGTGCCTCTGCC 180
QY 810 AACTGTGGAAATCATCGCCACTTCCAGCACCAGCCCAAGCCTAAACATCTTCCACAAGGAT 869
Db 181 AACTGTGGAAATCATCGCCACTTCCAGCACCAGCCCAAGCCTAAACATCTTCCACAAGGAT 240
QY 870 CCGATATGAACATGCTGCAACGTTTGTCTTGGGGAATGGAGCCCATCGAGTAGCGC 929
Db 241 CCGATATGAACATGCTGCAACGTTTGTCTTGGGGAATGGAGCCCATCGAGTAGCGC 300
QY 930 AAGA 933
Db 301 AAGA 304
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RESULT 31

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US-09-880-107-3920/c
; Sequence 3920, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3920
; LENGTH: 292
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Z40715
US-09-880-107-3920
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Query Match          9.2%; Score 292; DB 10; Length 292;
Best Local Similarity 100.0%; Pred. No. 2e-73;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2882 CTGAGCTGCTGTGCGAGTCTAACCCACTTAATCAGTTCTTAGATTTCAGGGGAAGGCGCAGC 2941
Db 292 CTGAGCTGCTGTGCGAGTCTAACCCACTTAATCAGTTCTTAGATTTCAGGGGAAGGCGCAGC 233
QY 2942 ACCAACAACCTCAGAATGGGGCTTTTGGGGAGGGCGCTAGTCCCCCAGCTCTAAGCAG 3001
Db 232 ACCAACAACCTCAGAATGGGGCTTTTGGGGAGGGCGCTAGTCCCCCAGCTCTAAGCAG 173
QY 3002 CCAGGAGGAGCTGCATCTAAGCATCTGGGTTGCCATGGCAATGGCATGCCCCCGCAGCTA 3061
Db 172 CCAGGAGGAGCTGCATCTAAGCATCTGGGTTGCCATGGCAATGGCATGCCCCCGCAGCTA 113
QY 3062 CTGTATGCCCGGACCCCGGAGGAGAGATGAACCATAGGAGCTGATCGTAAATGTT 3121
Db 112 CTGTATGCCCGGACCCCGGAGGAGAGATGAACCATAGGAGCTGATCGTAAATGTT 53
QY 3122 TATCATGTACTTCTCCCGCCCTACATTTTGTGAAATAAATAAGGAATTTT 3173
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Db 52 TATCATGTTACTTCCCCACCCCTACATTTTGTGAAATAAAATAAGGAATTTT 1

RESULT 32

US-09-873-319-740/c

Sequence 740, Application US/09873319A

Publication No. US20030134324A1

GENERAL INFORMATION:

APPLICANT: Mungez, William E.

APPLICANT: Kulkarni, Prakash

APPLICANT: Getzenberg, Robert H.

APPLICANT: Waga, Iwao

APPLICANT: Yamamoto, Jun

TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic

FILE OF INVENTION: Hyperplasia Using Gene Expression Profiles

FILE REFERENCE: 44921-5029-US

CURRENT APPLICATION NUMBER: US/09/873.319A

CURRENT FILING DATE: 2001-06-05

EARLIER APPLICATION NUMBER: US 60/223,323

EARLIER FILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 755

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 740

LENGTH: 292

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. US20030134324A1 Z40715

US-09-873-319-740

Query Match

Best Local Similarity 9.2%; Score 292; DB 13; Length 292;

Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2882 CTGAGCTGCTGTGAGTCTACCCACTAATCAGTCTTTAGATTGAGGGGAGGGCAGGC 2941

Db 292 CTGAGCTGCTGTGAGTCTACCCACTAATCAGTCTTTAGATTGAGGGGAGGGCAGGC 233

QY 2942 ACCAACAACCTAGAAATGGGGGCTTTCCGGGAGGGGCGCTAGTCCCCAGCTCTAAGCAG 3001

Db 232 ACCAACAACCTAGAAATGGGGGCTTTCCGGGAGGGGCGCTAGTCCCCAGCTCTAAGCAG 173

QY 3002 CCAGGAGGAGCTGATCTAAGCATCTGAGTCTGGGTTGGCATGGCAATGGCATGCCCGCCAGCTA 3061

Db 172 CCAGGAGGAGCTGATCTAAGCATCTGAGTCTGGGTTGGCATGGCAATGGCATGCCCGCCAGCTA 113

QY 3062 CTGTATGCCCCCGACCCCGCAGAGGAGCAATGAACCCATAGGAGCTGATCGTAATGTT 3121

Db 112 CTGTATGCCCCCGACCCCGCAGAGGAGGCGCTAGTCCCGCCAGCTCTAAGCAG 53

QY 3122 TATCATGTTACTTCCCGACCCCTACATTTTGTGAAATAAAATAAGGAATTTT 3173

Db 52 TATCATGTTACTTCCCGACCCCTACATTTTGTGAAATAAAATAAGGAATTTT 1

RESULT 33

US-09-960-706-1117/c

Sequence 1117, Application US/09960706

Publication No. US20030134280A1

GENERAL INFORMATION:

APPLICANT: Mungez, William E.

TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas

FILE OF INVENTION: Gene Expression Profiles

FILE REFERENCE: 44921-5029-01US

CURRENT APPLICATION NUMBER: US/09/960,706

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 60/223,323

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: 09/873,319

PRIOR FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 1124

SOFTWARE: PatentIn Ver. 2.1

Query Match

Best Local Similarity 8.0%; Score 253.8; DB 15; Length 473;

Matches 333; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1050 AAGAAGTGGGTGGACCTGGCGCTGGCGCTGAGTATCCCTTCTAGCGCTTCTTCTCTACTAT 68

Db 9 AAGAAGTGGGTGGACCTGGCGCTGGCGCTGAGTATCCCTTCTAGCGCTTCTTCTCTACTAT 68

QY 1110 ATCCCTTCTACGGCATCTCGGAGGCCCTCTTCTTCTCACTTCTAGGTTCTCTGGAG 1169

Db 69 GTGCCACTATGGGGCTGAAGCCCTCTCTGGCGCTTCTTCTTCTATAGTCTAGGTTCTCTGGAA 128

SEQ ID NO 1117

LENGTH: 292

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. US20030134280A1 Z40715

US-09-960-706-1117

Query Match

Best Local Similarity 9.2%; Score 292; DB 13; Length 292;

Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2882 CTGAGCTGCTGTGAGTCTAACCACCTAATCAGTCTTTAGATTGAGGGGAGGGCAGGC 2941

Db 292 CTGAGCTGCTGTGAGTCTAACCACCTAATCAGTCTTTAGATTGAGGGGAGGGCAGGC 233

QY 2942 ACCAACAACCTAGAAATGGGGGCTTTCCGGGAGGGGCGCTAGTCCCGCCAGCTCTAAGCAG 3001

Db 232 ACCAACAACCTAGAAATGGGGGCTTTCCGGGAGGGGCGCTAGTCCCGCCAGCTCTAAGCAG 173

QY 3002 CCAGGAGGAGCTGATCTAAGCATCTGAGTCTGGGTTGGCATGGCAATGGCATGCCCGCCAGCTA 3061

Db 172 CCAGGAGGAGCTGATCTAAGCATCTGAGTCTGGGTTGGCATGGCAATGGCATGCCCGCCAGCTA 113

QY 3062 CTGTATGCCCCCGACCCCGCAGAGGAGCAATGAACCCATAGGAGCTGATCGTAATGTT 3121

Db 112 CTGTATGCCCCCGACCCCGCAGAGGAGGCGCTAGTCCCGCCAGCTCTAAGCAG 53

QY 3122 TATCATGTTACTTCCCGACCCCTACATTTTGTGAAATAAAATAAGGAATTTT 3173

Db 52 TATCATGTTACTTCCCGACCCCTACATTTTGTGAAATAAAATAAGGAATTTT 1

RESULT 34

US-10-191-513A-36

Sequence 36, Application US/10191513A

Publication No. US20030104596A1

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Mukerji, Pardeep

APPLICANT: Leonard, Amanda E.

APPLICANT: Huang, Yung-Sheng

APPLICANT: Tapas, Das

TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

FILE REFERENCE: 6295,US.D3

CURRENT APPLICATION NUMBER: US/10/191,513A

CURRENT FILING DATE: 2002-09-25

PRIOR APPLICATION NUMBER: US 09/227,613

PRIOR FILING DATE: 1999-01-08

PRIOR APPLICATION NUMBER: PCT/US98/07422

PRIOR FILING DATE: 1998-04-10

PRIOR APPLICATION NUMBER: US 08/833,610

PRIOR FILING DATE: 1997-04-11

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 36

LENGTH: 473

TYPE: DNA

ORGANISM: Homo sapiens

US-10-191-513A-36

Query Match

Best Local Similarity 8.0%; Score 253.8; DB 15; Length 473;

Matches 333; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1050 AAGAAGTGGGTGGACCTGGCGCTGGCGCTGAGTATCCCTTCTAGCGCTTCTTCTCTACTAT 68

Db 9 AAGAAGTGGGTGGACCTGGCGCTGGCGCTGAGTATCCCTTCTAGCGCTTCTTCTCTACTAT 68

QY 1110 ATCCCTTCTACGGCATCTCGGAGGCCCTCTTCTTCTCACTTCTAGGTTCTCTGGAG 1169

Db 69 GTGCCACTATGGGGCTGAAGCCCTCTCTGGCGCTTCTTCTTCTATAGTCTAGGTTCTCTGGAA 128

RESULT 37

US-10-191-513A-37
 ; Sequence 37, Application US/10191513A
 ; Publication No. US20030104596A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pardeep
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Tapas, Das
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295 US D3
 ; CURRENT APPLICATION NUMBER: US/10/191,513A
 ; CURRENT FILING DATE: 2002-09-25
 ; PRIOR APPLICATION NUMBER: US 09/227,613
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422
 ; PRIOR FILING DATE: 1998-04-10
 ; PRIOR APPLICATION NUMBER: US 08/833,610
 ; PRIOR FILING DATE: 1997-04-11
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 37
 ; LENGTH: 449
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (5)...(5)
 ; OTHER INFORMATION: k = g or t/u at position 5
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (6)...(6)
 ; OTHER INFORMATION: m = a or c at position 6
 ; OTHER INFORMATION:
 ; US-10-191-513A-37

Query Match

Best Local Similarity 7.1%; Score 226.8; DB 15; Length 449;
 Matches 314; Conservative 0; Mismatches 127; Indels 1; Gaps 1;
 QY 1078 TCAGTACTATACGCTGCTTCTTCTATCATCATCATCTCTCTTCTACGGCATCTCTGGAGCCC 1137
 Db 7 TTACCTTCTAGCTGCGCTCTTCTCTCTATGTCACATATTGGGCT-GAAAGCTTC 65
 QY 1138 TCTTTTCTCTCACTCTATCATGCTTCTCTGGAGCCACTGTTTGTGTGGTTCACACAGA 1197
 Db 66 TGGGCTTTTCTTCTATCATGCTTCTCTGGAGCCACTGTTTGTGTGGTTCACACAGA 125
 QY 1198 TGAATCATCATCTCTATGAGATTGACAGGAGGCTTACCGTACTGTTTCTAGTACGACG 1257
 Db 126 TGAACCATATTCCCATGTCACATTGATCATGACCGAAACATGACTGGGTTTCCACCCAGC 185
 QY 1258 TGACAGCCACTGCAACGCTGGAGCAGTCTCTTCTTCAACGACTGTTTCTAGTGGACACCTTA 1317
 Db 186 TCCAGGCCACATGCAATGTCACAAAGTCTGCTTCAATGACTGTTTCTAGTGGACACCTCA 245
 QY 1318 ACTTCAGATTGAGCACCACCTCTTCCACCATCCCGGCACAACTTACACAAAGATCG 1377
 Db 245 ACTTCAGATTGAGCACCACCTCTTTCACCATGCTCGACAAATTACACAAAGTGG 305
 QY 1378 CCCCCTGTGTGAAGTCTCTATGTGCAAGCATGCGATTGAATPACCAAGAGAGCGGCTAC 1437
 Db 306 CTCCCTGTGTGAGTCTCTTGTGTGCAAGCATGCGATTGAATPACCAAGAGAGCGGCTAC 365
 QY 1438 TGAGGCCCTGTGTCACATCATGCTCTTCCCTCAAGAGTCTGGAAGCTGTGGTGGACG 1497
 Db 366 TGTACGCTTGGCCGACATCTCTCACTTAAGAGTTCAGGCGAGCTCTGGCTAGATG 425
 QY 1498 CCTACCTTCAAAATGAAGCCA 1519
 Db 426 CCTATCTTCAACCAATCAACA 447

RESULT 38

US-09-783-590-5518
 ; Sequence 5518, Application US/09783590
 ; Patent No. US20020110850A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Patrick J.
 ; APPLICANT: Haseltine, William A.
 ; APPLICANT: Li, Haodong
 ; APPLICANT: Rosen, Craig A.
 ; APPLICANT: Ruben, Steven M.
 ; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
 ; FILE REFERENCE: PO-16.2C1
 ; CURRENT APPLICATION NUMBER: US/09/783,590
 ; CURRENT FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: 08/420,856
 ; PRIOR FILING DATE: 1995-04-12
 ; PRIOR APPLICATION NUMBER: 08/346,731
 ; PRIOR FILING DATE: 1994-11-21
 ; NUMBER OF SEQ ID NOS: 12485
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5518
 ; LENGTH: 315
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (40)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (52)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (67)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (69)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (92)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (101)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (139)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (162)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (184)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (227)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (247)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (252)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (280)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (298)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (302)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (311)

Db 1 VFYFGNGWIPITLITAFVLATSOAQAGMLQHDYGHLSVYRKPKWNLVHKFVIGHLKGASA 60
Qy 211 NWNHHRHFQHHAKPNI FHKDPDNNMLHVFLVGEWQPIEYGGKKLKYLPYNHQBHEVFFLIG 270
Db 61 NWNHHRHFQHHAKPNI FHKDPDNNMLHVFLVGEWQPIEYGGKKLKYLPYNHQBHEVFFLIG 120
Qy 271 PELLIPMYFOYQIIMTMIVHKWVDLAWAVSYIRFFITY:PFYGIIGALLFLNFIRFLE 330
Db 121 PELLIPMYFOYQIIMTMIVHKWVDLAWAVSYIRFFIT-IPFYGIIGALLFLNFIRFLE 179
Qy 331 SHWFVWVTOMNHVMEIDQAYRDWFSQLTATCNVEQSFNDWFSCHLNFOIEHHLPPT 390
Db 180 SHWFVWVTOMNHVMEIDQAYRDWFSQLTATCNVEQSFNDWFSCHLNFOIEHHLPPT 239
Qy 391 MPRHNLKIAPLVKSCLAKHGIEYQEKPLLRALLDIIRSLKSKGKMLDAYLHK 444
Db 240 MPRHNLKIAPLVKSCLAKHGIEYQEKPLLRALLDIIRSLKSKGKMLDAYLHK 293

RESULT 4

US-10-102-806-650
; Sequence 650, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P403P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 650
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-102-806-650

Query Match 65.4%; Score 1594; DB 15; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.1e-154;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 159 IPTLITAFVLATSOAQAGMLQHDYGHLSVYRKPKWNLVHKFVIGHLKGASANNHHRFP 219
Db 1 IPTLITAFVLATSOAQAGMLQHDYGHLSVYRKPKWNLVHKFVIGHLKGASANNHHRFP 60
Qy 219 QHHAKPNI FHKDPDNNMLHVFLVGEWQPIEYGGKKLKYLPYNHQBHEVFFLIGPPLIPMY 278
Db 61 QHHAKPNI FHKDPDNNMLHVFLVGEWQPIEYGGKKLKYLPYNHQBHEVFFLIGPPLIPMY 120
Qy 279 FOYQIIMTMIVHKWVDLAWAVSYIRFFITY:PFYGIIGALLFLNFIRFLESFWVVT 339
Db 121 FOYQIIMTMIVHKWVDLAWAVSYIRFFIT-IPFYGIIGALLFLNFIRFLESFWVVT 180
Qy 339 OMNHVMEIDQAYRDWFSQLTATCNVEQSFNDWFSCHLNFOIEHHLPPTMPRNLHK 398
Db 181 OMNHVMEIDQAYRDWFSQLTATCNVEQSFNDWFSCHLNFOIEHHLPPTMPRNLHK 240
Qy 399 IAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSKGKMLDAYLHK 444
Db 241 IAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSKGKMLDAYLHK 286

RESULT 5

US-10-262-617-1
; Sequence 1, Application US/10262617
; Publication No. US2003007747A1
; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
; FILE REFERENCE: PF-0494-1 DIV
; CURRENT APPLICATION NUMBER: US/10/262,617
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 09/048,888
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CDI
US-10-262-617-1

Query Match 64.0%; Score 1560.5; DB 15; Length 445;
Best Local Similarity 62.3%; Pred. No. 5.4e-151;
Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;

Qy 1 MGKGGNQ--EGAAEREVSVPFSHEEIQKHLNRTDGLVIDRKYNITKNSIQHPGGOR 58
Db 1 MGVGEGPGREGPAQPGAPLTFCEQIRAHQDQKWLVIERRVYDTSRWACRHPGGSR 60
Qy 59 VIGHYAGEDATDAFRAHPDLDFVFGKFLKPLIGELAPEEPQDQHGKNSKITEDFRALK 118
Db 61 LIGHGAEADATDAFRAHQDLNFKVFLQPLIGELAPEEPQDQGPLNAQLVEDFRALHQ 120
Qy 119 TADNMNLFKTNHVFLLLAHIALESIAFWTFVFGNGWITLITAFVLATSOAQAGWL 178
Db 121 AEDMKLFDASPTFFAFLGHLAMEVLAWLLIYLLGPGWPSALAAFTLAISOQSACL 180
Qy 179 QHDYGHLSVYRKPKWNLVHKFVIGHLKGASANNHHRFQHHAKPNI FHKDPDNNMLHV 238
Db 181 QHDLGHASIFKSKWNNHVAQKFWMGOLKGFSAHWNFRHFQHHAKPNI FHKDPDNNMLHV 240
Qy 239 FVLGEWQPIEYGGKKLKYLPYNHQBHEVFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAW 298
Db 241 FLIGE--SSVEYGGKKRRLPYNQOHLFFLIGPPLITLVNFEVENLAYMLVCWQWADLLW 299
Qy 299 AVSYIRFFITY:PFYGIIGALLFLNFIRFLESFWVVTOMNHVMEIDQAYRDWFS 358
Db 300 AASFYARFFLSLIPFYGVGVLLFFVAVRVLESFWVVTOMNHVMEIDQAYRDWFS 359
Qy 359 QLTATCNVEQSFNDWFSCHLNFOIEHHLPPTMPRNLHKIAPLVKSCLAKHGIEYQEK 418
Db 360 QLAATCNVEPSLFTNWFSGHLNFOIEHHLPMPRPNYSRVAPLVKSLCAKHGLSYEVKP 419
Qy 419 LLRALDIIIRSLKSKGKMLDAYLHK 444
Db 420 FLTALVDIVRSLSKSGDIWLDAYLHQ 445

RESULT 6

US-10-262-617-3
; Sequence 3, Application US/10262617
; Publication No. US2003007747A1
; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
; FILE REFERENCE: PF-0494-1 DIV
; CURRENT APPLICATION NUMBER: US/10/262,617
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 09/048,888
; PRIOR FILING DATE: 1998-03-26

```

; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030077747A1 2056310CD1
US-10-262-617-3

Query Match      62.1%; Score 1515; DB 15; Length 444;
Best Local Similarity 62.0%; Pred. No. 2.5e-146;
Matches 272; Conservative 62; Mismatches 99; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEETQKINLRDTSGLVIDRKVNITKWSIOHPGGQVIGHYAGED 67
DB 7 AETAAGGTPRYFTWDEVAQRSGCEERWLVIDRKVNISEFTRRHPGGSRVISHYAGQD 66

QY 68 ATDAFAFPDLEFVCKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTAEQDNLFK 127
DB 67 ATDPFVAFHINKGLVKYNNLSLIGELSPQSPFETKKNKELTDFRELRAATVERMGLMK 126

QY 128 TNEVFPILLIAHIALESIAFWTFVFGNGWPTLTITAFVLATSOAQAGWLQHDYGHLSV 187
DB 127 ANHVFFLLYLLHLLDGAANLTLWVGTSFLPFLCAVLLSAVOAQAGWLQHDYGHLSV 186

QY 188 YRKPKNHLVHKFVIGHLKGASANNWNNHRRHQHAKPNIFHXDPDNNMLH--VFVLGEWQ 245
DB 187 FSTSKNNHLLHFFVIGHLKGAPASANNWNNHRRHQHAKPNCFRDXPDINN-HPFFALGKIL 245

QY 246 PIYGGKKLKYLPYNHQQEYFFLIGPPLIPMYFQYQIIMTVHKWVDLAWAVSYIR 305
DB 246 SVELGKQKKYMPYNHQQYFFLIGPALLPLYFQWYFYFVYFVYFVYFVYFVYFVYFVYR 305

QY 306 FFITYPFYIGLALLFLNFIRESHFWVWVTQNNHIVMEIDQAYRDFWFSQLTATCN 365
DB 306 FFLTYVPLGLKAFGLFFIVRLESNFWVWVTQNNHIMHIDHNDMDWSTQLQATCN 365

QY 366 VEGSFNDWFSGHNLFOIEHLLPPTWPRNHLKIAPLVKSCLAKHGIEYQEKPLLRALLD 425
DB 366 VHSKAFNDWFSGHNLFOIEHLLPPTWPRNHYHKAVALVQSLCAKHGIEYQSKPLLSAFAD 425

QY 426 IIRSLKSGKGLWDAYLHK 444
DB 426 IIRSLKSGGQLWDAYLHQ 444

RESULT 7
US-10-191-513A-12
; Sequence 12, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US D3
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (444)...(444)
; OTHER INFORMATION: Xaa = Unknown or other at position 444
US-10-191-513A-42

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```

; ORGANISM: Homo sapiens
US-10-191-513A-12

Query Match      61.9%; Score 1508; DB 15; Length 444;
Best Local Similarity 61.7%; Pred. No. 1.3e-145;
Matches 271; Conservative 62; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEETQKINLRDTSGLVIDRKVNITKWSIOHPGGQVIGHYAGED 67
DB 7 AETAAGGTPRYFTWDEVAQRSGCEERWLVIDRKVNISEFTRRHPGGSRVISHYAGQD 66

QY 68 ATDAFAFPDLEFVCKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTAEQDNLFK 127
DB 67 ATDPFVAFHINKGLVKYNNLSLIGELSPQSPFETKKNKELTDFRELRAATVERMGLMK 126

QY 128 TNEVFPILLIAHIALESIAFWTFVFGNGWPTLTITAFVLATSOAQAGWLQHDYGHLSV 187
DB 127 ANHVFFLLYLLHLLDGAANLTLWVGTSFLPFLCAVLLSAVOAQAGWLQHDYGHLSV 186

QY 188 YRKPKNHLVHKFVIGHLKGASANNWNNHRRHQHAKPNIFHXDPDNNMLH--VFVLGEWQ 245
DB 187 FSTSKNNHLLHFFVIGHLKGAPASANNWNNHRRHQHAKPNCFRDXPDINN-HPFFALGKIL 245

QY 246 PIYGGKKLKYLPYNHQQEYFFLIGPPLIPMYFQYQIIMTVHKWVDLAWAVSYIR 305
DB 246 SVELGKQKKYMPYNHQQYFFLIGPALLPLYFQWYFYFVYFVYFVYFVYFVYFVYR 305

QY 306 FFITYPFYIGLALLFLNFIRESHFWVWVTQNNHIVMEIDQAYRDFWFSQLTATCN 365
DB 306 FFLTYVPLGLKAFGLFFIVRLESNFWVWVTQNNHIMHIDHNDMDWSTQLQATCN 365

QY 366 VEGSFNDWFSGHNLFOIEHLLPPTWPRNHLKIAPLVKSCLAKHGIEYQEKPLLRALLD 425
DB 366 VHSKAFNDWFSGHNLFOIEHLLPPTWPRNHYHKAVALVQSLCAKHGIEYQSKPLLSAFAD 425

QY 426 IIRSLKSGKGLWDAYLHK 444
DB 426 IIRSLKSGGQLWDAYLHQ 444

RESULT 8
US-10-191-513A-42
; Sequence 42, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US D3
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (444)...(444)
; OTHER INFORMATION: Xaa = Unknown or other at position 444
US-10-191-513A-42

```

Query Match

61.3%; Score 1493.5; DB 15; Length 444;

```
Best Local Similarity 61.5%; Pred. No. 3.9e-144;
Matches 270; Conservative 62; Mismatches 100; Indels 7; Gaps 4;

QY 11 AAREVSVPT--PSWEEIOKHNLRDGLVIDRKVYNITKWSIQHPGGORVIGHYAGED 67
Db 7 AETAAGGTPRFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPGGSRVISHYAGQD 66

QY 68 ATDAFRAHPDLEFVGKFLKPLLIGELAPEPSODHGKNSKITEDFRALKRTAEDNNLKF 127
Db 67 ATDPFAFHINKGLVKYNNLSLIGELSPQSPSEPTKNKELTDEPE-LRATYERNGLMK 125

QY 128 TNHVFLLALLAHIIALESIAWFTVFYFGNGWIPITLITAFVLATSQAQAGWLQHDYGHLSV 187
Db 126 ANHVFFLLYLLHILLDGAAMLTLWVFGTSEFLPCLCAVLLSAVQAQAGWLQHDYGHLSV 185

QY 188 YRKPKNHVLHVKFVIGHLKGSANWNNHRRHQHAKPNIFHKDPDVNMLH--VFVLGEWQ 245
Db 186 PSTSKNNHLLHFFVIGHLKGPASWNNHMHFQHAKPNCFRKDPDINN-HPPFFALGKIL 244

QY 246 PIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMVHKNNWVDLAWAVSYIR 305
Db 245 SVELGKQKKYMPYNNHQHKKYFFLIGPPLIPMYFOYIFVFIQKRWVDLAWMITFYVR 304

QY 306 FFITYIPYIGLALLFNIRFLESHWVWVTQNNHIVMEIDQAYRDWFSQLTATCN 365
Db 305 FFLIVVPLLGKAFGLGFFIVRFLSNWVWVTQNNHIPMHDHNRNDWVSTQLTATCN 364

QY 366 VEQSFENDWFSCHLNFOIEHLLFPTMPRHNLKTAPLVKSICAKHGIEYQEKPLRALLD 425
Db 365 VHSFAFNWFSCHLNFOIEHLLFPTMPRHNVKRVAPLVQSLCAKGIEYQSKPLLSAFAD 424

QY 426 IIRSLKSGKWLMDAYLHK 444
Db 425 IIRSLKSGKWLMDAYLHQ 443

RESULT 9
US-10-191-513A-39
; Sequence 39, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10191,513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-191-513A-39

Query Match 46.3%; Score 1128; DB 15; Length 360;
Best Local Similarity 57.2%; Pred. No. 8e-107;
Matches 203; Conservative 56; Mismatches 90; Indels 6; Gaps 3;

QY 11 AAREVSVPT--PSWEEIOKHNLRDGLVIDRKVYNITKWSIQHPGGORVIGHYAGED 67
Db 7 AETAAGGTPRFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPGGSRVISHYAGQD 66

QY 68 ATDAFRAHPDLEFVGKFLKPLLIGELAPEPSODHGKNSKITEDFRALKRTAEDNNLKF 127
Db 67 ATDPFAFHINKGLVKYNNLSLIGELSPQSPSEPTKNKELTDEPE-LRATYERNGLMK 125

QY 128 TNHVFLLALLAHIIALESIAWFTVFYFGNGWIPITLITAFVLATSQAQAGWLQHDYGHLSV 187
Db 126 ANHVFFLLYLLHILLDGAAMLTLWVFGTSEFLPCLCAVLLSAVQAQAGWLQHDYGHLSV 185

QY 188 YRKPKNHVLHVKFVIGHLKGSANWNNHRRHQHAKPNIFHKDPDVNMLH--VFVLGEWQ 245
Db 186 PSTSKNNHLLHFFVIGHLKGPASWNNHMHFQHAKPNCFRKDPDINN-HPPFFALGKIL 244

QY 246 PIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMVHKNNWVDLAWAVSYIR 305
Db 245 SVELGKQKKYMPYNNHQHKKYFFLIGPPLIPMYFOYIFVFIQKRWVDLAWMITFYVR 304

QY 306 FFITYIPYIGLALLFNIRFLESHWVWVTQNNHIVMEIDQAYRDWFSQLTATCN 365
Db 305 FFLIVVPLLGKAFGLGFFIVRFLSNWVWVTQNNHIPMHDHNRNDWVSTQLTATCN 364

QY 366 VEQSFENDWFSCHLNFOIEHLLFPTMPRHNLKTAPLVKSICAKHGIEYQEKPLRALLD 425
Db 365 VHSFAFNWFSCHLNFOIEHLLFPTMPRHNVKRVAPLVQSLCAKGIEYQSKPLLSAFAD 424

QY 426 IIRSLKSGKWLMDAYLHK 444
Db 425 IIRSLKSGKWLMDAYLHQ 443

RESULT 10
US-10-191-513A-14
; Sequence 14, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10191,513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-191-513A-14

Query Match 45.2%; Score 1103; DB 15; Length 287;
Best Local Similarity 66.9%; Pred. No. 2.1e-104;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GMTPTLITAFVLATSQAQAGWLQHDYGHLSVYRKPKNHVLHVKFVIGHLKGSANWNNH 216
Db 8 GGIPAV-----QAQAGWLQHDYGHLSVSTSKNNHLLHFFVIGHLKGPASWNNH 58

QY 217 HFQHAKPNIFHKDPDVNMLH--VFVLGEWQIEYQEKKKLKYLPYNHGHYFFLIGPPL 274
Db 59 HFQHAKPNCFRKDPDINN-HPPFFALGKILSVELGKQKKYMPYNNHQHKKYFFLIGPPL 117

QY 275 IPMYFOYQIIMTMVHKNNWVDLAWAVSYIRFITYIPYIGLALLFNIRFLESHW 334
Db 118 LPLYFQWYIFVFIQKRWVDLAWMITFYVRFLTYVPLLGKAFGLGFFIVRFLSNW 177

QY 335 VWTQNNHIVMEIDQAYRDWFSQLTATCNVEQSFENDWFSCHLNFOIEHLLFPTMPRH 394
Db 178 VWTQNNHIPMHDHNRNDWVSTQLTATCNVHKSADFNSCHLNFOIEHLLFPTMPRH 237

QY 395 NLHKIAPLVKSLCAKGIEYQEKPLRALLDIIRSLKSGKWLMDAYLHK 444
Db 238 NYHKVAPLVQSLCAKGIEYQSKPLLSAFADIIIRSLKSGKWLMDAYLHQ 287
```

RESULT 11
US-10-191-513A-15
; Sequence 15, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardiip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.D3
; CURRENT APPLICATION NUMBER: US/10/191.513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (288)...(288)
; OTHER INFORMATION: Xaa = Unknown or other at position 288
US-10-191-513A-15

Query Match 45.2%; Score 1103; DB 15; Length 288;
Best Local Similarity 66.9%; Pred. No. 2.1e-104; Indels 12; Gaps 3;
Matches 194; Conservative 32; Mismatches 52

QY 157 GWIPTLITAFVLATSQAQAGWLQHDYGLSVYRKPNWHLVKFVIGHLKASANWNRH 216
DB 8 GGIPAV-----QAQAGWLQHDYGLSVYRKPNWHLVKFVIGHLKASANWNRH 58

QY 217 HFQHHAKPNIFKDPDVMNLH--VFVLGEMQPIEVYKGGKLLKPLVYNHGHYFFLLGPPLL 274
DB 59 HFQHHAKPNIFKDPDVMNLH--VFVLGEMQPIEVYKGGKLLKPLVYNHGHYFFLLGPPLL 117

QY 275 IPWVQVQIIMTMVHNKWNVDLAWAVSYIRFFITYIPFYIGLGAFLNFIPLFLESHWF 334
DB 118 LPLVYFQWYIFVYIQRKKWVDLAWMITFVYRFFLTVPVLLGLKAFGLFPIVRFLESNWF 177

QY 335 VWTQNNHIVMEIDQAYRDWSSQLTATCNVEQSFNDWFSGLNLFQIEHLLFPTMRH 394
DB 178 VWTQNNHIVMEIDQAYRDWSSQLTATCNVEQSFNDWFSGLNLFQIEHLLFPTMRH 237

QY 395 NLHKAIPLVKSLCAKHGIEQKPLLRALLDIRSLKSGKMLDAYLHK 444
DB 238 NYHKVAPLVQSLCAKHGIEQKPLLRALLDIRSLKSGKMLDAYLHK 287

RESULT 12
US-10-191-513A-40
; Sequence 40, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardiip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.D3
; CURRENT APPLICATION NUMBER: US/10/191.513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08

; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (251)...(251)
; OTHER INFORMATION: Xaa = Unknown or other at position 251
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (329)...(330)
; OTHER INFORMATION: Xaa = Unknown or other at these positions
US-10-191-513A-40

Query Match 37.3%; Score 909.5; DB 15; Length 347;
Best Local Similarity 58.6%; Pred. No. 1.8e-84; Indels 7; Gaps 4;
Matches 167; Conservative 43; Mismatches 68

QY 19 PT---ESWEEIQKHNLRTDGLVIDRKVYNIITKWSIQHPGQGVIGHYAGEDATDAFRAP 75
DB 3 PTPRYFTWDEVAQRSGCEERWLVIDRKVYNIITKWSIQHPGQGVIGHYAGEDATDAFRAP 62

QY 76 HPDLFVGVKFLKPLLLIGELAPESODHGKNSKITEDFALRKTAEKMLFKTNHVFLL 135
DB 63 HINKGLVKKYMSLLIGELSPQSPFETPKNKELTDFELRATVEMGLMKNHVFLL 122

QY 136 LLAAHIIALESIAWFTVYFNGWIPITLITAFVLATSQAQAGWLQHDYGLSVYRKPNWHL 195
DB 123 YLLHILLDDGAAMLTLWVFGTSPFLLCVLLSAVQAQAGWLQHDYGLSVYRKPNWHL 181

QY 196 LVHKFVIGHLKASANWNRHRRHFOHAKKNI PHKDPDVMNLH--VFVLGEMQPIEVYKGGK 253
DB 182 LLHFHFGVIGHLKASAPSWNNHMFQHHAKPNCFRKPDINN--HPFFPALGKILLSVELGKQK 240

QY 254 LKYLPNVNHQHYEYFFLIGPPLIIPMYFYQYQIIMTMVHNKWNVDLAW 298
DB 241 KKNYPNHNQHYEYFFLIGPPLIIPMYFYQYQIIMTMVHNKWNVDLAW 285

RESULT 13
US-10-191-513A-19
; Sequence 19, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardiip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.D3
; CURRENT APPLICATION NUMBER: US/10/191.513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-191-513A-19

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Query Match 32.2%; Score 784; DB 15; Length 219;
Best Local Similarity 61.7%; Pred. No. 6.9e-72;
Matches 137; Conservative 27; Mismatches 46; Indels 12; Gaps 3;

QY 157 GWITPILITAFVLTATSAQAAGLQHDYGHLSVYRKPKNNHLVHKFVIGHLKGASAKNNHR 216
DB 8 GGIPAV-----QAQAAGLQHDYGHLSVYRKPKNNHLVHKFVIGHLKGASAKNNHR 58

QY 217 HFQGHAKPNTFHKDPDNNMLH--VFVLGEQPIEYGGKGLKYLPPYNNHQHEYFPLIGPPLL 274
DB 59 HFQGHAKPNCFRKDPDNNM--HPFFALGKLSVELGKQKKYNNHQYFPLIGPPAL 117

QY 275 IPMYFOYIIMTVMVHQNVDLAWAVSYIRFTTIPFYGLGALLNFNIRPLESHWF 334
DB 118 LPLFYQYIYFVYIQRKKVDLAWMITFYRFLLTYVPLGLKFAFLGFFIVRFLSNWF 177

QY 335 VVYQNNHIVMEIDOEAYRDWFSQLTATCNVQSPPNDWFS 376
DB 178 VVYQNNHIVMEIDOEAYRDWFSQLTATCNVKSAPNDWFS 219

RESULT 14
US-10-191-513A-20
; Sequence 20, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.B3
; CURRENT APPLICATION NUMBER: US/10191.513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (128)...(128)
; OTHER INFORMATION: Xaa = Unknown or other at position 128
US-10-191-513A-20

Query Match 24.1%; Score 587.5; DB 15; Length 182;
Best Local Similarity 62.3%; Pred. No. 7.1e-52;
Matches 101; Conservative 22; Mismatches 36; Indels 3; Gaps 2;

QY 139 HIIALESIAFWTFVYFGNGWIPITLITAFVLTATSAQAAGLQHDYGHLSVYRKPKNNHLVH 198
DB 2 HILLDGAALTLWVFGTSFLPFLLCVALLSAGVQAAGLQHDYGHLSVYRKPKNNHLVH 61

QY 199 KPVIGHLKGASANNHRRHFQGHAKPNTFHKDPDNNMLH--VFVLGEQPIEYGGKGLK 256
DB 62 HFVIGHLKGASANNHRRHFQGHAKPNCFRKDPDNNM--HPFFALGKLSVELGKQKKY 120

QY 257 LPPYNNHQHEYFPLIGPPLLIPMYFOYIIMTVMVHQNVDLAW 298
DB 121 MPYNNHQHYFPLIGPPLLIPMYFOYIIMTVMVHQNVDLAW 162

RESULT 15
US-09-967-477B-8
; Sequence 8, Application US/09967477B
```

```
; Patent No. US20020156254A1
; GENERAL INFORMATION:
; APPLICANT: Xiac Qiu
; APPLICANT: Haijing Hong
; TITLE OF INVENTION: PAD4, FADS-2, AND FADS6, NOVEL
; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: BNZ-001
; CURRENT APPLICATION NUMBER: US/09/967,477B
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/236,303
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/297,562
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Thraustochytrium sp.
US-09-967-477B-8

Query Match 20.4%; Score 497; DB 10; Length 459;
Best Local Similarity 27.7%; Pred. No. 4.7e-42;
Matches 132; Conservative 79; Mismatches 176; Indels 90; Gaps 16;

QY 22 SWEEIOKHNLRDTSGLVIDRKVYNNITKWSIOHGGQORVIGHYAGEDATDAFRAHPDLEF 81
DB 13 SWKEIREHATPATAVIVHKKVYDISKWD--SHPGGS--VMTQAGEDATDAFVHPSSAL 70

QY 82 VGKFLKPLLIIGEL-----APEEPSQD--HGKSKITE---DPRALKRKTADNNLFTKN 129
DB 71 --KLEQFYVGVDDTETSKAE--EGEPASDEERARRERINEFTIAYRRLRVKYGKGLYDAS 128

QY 130 HVFFELLALHIIALESIAFWTFVYFGNGWIPITLITAFVLTATSAQAAGLQHDYGHLSVYR 189
DB 129 ALUYANKLVSTFGIAVLSNAICFPF--NSFAMVWAGVINGLGYQSGWLAHDFLENQVCE 187

QY 190 KPKNNHLVHKFYVIGHLKGASANNHRRHFQGHAKPNT-----FHKDPDNNMLHVFVLG 242
DB 188 NRTGLNGLICLVGNAWQGFVSQWKKNNKLNHAAVFNLSAKDEGFIGDPDIDTM----- 241

QY 243 EQWPIEYGGKGLKYLPPYNNHQHEYF-----FLIGPPLLIPMY-----FOYQI 283
DB 242 ---PILAWSKENARKAFESAHHGPFPIRNOAFLYFPLLLALRLSLWLAQSFYVTFEFSFI 298

QY 284 I-----MTMIVHKNVVDLAWAVSY-----IRFFITYIPFYGILGALLFNLF 325
DB 299 FDKVEFDGPEKAGLIVHYI---QLAIFYFCNMSLFEGVAYFLMQASCGLLALVF--- 352

QY 326 IRFLESHWFVWTONHIVMEI--DOEAYRDWFSQLTATCNVQSPPNDWFSGHNLNFOIE 384
DB 353 -----SIGHNGMSVYERETKPDQWQGVVTRIRASVFMDFWFGGLNLYQID 399

QY 385 HHLFPTMPRNLHKLAPLVKSLCAKHGIEYQKPLLRALLDLIRSLKSKGKLWLDAY 441
DB 400 HHLFPLVPRNLKPNVNLKSLCKEFDIPFHETGWEIGIYEVVDHLADISKEFITEF 456

RESULT 16
US-09-769-863-14
; Sequence 14, Application US/09769863
; Publication No. US20030157144A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.O1
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
```

```
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-09-769-863-14

Query Match      20.0%; Score 487.5; DB 12; Length 453;
Best Local Similarity 27.9%; Pred. No. 4.3e-41;
Matches 133; Conservative 92; Mismatches 164; Indels 87; Gaps 19;

QY 7 QGGAAREVSVPTFSWEEIQKHLRTDGLVDRKYNITKWSIQHPGQORVIGHAGE 66
Db 3 QGQKAEK-----ISWATIREHNRQDNAMIVIHKKYVDISAFE-DHPGGV-VNFTQAGE 53

QY 67 DATDAFAFHDPDLREVGVKFLKPLLIGEL-----APEPSQDHGKNSK--ITEDFRALRKT 119
Db 54 DATDAFAVHFSSAL--KLEQYVGVDDQSTAAVDTSISDEVKKSQSDFIASVKLRLE 111

QY 120 AEDMNLFTKNHVFLLLAHIIALESIAFTVFVFGNGWIPTLITAFVLATSOAQAGWLQ 179
Db 112 VKRLGLYDSSKLYLYKCASTLSIALVSAACILHF-DSTAMYMVAAVILGLFYQCCGWL 170

QY 180 HDYGHLSYVRKPKNHLVHKFV---IGHL-KGASANMNNHRHFOHAKPNI-----FH 228
Db 171 HDFLHQVFE---NHLFGDLGVNMGVNLQGFVSQVQWKNKXNTHAIPNLHATPEIAFH 226

QY 229 KDPDYNMLHFVILGEQWPIEGKKLYLPYNHQQEYFFLIGPPLLIPIFYQYQIIMTI 289
Db 227 GPDIDITPILA--W-----SLKWA---CHAVDSPVG---LFFMRYQAYLYPFI 268

QY 289 VHKNWVDLAWAYSIVIRFITVIP-----FYGILGALLFLNFIREFL 329
Db 269 L---FARISWVTSQAWYAFYNNVPGGTDKVOYPLERAGLLLYGWNGLVYVAAWMSLL 325

QY 330 ESHWFVWVTQ-----MNHVMEI-DQEAAYRDMFSSQLPATCNVQSFNDWFS 376
Db 326 QAAAFVFSQASCGGLFLAMVFSVGHNGMEVFDKSKDPFWKLQVLSTRNVTSSLWIDWFM 385

QY 377 GHNLFOIEHLFPTRHNLHIAPIVKSCLAKHGIEYQEKPLLRALLDIIRSLKK 432
Db 386 GGLNYQIDHLLFPWPRHNLPALNVLSLCKQYDIPYHETGFIAGMAEVVHLE 441

RESULT 18
US-10-431-952-14
; Sequence 14, Application US/10431952
; Publication No. US20030190733A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/10/431,952
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US/09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-10-431-952-14

Query Match      20.0%; Score 487.5; DB 12; Length 453;
Best Local Similarity 27.9%; Pred. No. 4.3e-41;
Matches 133; Conservative 92; Mismatches 164; Indels 87; Gaps 19;

QY 7 QGGAAREVSVPTFSWEEIQKHLRTDGLVDRKYNITKWSIQHPGQORVIGHAGE 66
Db 3 QGQKAEK-----ISWATIREHNRQDNAMIVIHKKYVDISAFE-DHPGGV-VNFTQAGE 53

QY 67 DATDAFAFHDPDLREVGVKFLKPLLIGEL-----APEPSQDHGKNSK--ITEDFRALRKT 119
Db 54 DATDAFAVHFSSAL--KLEQYVGVDDQSTAAVDTSISDEVKKSQSDFIASVKLRLE 111

QY 120 AEDMNLFTKNHVFLLLAHIIALESIAFTVFVFGNGWIPTLITAFVLATSOAQAGWLQ 179
Db 112 VKRLGLYDSSKLYLYKCASTLSIALVSAACILHF-DSTAMYMVAAVILGLFYQCCGWL 170

QY 180 HDYGHLSYVRKPKNHLVHKFV---IGHL-KGASANMNNHRHFOHAKPNI-----FH 228
Db 171 HDFLHQVFE---NHLFGDLGVNMGVNLQGFVSQVQWKNKXNTHAIPNLHATPEIAFH 226

QY 229 KDPDYNMLHFVILGEQWPIEGKKLYLPYNHQQEYFFLIGPPLLIPIFYQYQIIMTI 289
Db 227 GPDIDITPILA--W-----SLKWA---CHAVDSPVG---LFFMRYQAYLYPFI 268

QY 289 VHKNWVDLAWAYSIVIRFITVIP-----FYGILGALLFLNFIREFL 329
Db 269 L---FARISWVTSQAWYAFYNNVPGGTDKVOYPLERAGLLLYGWNGLVYVAAWMSLL 325

QY 330 ESHWFVWVTQ-----MNHVMEI-DQEAAYRDMFSSQLPATCNVQSFNDWFS 376
Db 326 QAAAFVFSQASCGGLFLAMVFSVGHNGMEVFDKSKDPFWKLQVLSTRNVTSSLWIDWFM 385

QY 377 GHNLFOIEHLFPTRHNLHIAPIVKSCLAKHGIEYQEKPLLRALLDIIRSLKK 432
Db 386 GGLNYQIDHLLFPWPRHNLPALNVLSLCKQYDIPYHETGFIAGMAEVVHLE 441

RESULT 17
US-10-054-534B-14
; Sequence 14, Application US/10054534B
; Publication No. US20030167525A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.P1
; CURRENT APPLICATION NUMBER: US/10/054,534B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-10-054-534B-14

Query Match      20.0%; Score 487.5; DB 12; Length 453;
Best Local Similarity 27.9%; Pred. No. 4.3e-41;
Matches 133; Conservative 92; Mismatches 164; Indels 87; Gaps 19;
```


Db 112 VKRLGLYDSSKLYLYKCASTLSIALVSAACILHP-DSTAMVVAARVILGLFYQCGWLA 170
Qy 180 HDYCHLSVYKPKWNLVHKPV---ICHL-KGASANWNRHHRFHAKNMI-----EH 228
Db 171 HDFLHQVFE---NHLGDLGVGVGNLWQGSVQWKKRNTTHAIPNLHATPIAPH 226
Qy 229 KDPDNNMLHVFVLGEMQPIBYGKKKLYLPYNHCHYEYFFLIGPPLIPMYFYQYIIMTWI 288
Db 227 GDDIDTMPILA---W-----SLKWA---QHAVDSPVG---LFFMYQAYLYFPIL 268
Qy 289 VHKWVDLAVNAVSYIRFFITYP-----FYGLGALLFLNIREL 329
Db 269 L---FARISVIOASMYAFYVNGVGGTFDKVQVPELLERAGLLIYGNLGLVFAANWSLL 325
Qy 330 ESHWFVWVTO-----MMHIVMEI-DOEAYRDNFSSQLTATCNVEQSFDFNDFS 376
Db 326 QAAFLVFSQASGLFLAMVFSVGHNGMEYFDKSKDFKQLVLSRNVTSLLWIDWFM 385
Qy 377 GHLNFQIEHLFPMPRHNHKLAPLVKSLCAKHGIEYQKPLRALLDIIRSLKK 432
Db 386 GGLNYQIDHLLFPMVPRHNLPALNVLSLCKQYDIPYHETGFIAGNAEVVYVHLER 441

RESULT 19
US-10-278-391-4
; Sequence 4, Application US/10278391
; Publication No. US20030159164A1
; GENERAL INFORMATION:
; APPLICANT: KOPCHIK, JOHN J.
; KELDER, BRUCE
; HUANG, YUNG-SHENG
; KIRCHNER, STEPHEN J.
; MUKERJI, PRADIP
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
; PRODUCTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,391
; FILING DATE: 23-Oct-2002
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,578
; FILING DATE: 29-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-03348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030159164A1 Relevant
; TOPOLOGY: No. US20030159164A1 Relevant
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-278-391-4

Query Match. 18.8%; Score 459; DB 12; Length 457;
Best Local Similarity 24.9%; Pred. No. 3.6e-38;
Matches 118; Conservative 88; Mismatches 183; Indels 84; Gaps 14;
Qy 17 SVTPFSWEEI-----QKNLRTDSGLVTRKVVYNTKWSIOHPOGQORVIGHVAGEDA 68
Db 6 SVRTFTRAEVFNABALNEGKDAEPFLMIIDNKVYDVREFFVDPHPPGGSVILTH-VGKDG 64
Qy 69 TDAFRAPHDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEDMNLKPT 128
Db 65 TDVPTDTHP--EAAWETLANFVVGDI--DESDRDI-KXDDFAAEVRKLRITLFSGLGYDS 119
Qy 129 NHVFFLLLAHIIALESIAWTFVYFG-NGWIPILITAFVLATSAQAQAGMLQHDYGHLSV 187
Db 120 SKAYAFKVSFNLCTIGWGLSTVIVAKGQSTLANVLSAALLGLFWQCGGWLHDFLHHQV 179
Qy 188 YRKPKNHNLVHKFVIGHLKGASANWNRHHRFHAKNIPHKDPDNNMLHVFVLGEMQPI 247
Db 180 FQDRFWGLDFGAFLGVCQGFSSSWWKDKHNTHAAPNVHGEDPDIDTHPLTWSE---- 235
Qy 248 EYGKKKLYLPYNHCHYEYFFLIGPPLIPMYFYQYIIMTWIHKW-----VDLAWA 299
Db 236 -----HALENFSDVPDBELTRMSRF-----MVLNQTFWFFPILSFARLSWC 277
Qy 300 VSYIRFFITYPYGILGALLFLNFIR--FLESHWFVW----- 336
Db 278 LQ-SILFVLPGQAKHPSGARVPISLVQSLAMEN-TWYLATMELFIKDPNNMLVYFLV 335
Qy 337 -----VTQNNHIVMEI---DQEAYRDNFSSQLTATCNVEQSFDFNDFSGLHNFQ 382
Db 336 SQAVCGNLLAIIVFSLNHNMPVISKEEAVDMDFTKQIITGRDVHPGLFANWFTGGLNYQ 395
Qy 383 IEHLFPMPRHNHKLAPLVKSLCAKHGIEYQKPLRALLDIIRSLKKSGK 435
Db 396 IEHLFPMPRHNHKLAPLVKSLCAKHGIEYQKPLRALLDIIRSLKKSGK 448

RESULT 20
US-10-191-513A-11
; Sequence 11, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (458)...(458)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-11

Query Match. 18.8%; Score 459; DB 15; Length 458;
Best Local Similarity 24.9%; Pred. No. 3.6e-38;
Matches 118; Conservative 88; Mismatches 183; Indels 84; Gaps 14;

QY		17	SVPFSEMEI-----QKNLRTDGLVIDRKVNNTKWSIOHQGGORVIGHYAGEDA	68
			: : : : : :	
Db		6	SVRTFTRAEVLNAEALNEGKDABAPFLMIIDNKVDVREFPDPHGGGVILTH-VGXDG	64
			: : : : : :	
QY		69	TDAFRAPHDPDEFVGKTLKPLLIGELAPEPSSODHGKNSKITEDFPALAKTAEDMNLFKT	128
			: : : : : :	
Db		65	TDVCTRHP--EAWEFLANFYVGDJ--DSDDRDI-KNUDFAAEVKRKLTLFQSIGYYDS	119
			: : : : : :	
QY		129	NHVFFLLLAHHIALESIANFTVEYFG-NGWIPITLITAFVLATSOAQAGMLQHDYCHLSU	187
			: : : : : :	
Db		120	SKAYYAFKVSNLCIWGLSTVIIVAKWGOTETLANVLSAALLGLFWQCQGLAHDFLHQV	179
			: : : : : :	
QY		188	YRKPKWNHLVHKPFYGHLGKASANNWNRHFQHWAKPNIFPHKDPDYNMMLHVFLGEWQPI	247
			: : : : : :	
Db		180	FQDRFWDGLFAFJGGVCQGFSNKKWKDKNTTHAAPNVGEHPDIDTHPLTWSE----	235
			: : : : : :	
QY		248	EYGKKKIKLYLPYNHQHEHYFFLIGPLLIPIYFOYQIIIMTIMVHKNW-----VDLAWA	299
			: : : : : :	
Db		236	-----HALEWFSDVDPDEELTRMSRF-----MVLNQTWFYPILLSFAELSHWC	277
			: : : : : :	
QY		300	VSYIRPFTITIPYGILGALLFNFR--FLASHWFW-----	336
			: : : : : :	
Db		278	LQ-SILFVLPNGOAHKPSGARVPISLVEQLSLAMHW-TWYLATMTFLFDYPNMMLVFVLV	335
			: : : : : :	
QY		337	-----VTOMNHVMEI---DOEARVDFSSOLTATCNVEOSFENDAFSGHLNFQ	382
			: : : : : :	
Db		336	SOAVCGNLLAIVPSLNHNHNPVISKEBAVMDWDFTKQITGRDVHPCLFANWFTGGLNYQ	395
			: : : : : :	
QY		383	IEHLLFPTMPRHNLHIAPLVKSICAKHGIEYOEKPLLRALLDIITRSLKXSK	435
			: : : : : :	
Db		396	IEHLLFSPMPHNFSKIQPAAVELICKRYNNRYHTTGMIETGAEEVFSRLANEVK	448
			: : : : : :	

```

RESULT 21
US-10-191-513A-41
; Sequence 41, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardiip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US96/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (458)...(458)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-41

```

```

69 QY TDAPRAFPDLEFVGKFLKPLTIGELAPPEPQDGHGKNSKITEDPRALRKTAEDMNLKFT 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 Db TDVFDTEHP -EAAWETLANFYVGDI--DESORDI-KXDDFAAEVRKLRTLFQSLGYVDS 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
129 QY NHVFFLLLAHIALESIAFWVFVG-NGWTFTLITAPVLATSOAQAGWLOHDYGHLSV 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 Db SKAYIAFKVFNICIGLSTVIIVAKWGQTSTLIANVLSAALLGLEFWQCGWLAHDFLHHQV 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
198 QY YRKPKMNLHVKEVIGHLKGASANNMNRHHFOHAKPNI FHKDPDVNMLHVFVLGEWQPI 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
180 Db FQDRFWDGLFGALFGVCGQFSSWKCXKHNTHAAPNVHGDEPDIDTHPLLTWSE--- 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
248 QY EYGKKLXKLPYNHQHSEYFFLIGPPLIPMYFOYQIIMTIVHKNW-----VDLAWA 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
236 Db -----HALEMFSDPDELTAKMRSF-----MVLNQTWFFPILSPARLUSWC 277
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
300 QY VSYVIRFFITYIPFYGILGALLFLNPIR--FLESHWFVW----- 336
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
278 Db LQ-SILEVLPNGQAHKPSGARVPISLVEQLSLAMHW-TWILATWFLFIKDPVNMVYFLV 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
337 QY -----VTCMHNIWEI-----DOEAYRWFSQUTATCNVEQSFNDWFGSHLNFQ 382
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
336 Db SQAVCGNLLAIVFSLNHNGMPVISEAEVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQ 395
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
383 QY IEHLFPTMPRNLHIAPLVLSLCAKHGIEYOEKPLLRALLIDIRSLKSGK 435
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
396 Db IEHLFSPMRPNFSKIQPAVETLCKYVRYHTTGMEGTAEVFSRLNEVSK 448
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 22
US-10-340-779A-11
; Sequence 11, Application US/10340779A
; Publication No. US20030152963A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Johnathan A.
; APPLICANT: Michaelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340,779A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Helianthus annuus
US-10-340-779A-11

```

QY 197 VHKFVIGHLKASANNWNRHFOHAKPNIPHKDPDVNMLHF-----VLGEWQPIBYGK 251
DB 186 AGIFIGNCITGISIAWKTNAHIAACNSLDYDPLQHLPLMVAASKLNSITSFYG- 244
QY 252 KKLKXLP-----YHQHEFFELIGPPLIPMYFOYQIIMTMIVHKWVDLAWAVSYIRF 306
DB 245 RQLFDFPLARFVSQVHYLYPIMCVARNVLYL--QILLISRK- 288
QY 307 FITPIFYG--ILGALLFLNFIRESHWFW-----VTOMNHVMEIDQ--- 349
DB 289 ----IPDRGLNLGLTFTWTFPLVLSRLPNPBRVAFVLVSFCVTGICHIQITLNFSG 344
QY 350 EAY-----RDWFSQLTATCNVEOSPFNDWFSGLHNFQIEHHLFPTMPRHNLHKAIPLV 403
DB 345 DVIYGPCKDNWFEKQRTGTIDACSSWMDNFFGGLQFQLEHHLFPLPCHLSISIPIC 404
QY 404 KSLCAKHGIEYOEKPLLRALLDIIRSLK 431
DB 405 RELCKKNLPYVSLSFYDANVTTLKTLR 432
RESULT 23
US-10-340-779A-13
; Sequence 13, Application US/10340779A
; Publication No. US20030152983A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Johnathan A.
; APPLICANT: Michaelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340,779A
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Borago officinalis
US-10-340-779A-13
Query Match 17.9%; Score 436.5; DB 12; Length 448;
Best Local Similarity 29.0%; Pred. No. 7,1e-36;
Matches 130; Conservative 63; Mismatches 182; Indels 73; Gaps 16;
QY 24 BEIQKHLRTDSGLVIDRKVYNTKWSIQHPGQQRVIGHYAGEDATDAFRAHP----- 77
DB 12 DELKNDKPGDLWISIQKAYDVSDWKDPHGGSPFLKSLAQEVTDFAVAFHPASTWKN 71
QY 78 -DLEFVGKELKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNLP-KTNHVFLL 135
DB 72 LDKFETGYLKYDVS-----SEVSKDYRLKLVFEFSKGLYDKKGHMF-A 115
QY 136 LLAHIIALESIAWFTVYFGNGWIPITLITAFVATSQAQAGLQHDYHLSVYRKPKWNH 195
DB 116 TLCFIAMLFAMSVYGVLFCEGVVLHFLSGCLMGFLWISQGWIGHDAGHVMVSDSLNK 174
QY 196 LVHKFVIGHLKASANNWNRHFOHAKPNIPHKDPDVNMLHFVL-----CEWPIYSG 250
DB 175 FMGIFAANCLSGISIGWKNWNAHIAACNSLEYDPLQYIPPLVSSKFFGSLTSHFYE 234
QY 251 KK----KLKYLPNHGHVFFELIGPPLIPMYFOYQIIMTMIVHKWVDLAWAVSYIRF 306
DB 235 KRLTFDSLSPFFVSQHWTFYPLMCAARLNMVQ-SLIM-LITKEN-----VSRA-- 283

QY 307 FITPIFYGILGALLFLNFIRES-----HV-----FV-----KVTONNHVMEID--QEA 351
DB 284 -----HELLCCLVFSIWPVLVCLNPNWGRINMFVTSVGNQVQVSLNHFSSV 336
QY 352 Y-----RDWFSQLTATCNVEOSPFNDWFSGLHNFQIEHHLFPTMPRHNLHKAIPLVKS 405
DB 337 YVGKPKGNWFEKQRTGTIDLISCPWMDWFGGLQFQIEHHLFPPKPRCNLRKISPYVIE 396
QY 406 LCAKHGIEYOEKPLLRALLDIIRSLKS 433
DB 397 LCKKNLPYNYASFASKANEMTURTURT 424
US-10-029-756-5
; Sequence 5, Application US/10029756
; Publication No. US20020108147A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/029,756
; FILING DATE: 21-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-029-756-5
Query Match 17.6%; Score 429.5; DB 14; Length 448;
Best Local Similarity 28.8%; Pred. No. 3.7e-35;
Matches 129; Conservative 63; Mismatches 183; Indels 73; Gaps 16;
QY 24 BEIQKHLRTDSGLVIDRKVYNTKWSIQHPGQQRVIGHYAGEDATDAFRAHP----- 77
DB 12 DELKNDKPGDLWISIQKAYDVSDWKDPHGGSPFLKSLAQEVTDFAVAFHPASTWKN 71
QY 78 -DLEFVGKELKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNLP-KTNHVFLL 135
DB 72 LDKFETGYLKYDVS-----SEVSKDYRLKLVFEFSKGLYDKKGHMF-A 115
QY 136 LLAHIIALESIAWFTVYFGNGWIPITLITAFVATSQAQAGLQHDYHLSVYRKPKWNH 195
DB 116 TLCFIAMLFAMSVYGVLFCEGVVLHFLSGCLMGFLWISQGWIGHDAGHVMVSDSLNK 174

Db 199 IYGLGCMSCYWRNHNKHAATPOKLGTDPLQTMPLVAFHAKVAKARGKAWLAW- 257
Qy 261 HQHEYFLGPPILLIPMYFOYQIIM- - - - - TMIVHKNWDLAWAVSYIRFFIT- - - - - 309
Db 258 -QAPLFF- - - - - GGIICSLVSFGQVFLHFNHAIKRVH- - - - - NHLELAYMGLRYLVHIAFGHLGL 313
Qy 310 - - - - - YIPFYGILGALLFNFIRFLESHWVFWVVTQNNHIVMEIDOEAYRDFSSQJATC 364
Db 314 SSLRLAFYVAVGTVFTNF- - - - - AVSHTHKDV- - - - - VPPTKHI- - - - - SWALYSANHTT 361
Qy 365 NVQSPFNDFSHLAFNFOIEHHLPPTMPRNLHKAIPLYKSLCAKHGIEYQEKPL 420
Db 362 NCSDSPFVNMWMLNFOIEHHLPPTMPRNLHKAIPRYALFEKHGVEYDVRPYL 417
RESULT 27
US-09-769-863-29
; Sequence 29, Application US/09769863
; Publication No. US20030157144A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Thraustochytrium aureum
US-09-769-863-29
Query Match 16.3%; Score 398; DB 12; Length 439;
Best Local Similarity 28.1%; Pred. No. 6.1e-32;
Matches 129; Conservative 74; Mismatches 202; Indels 54; Gaps 15;
Qy 1 MGKGNQGEAAERESVPTFSWBEIQKHNLRDTSGLVIDRKVYNITKWSIQHPGGQRV 60
Db 1 MGRGEGGVNSA- - - - - QVAGGAGTRKTILIEGEVDVT- - - - - NFRHPGGS-II 45
Qy 61 GHYAGE- - - - - DATDAFRAHPDLEFVGKFLKPL-LIGELAPEE- - - - - PSQDHGKNSKITE 111
Db 46 KFLTTDGTAEVDATNAFREFHCRSGKAEKYLKSLPKLG- - - - - APSQKFDKEQARRDAITR 103
Qy 112 DFRALRKTAEADNLFKTNHVFLLLAHIIAIESIAWFTVYFGNGWIPTLITAFVLATS 171
Db 104 DYVKLEEMVAEGLFKPAPLHIVYRFAEIALFAASFLPSMRGNVF-ATLAAIAGVGGIA 162
Qy 172 QAQAGWLQHDYGHLSVYKPKKNHVLHVFVGHUKGASANNWNRHFOHAKPNIHFKDP 231
Db 163 QGRGWLMECHGCHFSMTGYIPLDVRLOELVYGVCSMSASWRYOHNKHATPOKLKHDV 222
Qy 232 DVNMLHVFVLGE- - - - - WQPIEYGGKKLKYLPYNHQBHYFFLIG- - - - - PPLLIPIMYF 279
Db 223 DDTLPLVAFNEKIAKVRPSFOAKWLSAQAYIFAPVSCFLVGLFWTLFLHPRMPTS 282
Qy 280 QYQIIMTIVH-KNWVDLAWAVSY-IRFFITYIPFYGILGALLFLNFIRFLESHWVFW 337
Db 283 HFAEMAAVAVRVVGVGWAALMHSGSDSFGLYMATFGCTGYIFTN- - - - - FAVSHTHLDV 339
Qy 338 TQNNHIVMEIDOEAYRDFSSQJATCNV-BQSFPNDWFSGLHNFQIEHLPPTMPRNL 396
Db 340 T- - - - - EPDEFHVVVEAALHTTNVSDNSWFIITWMSYLANFQIEHLPFSLPQLNA 390
Qy 397 HKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSKG 435
Db 391 PRVAPRVRALFEKHGMAYDERPYLTALGDTFANLHAVGQ 429

Db 391 PRVAPRVRALFEKHGMAYDERPYLTALGDTFANLHAVGQ 429
RESULT 28
US-10-054-534B-29
; Sequence 29, Application US/10054534B
; Publication No. US20030167525A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/10/054,534B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Thraustochytrium aureum
US-10-054-534B-29
Query Match 16.3%; Score 398; DB 12; Length 439;
Best Local Similarity 28.1%; Pred. No. 6.1e-32;
Matches 129; Conservative 74; Mismatches 202; Indels 54; Gaps 15;
Qy 1 MGKGNQGEAAERESVPTFSWBEIQKHNLRDTSGLVIDRKVYNITKWSIQHPGGQRV 60
Db 1 MGRGEGGVNSA- - - - - QVAGGAGTRKTILIEGEVDVT- - - - - NFRHPGGS-II 45
Qy 61 GHYAGE- - - - - DATDAFRAHPDLEFVGKFLKPL-LIGELAPEE- - - - - PSQDHGKNSKITE 111
Db 46 KFLTTDGTAEVDATNAFREFHCRSGKAEKYLKSLPKLG- - - - - APSQKFDKEQARRDAITR 103
Qy 112 DFRALRKTAEADNLFKTNHVFLLLAHIIAIESIAWFTVYFGNGWIPTLITAFVLATS 171
Db 104 DYVKLEEMVAEGLFKPAPLHIVYRFAEIALFAASFLPSMRGNVF-ATLAAIAGVGGIA 162
Qy 172 QAQAGWLQHDYGHLSVYKPKKNHVLHVFVGHUKGASANNWNRHFOHAKPNIHFKDP 231
Db 163 QGRGWLMECHGCHFSMTGYIPLDVRLOELVYGVCSMSASWRYOHNKHATPOKLKHDV 222
Qy 232 DVNMLHVFVLGE- - - - - WQPIEYGGKKLKYLPYNHQBHYFFLIG- - - - - PPLLIPIMYF 279
Db 223 DDTLPLVAFNEKIAKVRPSFOAKWLSAQAYIFAPVSCFLVGLFWTLFLHPRMPTS 282
Qy 280 QYQIIMTIVH-KNWVDLAWAVSY-IRFFITYIPFYGILGALLFLNFIRFLESHWVFW 337
Db 283 HFAEMAAVAVRVVGVGWAALMHSGSDSFGLYMATFGCTGYIFTN- - - - - FAVSHTHLDV 339
Qy 338 TQNNHIVMEIDOEAYRDFSSQJATCNV-BQSFPNDWFSGLHNFQIEHLPPTMPRNL 396
Db 340 T- - - - - EPDEFHVVVEAALHTTNVSDNSWFIITWMSYLANFQIEHLPFSLPQLNA 390
Qy 397 HKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSKG 435
Db 391 PRVAPRVRALFEKHGMAYDERPYLTALGDTFANLHAVGQ 429
RESULT 29
US-10-431-952-29
; Sequence 29, Application US/10431952
; Publication No. US20030190733A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng

APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763.US.01
CURRENT APPLICATION NUMBER: US/10/431,952
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 439
TYPE: PRT
ORGANISM: Thraustochytrium aureum
US-10-431-952-29

Query Match 16.3%; Score 398; DB 12; Length 439;
Best Local Similarity 28.1%; Pred. No. 6.1e-32;
Matches 129; Conservative 74; Mismatches 202; Indels 54; Gaps 15;

QY 1 MGKGGNCGEAGAEVSVPTFSWEEIQKHNLRTDSGLVIDRKVYNITKWSIQHFGQGV 60
Db 1 MGRGEGQUNSA-----QVAGGAGTRKTIIEGEVYDVT--NERHFGGS-II 45
QY 61 GHYAGE-----DATDAFRAHFDLEFVGKFLKPL-LIGELAPEE---PSQDHGKNSKITE 111
Db 46 KELTIDGTAEVADATNAFREFHCRSGKAEKYLKSLPKLG--APSKMKFPAKQARRDAITR 103
QY 112 DFRALRKAEDNMLKTNHVPFLLLLAHIALESIAWFTVFGNGMPTLITAFVLATS 171
Db 104 DTVKUREEMVAGLEKPAFLHIVYFASIALFAASFVLFSGNGVF-ATLAAAVGGIA 162
QY 172 QAQAGHLQHDYGHLSYRKPKNHVLKVFVIGHLKGASANNWNHHRFOHAKPNIFHQP 231
Db 163 QCRGGLMHECHGFSMTGYIPLDVRLQELVYGVGSGMSASWVQHNKHATPQKLKHDV 222
QY 232 DVNMLHVFVLGE-----WQPIEGYKKLKLKLYPNHQHEYFFLIG-----PPLLIPMYF 279
Db 223 DTDITLVAFNKIAKVPFGSQKWLISAQAYIFAPVSCFLVGLFWTLFLHPRHPTS 282
QY 280 QYQIIMTIVH-KNNVVDLAWAYSYY-IRFFITYIPYGLGALLFLNFIRESHFWVW 337
Db 283 HFAEMAARVAVRVGVMAALMHSFGYSGDSFGLYMATFGCTYIFTN---FAVSHTHLDV 339
QY 338 TQNHVIMDEQAEYRDWESSQLTATCV-EOSFNDWFSGLHNFQIEHLLPPTMRENL 396
Db 340 T-----EPDEFUHWVEYAAALHTNVNSDWSFITWMSYLNFIQIEHLLFPSLPQLNA 390
QY 397 HKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKXSGK 435
Db 391 PRVAPRVRALFEKGHWAYDERPVLTAIGDTFANLHVGQ 429

RESULT 30
US-10-340-779A-20
Sequence 20, Application US/10340779A
Publication No. US20030152983A1
GENERAL INFORMATION:
APPLICANT: Napier, Johnathan A.
APPLICANT: Michaelson, Louise
APPLICANT: Stobart, Keith
TITLE OF INVENTION: Desaturase
FILE REFERENCE: 005407.00004
CURRENT APPLICATION NUMBER: US/10/340,779A
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 09/582,034
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: FCT/GB98/03895
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: UK 9727256.1

PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 443
TYPE: PRT
ORGANISM: C. elegans
US-10-340-779A-20

Query Match 16.2%; Score 395.5; DB 12; Length 443;
Best Local Similarity 28.0%; Pred. No. 1.1e-31;
Matches 122; Conservative 62; Mismatches 174; Indels 77; Gaps 18;

QY 37 LVIDRKVYNIT-----KWSI-----QHPGQORVICHYAGEDATDAFRAHP----- 77
Db 1 MVVDKNASGLRMKVDGKMLYSEELVKKHPGG-AVIEQYKNSDATHIFHAPHEGSSQAYK 59
QY 78 --DL-----EFVGKFL-KPLLIGELAPEEPSQDHGKNSKITEDFRALRKAEDNMLF 126
Db 60 QLDLLKKHGEHDEFFLEKLEKLDKVDINVSAYDVSAQEKWVESFEKLRQKLDHDDGLM 119
QY 127 KTNHVFLLLAHIALESIAWFTVFGNGMPTLITAFVLATSQAQAGHLQHDYGHLS 186
Db 120 KANETVFLFAISTLSINAFAYLQYL---GWYIT--SACLLALAWQOFGWLTHEFCQQ 174
QY 187 VYRKPKNHVLKVFVIGHLKGASANNWNHHRFOHAKPNIFHKDPDVNM--LRHVFVLGEW 244
Db 175 PFKNRRLNTISLFGNFGLOGFSRDKWKDKNTHAATNVIDHGDIDLAPLFAIPGDL 234
QY 245 --QPIEYGGKKLKLKLYPNHQHEYFFLIGPPL-----LIPMYFQYQIIMTIVHKN--W 293
Db 235 CKYKASFEKAILKIVPY--CHLYFTAMPLRFSWTGQSVQVWFKENQMEYKYQORNAFW 292
QY 294 VDLA-----NAVSVYIRFFITYIPF---YGIL---GALLFLNFIRESHFWVWVQNMH 342
Db 293 EQATVGHWAQVYQFLPTPLRVAVYFIISQMGGLIAHVVF-----NH 340
QY 343 IVME---IDQAYRDNFSSQLTATCVESQFNDWFSGLHNFQIEHLLPPTMRENLHKI 399
Db 341 NSVDKYPANSRIINLFAALQILTRNMTSPFIDMLWGLNFIQIEHLLPPTMRENLNAC 400
QY 400 APLVKSCLCAKHGIEY 414
Db 401 VKYVKGWCKENNLUPY 415

RESULT 31
US-09-967-477B-6
Sequence 6, Application US/09967477B
Patent No. US20020156254A1
GENERAL INFORMATION:
APPLICANT: Xiao Qiu
APPLICANT: Haiping Hong
TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
FILE REFERENCE: ENZ-001
CURRENT APPLICATION NUMBER: US/09/967,477B
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/236,303
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/297,562
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 456
TYPE: PRT
ORGANISM: Thraustochytrium sp.
US-09-967-477B-6

Query Match 15.2%; Score 369.5; DB 10; Length 456;
Best Local Similarity 24.3%; Pred. No. 5.3e-28;
Matches 118; Conservative 86; Mismatches 179; Indels 103; Gaps 21;

APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763.US.01
CURRENT APPLICATION NUMBER: US/10/431,952
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 439
TYPE: PRT
ORGANISM: Thraustochytrium aureum
US-10-431-952-29

Query Match 16.3%; Score 398; DB 12; Length 439;
Best Local Similarity 28.1%; Pred. No. 6.1e-32;
Matches 129; Conservative 74; Mismatches 202; Indels 54; Gaps 15;

QY 1 MGKGGNCGEAGAEVSVPTFSWEEIQKHNLRTDSGLVIDRKVYNITKWSIQHFGQGV 60
Db 1 MGRGEGQUNSA-----QVAGGAGTRKTIIEGEVYDVT--NERHFGGS-II 45
QY 61 GHYAGE-----DATDAFRAHFDLEFVGKFLKPL-LIGELAPEE---PSQDHGKNSKITE 111
Db 46 KELTIDGTAEVADATNAFREFHCRSGKAEKYLKSLPKLG--APSKMKFPAKQARRDAITR 103
QY 112 DFRALRKAEDNMLKTNHVPFLLLLAHIALESIAWFTVFGNGMPTLITAFVLATS 171
Db 104 DTVKUREEMVAGLEKPAFLHIVYFASIALFAASFVLFSGNGVF-ATLAAAVGGIA 162
QY 172 QAQAGHLQHDYGHLSYRKPKNHVLKVFVIGHLKGASANNWNHHRFOHAKPNIFHQP 231
Db 163 QCRGGLMHECHGFSMTGYIPLDVRLQELVYGVGSGMSASWVQHNKHATPQKLKHDV 222
QY 232 DVNMLHVFVLGE-----WQPIEGYKKLKLKLYPNHQHEYFFLIG-----PPLLIPMYF 279
Db 223 DTDITLVAFNKIAKVPFGSQKWLISAQAYIFAPVSCFLVGLFWTLFLHPRHPTS 282
QY 280 QYQIIMTIVH-KNNVVDLAWAYSYY-IRFFITYIPYGLGALLFLNFIRESHFWVW 337
Db 283 HFAEMAARVAVRVGVMAALMHSFGYSGDSFGLYMATFGCTYIFTN---FAVSHTHLDV 339
QY 338 TQNHVIMDEQAEYRDWESSQLTATCV-EOSFNDWFSGLHNFQIEHLLPPTMRENL 396
Db 340 T-----EPDEFUHWVEYAAALHTNVNSDWSFITWMSYLNFIQIEHLLFPSLPQLNA 390
QY 397 HKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKXSGK 435
Db 391 PRVAPRVRALFEKGHWAYDERPVLTAIGDTFANLHVGQ 429

RESULT 30
US-10-340-779A-20
Sequence 20, Application US/10340779A
Publication No. US20030152983A1
GENERAL INFORMATION:
APPLICANT: Napier, Johnathan A.
APPLICANT: Michaelson, Louise
APPLICANT: Stobart, Keith
TITLE OF INVENTION: Desaturase
FILE REFERENCE: 005407.00004
CURRENT APPLICATION NUMBER: US/10/340,779A
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 09/582,034
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: FCT/GB98/03895
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: UK 9727256.1

PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 443
TYPE: PRT
ORGANISM: C. elegans
US-10-340-779A-20

Query Match 16.2%; Score 395.5; DB 12; Length 443;
Best Local Similarity 28.0%; Pred. No. 1.1e-31;
Matches 122; Conservative 62; Mismatches 174; Indels 77; Gaps 18;

QY 37 LVIDRKVYNIT-----KWSI-----QHPGQORVICHYAGEDATDAFRAHP----- 77
Db 1 MVVDKNASGLRMKVDGKMLYSEELVKKHPGG-AVIEQYKNSDATHIFHAPHEGSSQAYK 59
QY 78 --DL-----EFVGKFL-KPLLIGELAPEEPSQDHGKNSKITEDFRALRKAEDNMLF 126
Db 60 QLDLLKKHGEHDEFFLEKLEKLDKVDINVSAYDVSAQEKWVESFEKLRQKLDHDDGLM 119
QY 127 KTNHVFLLLAHIALESIAWFTVFGNGMPTLITAFVLATSQAQAGHLQHDYGHLS 186
Db 120 KANETVFLFAISTLSINAFAYLQYL---GWYIT--SACLLALAWQOFGWLTHEFCQQ 174
QY 187 VYRKPKNHVLKVFVIGHLKGASANNWNHHRFOHAKPNIFHKDPDVNM--LRHVFVLGEW 244
Db 175 PFKNRRLNTISLFGNFGLOGFSRDKWKDKNTHAATNVIDHGDIDLAPLFAIPGDL 234
QY 245 --QPIEYGGKKLKLKLYPNHQHEYFFLIGPPL-----LIPMYFQYQIIMTIVHKN--W 293
Db 235 CKYKASFEKAILKIVPY--CHLYFTAMPLRFSWTGQSVQVWFKENQMEYKYQORNAFW 292
QY 294 VDLA-----NAVSVYIRFFITYIPF---YGIL---GALLFLNFIRESHFWVWVQNMH 342
Db 293 EQATVGHWAQVYQFLPTPLRVAVYFIISQMGGLIAHVVF-----NH 340
QY 343 IVME---IDQAYRDNFSSQLTATCVESQFNDWFSGLHNFQIEHLLPPTMRENLHKI 399
Db 341 NSVDKYPANSRIINLFAALQILTRNMTSPFIDMLWGLNFIQIEHLLPPTMRENLNAC 400
QY 400 APLVKSCLCAKHGIEY 414
Db 401 VKYVKGWCKENNLUPY 415

RESULT 31
US-09-967-477B-6
Sequence 6, Application US/09967477B
Patent No. US20020156254A1
GENERAL INFORMATION:
APPLICANT: Xiao Qiu
APPLICANT: Haiping Hong
TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
FILE REFERENCE: ENZ-001
CURRENT APPLICATION NUMBER: US/09/967,477B
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/236,303
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/297,562
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 456
TYPE: PRT
ORGANISM: Thraustochytrium sp.
US-09-967-477B-6

Query Match 15.2%; Score 369.5; DB 10; Length 456;
Best Local Similarity 24.3%; Pred. No. 5.3e-28;
Matches 118; Conservative 86; Mismatches 179; Indels 103; Gaps 21;


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Db 225 LDTPLVANNKEIARRVKPGSQAKWL---HLQGYIAPVSCLLVGLFWLYLHPHMIR 281
Qy 280 ---QYIIMTMIHKNWVDLAWAVSYIRPFI-TYIPFYGLGALLFLNFIRESHWFV 335
Db 282 TKRNFELFSVALRVVCPMLLSMGYTVGESLGYVLTFTG-LGCTYI--FTHFAVSH--- 335
Qy 336 WVTQNMHIVMEIDQEAERDFSSQLTATCNVE-QSFFNDWFSGLHNFQIEHHLFPPTMPRH 394
Db 336 -----THLPVS-EDEYLHWVEYAAALHTTNVAIDSYVVTWLMSTVNFQIEHHLPCCPQF 389
Qy 395 NLHKIAPLVKSLCAKHGIEQKPLRALLDIIRSLKKS 434
Db 390 RHPALSSRVKLFEDNGLVDARSYQALKDTFGLNHEVG 429

RESULT 34
US-09-967-477B-4
; Sequence 4, Application US/09967477B
; Patent No. US20020156254A1
; GENERAL INFORMATION:
; APPLICANT: Xiao Qiu
; APPLICANT: Haiping Hong
; TITLE OF INVENTION: PAD4, PAD5, PAD6, AND PAD7, NOVEL
; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: ENZ-001
; CURRENT APPLICATION NUMBER: US/09/967,477B
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/236,303
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/297,562
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Thraustochytrium sp.
US-09-967-477B-4

Query Match 14.6%; Score 355; DB 10; Length 439;
Best Local Similarity 25.3%; Pred. No. 1.5e-27;
Matches 120; Conservative 85; Mismatches 182; Indels 88; Gaps 18;

Qy 1 MGKGGNGGGAAREVSVPTFSWEEIQKHLRDTSGLVDRKVNITKWSIQHPGGQRI 60
Db 1 MGK-GSEGRSAA-RENTA-----EANGDKRKT---ILLEGVLYDATT-NFKHPGGS-II 46
Qy 61 GHY-----AGEDATDAFRAHPDLEFVGKFLKPLLIGELAPEE---PSQDHGKNSKITEDF 113
Db 47 NFLTEGAGVDATQAYREFHQRSQKADKYLKSLPLKLDASKVESRFSKAQEARDAWTRDY 106
Qy 114 RALRKTAEADNNLFTKTHVFLPALLAHIALESIAFTVFYFGNGWIPFTLIITAFVL-ATS 171
Db 107 AAPREELVARGYDPSLPNMIYRVEIVAFALFALS-----FWLSKASPTSLVGVWNGIA 162
Qy 172 QAQAGMLQHDYGHLSVYRKPKNHLVHKFVIGHLKGASANNWNRHFQHAKPNIFHKDPD 231
Db 163 QGRGCVWMEHWGSGSFTGVWLDDBMCEFPYGVGCGMSGHYKKNQHSKHAAPNRLHEDV 222
Qy 232 DVNMLHVFVGEWQPIEGYKGLKLYPNHQHVEYFLLIGPPLIIPWFOYQIIMTMIHVK 291
Db 223 DLNLFPLVARN-----BRVRKVK-----PGSLALNLRVQAVLFPAPVC 262
Qy 292 NWVDLAWAVSYIRF-----FITYIPFYGILGAL-----LFL----- 323
Db 263 LLIGLWTLVLPYMLRTRKHBFEVMI FARYIGWPSLMGALGYSPTSGVMYLCFGLG 322
Qy 324 ---NFIRPLESHWFVWVTOMNHIVMEIDQEAERDFSSQLTATCNVE-QSFFNDWFSGLH 379
Db 323 CIYIFLQFAVSHTHLPVT-----NPDQLNLEVAADHTVNISTKSLWLVWMSNL 373
Qy 380 NFQIEHHLFPPTMPRHNLHKIAPLVKSLCAKHGIEQKPLRALLDIIRSLKKS 434

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Db 374 NFQIEHHLFPPTAPQPRFKEISPRVEALFKRHLNLPYDLPYTSVAVSTTFANLYSVG 428

RESULT 35
US-09-769-863-20
; Sequence 20, Application US/09769863
; Publication No. US20030157144A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Jung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.O1
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-09-769-863-20

Query Match 14.3%; Score 348; DB 12; Length 470;
Best Local Similarity 24.9%; Pred. No. 8.8e-27;
Matches 123; Conservative 91; Mismatches 183; Indels 96; Gaps 24;

Qy 11 AABREYSV---PTFSWEEIQKHLRDTSGLVDRKVNITKWSIQHPGGQRIYHAGD 67
Db 12 AAVAETPVAGKAKFTWQEAQNTASAWIIIRGVYDVTWANKPGGEMVLLHAGRE 71
Qy 68 ATDAFRAHPDLEFVGKFLKPLLIG-----ELAPEEPSQDHGKNSKITEDFALRKTA 121
Db 72 ATDTFDSYHPFSDKASILNKYBIGTFTGPFEPFTKPD-----TGFYKCKRKG 122
Qy 122 DMNLFKTNHVF-----FLLLAHIALESIAFTVFYFGNGWIPFTLIITAFVLATSQA-Q 174
Db 123 E--YFKQNNLHPQDGPGLWRWMMVFAVAGLALYGM-HESTIPALQAAAAFGVCQALP 179
Qy 175 AGMLQHDYGHLSVYRKPKNHLVHKFVIGHLKGAS-ANNWNRHFQHAKPNIFHKDPD- 232
Db 180 LLHWHDSSHASVTNMPFFHYVYVGRFAMDFAGGSVMWLNQHVGHYITNVAGSDPOL 239
Qy 233 -VNN-----LHVFVLGEWQPIEGYKGLKLYPNHQHVEYFLLIGPPL--LIIPWFO 280
Db 240 PVNMDGDIRIVNRQVF-----QPM-----YAFQHIYL-----PPLYGVGLKPR 279
Qy 281 YQ-IIMTMIHKN-----WVDLAWAVSYIRPFTIIPFYGILG-----AL 320
Db 280 IQDFTDTFGSHNGPIRVNPHALSTWAMISKSFV-AFYRVYLPL-AVLQMPIKTVLAI 337
Qy 321 LFLNFIPLFLESHWFVWVTOMNHIVMEID-----QEAERD-WFSSOL-TATCNVEQSFF 371
Db 338 PFL--AEFVTGWYLAFFQVSHVSTEGYPCGEAKWALQDENAVSQVTSVDYAHGSM 395
Qy 372 NDWFSGLHNFQIEHHLFPPTMPRHNLHKIAPLVKSLCAKHGIEYQKXP-LRALLDIIRSL 430
Db 396 TTFLAGALNYQVWVHLLPFSVSQVHYPAIPIIVDVCKEYNIKAILPDFTAFAVHLKHL 455
Qy 431 KKSGLWLDALH 443
Db 456 RNMGQGGIAATH 468

RESULT 36
US-10-054-534B-20
; Sequence 20, Application US/10054534B
; Publication No. US20030167525A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories

```


APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer M.
APPLICANT: Pereira, Suzette L.

TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF

FILE REFERENCE: 6763.US.P1

CURRENT APPLICATION NUMBER: US/10/054.534B

CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: US 09/769,863

PRIOR FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 55

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 20

LENGTH: 470

TYPE: PRT

ORGANISM: Saprolegnia diclina

US-10-054-534B-20

Query Match 14.3%; Score 348; DB 12; Length 470;

Best Local Similarity 24.9%; Pred. No. 8.8e-27;

Matches 123; Conservative 91; Mismatches 183; Indels 96; Gaps 24;

QY 11 AAAREVSV---PTFSWEIEIQHNLRDTSGLVIDRKNVNIKWSIQHPGQGVIGHVAGED 67

DB 12 AAVATPVAGKKAFTWQEVAGHNTAASAWIIRGVYDVTEWANKHPPGGRVLLHAGRE 71

QY 68 ATDAFRAHPDLEFVGKFLKPLLIG-----ELAPEEPSQDHGKNSKITEDFRALKRTAE 121

DB 72 ATDTFDSYHPFSDKAESILNKYEIGTFTGPSEFFTFKPD-----TGFYKECKRVG 122

QY 122 DMNLFKTNHVF-----FLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFVLATSOA-Q 174

DB 123 E--YFKKNLHPQDGFPGGLWRMMVVFVAVAGLALYGM-HFSTIFALQLAAALFGVCOALP 179

QY 175 AGWLQHDYGHLSVYRKPKNHLVHKFVIGHLKGAS-ANWNNHRRHFQHHAKNIFHKDPD- 232

DB 180 LLHVMDSDSHASYTNMPPFFHYVVGFRFAMDWFAGGSMVSNLQHVGHYITNVAGSDPDL 239

QY 233 -VNM-----LHVFLVGEWQPIEYGGKKLVLPYNHQHXYFFLIGPPL--LIPMYFQ 280

DB 240 PVNMGDTRIRVNRQVF-----QPM-----YAFQHIYL-----PPLYGVGLKFR 279

QY 281 YQ-IIMTMIVHKQ-----WDLAWAVSYIIRFFITYIPFYGILG-----AL 320

DB 280 IQDFTDTFGSHNGPIRVNPHALSTWAMISKSFV-AFYRVYLPL-AVLQMPIKTYLAI 337

QY 321 LFLNFIREFLESHFWVVTQNMHIVMEID-----QEAYRD-WFSSQL-TATCNVEQSF 371

DB 338 FFL--AEFTVGYLAFNQVSHVSTECGPGCDEAKMALQDEWAVSQVKTSDVYAHGSMW 395

QY 372 NDFSGHLNFQIEHLLFPTMPRHNLHKIAPLVKSLCAKHGIEYQEKP--LLRALLDIIRSL 430

DB 396 TTFLAGALNYQVWHLPFSVQYHYPALAPIIVDVCKEYNIKYAILPDFTAAFAVHLKHL 455

QY 431 KKSGLWLDAYLH 443

DB 456 RNMGOOGIAATH 468

RESULT 37

US-10-431-952-20

Sequence 20, Application US/10431952

Publication No. US20030190733A1

GENERAL INFORMATION:

APPLICANT: Mukerji, Pradip

APPLICANT: Huang, Yung-Sheng

APPLICANT: Das, Tapas

APPLICANT: Thurmond, Jennifer

APPLICANT: Pereira, Suzette L.

TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF

FILE REFERENCE: 6763.US.O1

CURRENT APPLICATION NUMBER: US/10/431.952

CURRENT FILING DATE: 2003-05-08

PRIOR APPLICATION NUMBER: US/09/769,863

PRIOR FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 20

LENGTH: 470

TYPE: PRT

ORGANISM: Saprolegnia diclina

US-10-431-952-20

Query Match 14.3%; Score 348; DB 12; Length 470;

Best Local Similarity 24.9%; Pred. No. 8.8e-27;

Matches 123; Conservative 91; Mismatches 183; Indels 96; Gaps 24;

QY 11 AAAREVSV---PTFSWEIEIQHNLRDTSGLVIDRKNVNIKWSIQHPGQGVIGHVAGED 67

DB 12 AAVATPVAGKKAFTWQEVAGHNTAASAWIIRGVYDVTEWANKHPPGGRVLLHAGRE 71

QY 68 ATDAFRAHPDLEFVGKFLKPLLIG-----ELAPEEPSQDHGKNSKITEDFRALKRTAE 121

DB 72 ATDTFDSYHPFSDKAESILNKYEIGTFTGPSEFFTFKPD-----TGFYKECKRVG 122

QY 122 DMNLFKTNHVF-----FLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFVLATSOA-Q 174

DB 123 E--YFKKNLHPQDGFPGGLWRMMVVFVAVAGLALYGM-HFSTIFALQLAAALFGVCOALP 179

QY 175 AGWLQHDYGHLSVYRKPKNHLVHKFVIGHLKGAS-ANWNNHRRHFQHHAKNIFHKDPD- 232

DB 180 LLHVMDSDSHASYTNMPPFFHYVVGFRFAMDWFAGGSMVSNLQHVGHYITNVAGSDPDL 239

QY 233 -VNM-----LHVFLVGEWQPIEYGGKKLVLPYNHQHXYFFLIGPPL--LIPMYFQ 280

DB 240 PVNMGDTRIRVNRQVF-----QPM-----YAFQHIYL-----PPLYGVGLKFR 279

QY 281 YQ-IIMTMIVHKQ-----WDLAWAVSYIIRFFITYIPFYGILG-----AL 320

DB 280 IQDFTDTFGSHNGPIRVNPHALSTWAMISKSFV-AFYRVYLPL-AVLQMPIKTYLAI 337

QY 321 LFLNFIREFLESHFWVVTQNMHIVMEID-----QEAYRD-WFSSQL-TATCNVEQSF 371

DB 338 FFL--AEFTVGYLAFNQVSHVSTECGPGCDEAKMALQDEWAVSQVKTSDVYAHGSMW 395

QY 372 NDFSGHLNFQIEHLLFPTMPRHNLHKIAPLVKSLCAKHGIEYQEKP--LLRALLDIIRSL 430

DB 396 TTFLAGALNYQVWHLPFSVQYHYPALAPIIVDVCKEYNIKYAILPDFTAAFAVHLKHL 455

QY 431 KKSGLWLDAYLH 443

DB 456 RNMGOOGIAATH 468

RESULT 38

US-10-029-386-29651

Sequence 29651, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: A60MICA-X-2

EXPRESSION ANALYSIS TWO

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 29651

LENGTH: 76

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO CHR11.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.9
US-10-029-386-29651

Query Match 14.2%; Score 347; DB 12; Length 76;
Best Local Similarity 94.4%; Pred. No. 9.2e-28;
Matches 67; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 104 GNSKITEDFRALRKTADNMLFKTNHVFLLLAHIALESIAHFTVFYFGNGWIPTLI 163
DB 4 GQSKITEDFRALRKTADNMLFKTNHVFLLLAHIALESIAHFTVFYFGNGWIPTLI 63
QY 164 TAFVLATSOAQ 174
DB 64 TAFVLATSOVR 74

RESULT 39
US-09-903-456-30
Sequence 30, Application US/09903456
Patent No. US20020138874A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 446
TYPE: PRT
ORGANISM: Mortierella alpina
US-09-903-456-30

Query Match 14.0%; Score 342.5; DB 10; Length 446;
Best Local Similarity 26.0%; Pred. No. 3e-26;
Matches 121; Conservative 64; Mismatches 184; Indels 97; Gaps 22;
QY 4 GGNQGEAAREVSVPFTSWEEIKQKNLRTDGLVIDRKVNTKWSIQHPGQGVIGHY 63
DB 2 GTDQCK-----TFTWEELAAHNTKDDLLAIRGRVYDVKFLSRHPGQGVTLILG 51
QY 64 AGEDATDAFRAFPDLEFVGKFLKPLLIGELAPE-----EPSQDHGKNKSKITEDFRALR 117
DB 52 AGRDVTPVPMYHA-FGAADAIKMYVGTLSNELPIPEPTVFH-----KTIK 100
QY 118 KTAE-----DNVLEKTHV-----FFLLLAHIALESIAHFTVFYFGNGWIPTLITAFVLA 169
DB 101 TRVEGYFTDRNDPKRPEIHWGRIALIFGSLIASYVAQLFVFFVVERTWL-QVFAILING 159
QY 170 TSOAQAGWLQ-HDYGHLSVYRKEK-WNHL--VHKFVIGHLKGSANWNHRE-FOHAKP 224
DB 160 FACAQVGLNPLHDASHFVSHTNVTWKILGATHDF----FNGASYLVVMYQHMGLGHPYT 215
QY 225 NIFHKDPDVM-----LHVFLGEMQPIEYCKKXKLYLPYNNQHE 264

DB 216 NIAGADPDVSTSEBDVRRIKQKWFVNHINQENFV-----PFLYGLLAFKVRQDINIL 270
QY 265 YFFLIGPELLIPMYFQVQIIMTIVHKWVDLAWAVSYIRFFTYIPFYIIGALLFLN 324
DB 271 YFVKINDAIRVNPISATWHTVMF-----WGGKAPFVWYRLIVPLQYLP-----LGKVLILF 320
QY 325 FIR-FLESHWFVWVQNMHIWMEI-----DOEA--YRDWFSQLTATCNVQSPFND--- 373
DB 321 TVADMVSSYIWLALTFQANHVVEVQWPLPDENGILQKDMAAQVETT-----QDYAHDHSL 376
QY 374 WFS--GHLNFQIEHRLFTMPRNLHKTAPLKVSLCAKGIYEYOEK 417
DB 377 WTSITGSLNYQAVHHLFFNVSOHYPDILAIKNTCTSEYKVPYLK 422
RESULT 40
US-10-278-391-2
Sequence 2, Application US/10278391
Publication No. US20030159164A1
GENERAL INFORMATION:
APPLICANT: KOPCHIK, JOHN J.
KELDER, BRUCE
HUANG, YUNG-SHENG
KIRCHNER, STEPHEN J.
MUKERJI, PRADIP
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
PRODUCTS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,391
FILING DATE: 23-Oct-2002
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/087,578
FILING DATE: 29-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OHU-03348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030159164A1 Relevant
TOPOLOGY: No. US20030159164A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-278-391-2

Query Match 14.0%; Score 342.5; DB 12; Length 446;
Best Local Similarity 26.0%; Pred. No. 3e-26;
Matches 121; Conservative 64; Mismatches 184; Indels 97; Gaps 22;
QY 4 GGNQGEAAREVSVPFTSWEEIKQKNLRTDGLVIDRKVNTKWSIQHPGQGVIGHY 63
DB 2 GTDQCK-----TFTWEELAAHNTKDDLLAIRGRVYDVKFLSRHPGQGVTLILG 51

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2003, 19:33:52 ; Search time 330 Seconds

(without alignments)
4471.752 Million cell updates/sec

US-09-719-601-5

Title: 2438

Perfect score: 2438

Sequence: 1 MGKGGNQGEAARREVSPT.....DIIRSLKSGKLWDAYLHK 444

Scoring table:

BLOSUM62
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Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US09719601/runat_09122003_094910_21283/app_query.fasta_1.583
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cgi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09719601@cgn_1_164@runat_09122003_094910_21283
-NCPU=6 -ICPU=3 -NO WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
- 17: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 18: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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1	1935	79.4	2257	15	US-10-191-513A-8	Sequence 8, Appli
2	1646	67.5	1843	15	US-10-191-513A-7	Sequence 7, Appli
3	1594	65.4	1474	15	US-10-102-806-232	Sequence 232, App
4	1560.5	64.0	1717	15	US-10-262-617-2	Sequence 2, Appli
c	1516	62.2	1972	9	US-09-822-849A-485	Sequence 485, App
5	1516	62.2	4213	13	US-10-133-937-7	Sequence 7, Appli
6	1515	62.1	1928	15	US-10-262-617-4	Sequence 4, Appli
7	1508	61.9	1335	15	US-10-191-513A-1	Sequence 1, Appli
8	1348	55.3	1686	15	US-10-191-513A-6	Sequence 6, Appli
9	1300	53.3	1478	11	US-09-981-876-63	Sequence 63, Appli
10	1300	53.3	1478	11	US-09-148-545-63	Sequence 63, Appli
11	1162	47.7	2016	10	US-09-981-876-119	Sequence 119, App
12	1162	47.7	2016	11	US-09-148-545-119	Sequence 119, App
13	1103	45.2	864	15	US-10-191-513A-13	Sequence 13, Appli
14	960	39.4	990	15	US-10-191-513A-34	Sequence 34, Appli
15	923	38.3	960	15	US-10-191-513A-35	Sequence 35, Appli
16	923	37.9	918	15	US-10-191-513A-5	Sequence 5, Appli
17	923	34.2	446	9	US-09-604-287A-425	Sequence 425, App
18	834	34.2	446	11	US-09-551-821-425	Sequence 425, App
19	834	34.2	446	13	US-10-124-805-313	Sequence 313, App
20	834	34.2	446	14	US-10-007-805-313	Sequence 313, App
21	834	34.2	446	14	US-10-076-622-313	Sequence 313, App
22	834	34.2	446	15	US-10-076-622-425	Sequence 425, App
23	834	34.2	456	9	US-09-604-287A-313	Sequence 313, App
24	834	34.2	456	10	US-09-339-338-313	Sequence 313, App
25	834	34.2	456	11	US-09-551-821-313	Sequence 313, App
26	834	34.2	456	13	US-10-124-805-313	Sequence 313, App
27	834	34.2	456	14	US-10-007-805-313	Sequence 313, App
28	834	34.2	456	15	US-10-076-622-313	Sequence 313, App
29	705	28.9	453	11	US-09-918-995-29095	Sequence 29095, A
30	620	25.4	473	15	US-10-191-513A-36	Sequence 36, Appli
31	585	24.0	304	15	US-10-191-513A-4	Sequence 4, Appli
32	566	23.2	449	15	US-10-191-513A-37	Sequence 37, Appli
33	566	23.2	449	15	US-10-191-513A-3	Sequence 3, Appli
c	499	20.5	567	13	US-10-029-386-3070	Sequence 3070, Ap
34	497	20.4	1380	10	US-09-967-477B-7	Sequence 7, Appli
35	487.5	20.0	1362	13	US-09-769-863-13	Sequence 13, Appli
36	487.5	20.0	1362	13	US-10-054-534B-13	Sequence 13, Appli
37	487.5	20.0	1362	13	US-10-431-952-13	Sequence 13, Appli
38	459	18.8	1374	13	US-10-278-391-3	Sequence 3, Appli
39	435.5	17.9	1685	14	US-10-029-756-4	Sequence 4, Appli
40	434	17.8	475	9	US-09-864-761-6399	Sequence 6399, Ap
c	426.5	17.5	1350	10	US-09-938-842A-558	Sequence 558, App
41	426.5	17.4	493	10	US-09-728-445-595	Sequence 595, App
42	426.5	17.4	493	10	US-09-728-445-595	Sequence 595, App
43	426.5	17.4	493	10	US-09-728-445-595	Sequence 595, App
44	420	17.2	315	10	US-09-783-590-5518	Sequence 5518, Ap
45	411.5	16.9	1702	14	US-10-029-756-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1

US-10-191-513A-8
; Sequence 8, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Faridip
; APPLICANT: Leonard, Ananda B.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2257

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-8

Alignment Scores:
  Pred. No.:      3,266-216      Length:      2257
  Score:          1935.00        Matches:      352
  Percent Similarity: 88.84%      Conservative: 30
  Best Local Similarity: 81.86%    Mismatches:   44
  Query Match:     79.37%        Indels:       4
  DB:              15           Gaps:         2

US-09-719-601-5 (1-444) x US-10-191-513A-8 (1-2257)
QY 19 ProThr-----PheSerTrpGluGluGluGlnLysHisAsnLeuArgThrAspSer 35
Db 7 CCAACCCCGCGTACTTACCTGGACGAGGCGGCGGCGCTCAGGTCGCGAGAGCGG 66
QY 36 GlyLeuValIleAspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGly 55
Db 67 TGGCTAGTGTATGACCGTAAGGTGTACAAACATCATCAGCAGATTCCACCGCGCGCATCCAGG 126
QY 56 GlyGlnArgValIleGlyHisIleAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
Db 127 GGTCTCCGGGTGTCATCAGCCATCAGCCGCGGCGAGATGCCAGATCCCTTTGTGGCTTC 186
QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95
Db 187 CATCATCAACAGGCGCTTGTGAAGAATATATGAATCTCTCTGATTGGAGAACTGTCT 246
QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115
Db 247 CAGAGCAGCCCGCTTTGAGCCCGCCCAAGATAAAGAGCTGACAGATGAGTTCCGGAG 306
QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135
Db 307 CTGCGGCGCACAGTGAGCGGATGGGCTCATGAAGGCCAACCATGTCTTCTTCTGCTG 366
QY 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGly 155
Db 367 TACCTCTGCATCATCTGTCTGTGATGGTGAGCGCTGCTCACCCTTTGGTCTTTGGG 426
QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln 174
Db 427 ACGTCCTTTTGGCTTCTCTCTCTGCGGCTGCTCAGTGCGAGTTCCAGCAGGCCCAA 486
QY 175 AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194
Db 487 GCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAACCCCAAGTGGAA 546
QY 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyValAsnSerAlaAsnTrpTrpAsn 214
Db 547 CACCTTGTCCAAATTCGTATGGCCACTTAAAGGGTGCCTTGCCTGCAACTGGTGAAT 606
QY 215 HisArgHisPheGlnHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234
Db 607 CATCGCAGCTTCAGACACACGACGCAAGCCCTAATCTTCCAAAGATCCCGATGTGAAC 666
QY 235 MetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLeu 254
Db 667 ATGCTGACAGTGTGTTGTTCTGGCGAATGGCAGCCCATCGAGTACGCGCAAGAAGCTG 726
QY 255 LysTrpLeuProTrpAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeu 274
Db 727 AAATACCTGCGCTTACCAATCACCAGCAGATATCTTCTCTGATTGGCGCGCGCTGCTC 786
QY 275 IleProMetTyrPheGlnTrpGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294
Db 787 ATCCCAATGATTTCCAGTACCAAGATCATCATCATGATCGTCCATGAAGACTGGGTG 846
QY 295 AspLeuAlaTrpAlaValSerTyrTrpIleArgPhePheIleThrTrpIleProPheTyr 314
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RESULT 2
US-10-191-513A-7
; Sequence 7, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardi
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-7

Alignment Scores:
  Pred. No.:      1,966-182      Length:      1843
  Score:          1646.00        Matches:      294
  Percent Similarity: 100.00%      Conservative: 0
  Best Local Similarity: 100.00%    Mismatches:   0
  Query Match:     67.51%        Indels:       0
  DB:              15           Gaps:         0

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Db 1 GTCCTTTTACITTTGGCAATGCTGGATTCTTACCTCATCAGCGCTTTGCTTGTCTAC 60
QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
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Db	61	TTTCAGGCCCAAGCTGGATGGCTGCACATGATTATTGGCCACCTGTCTGTCTACAGAAA	120
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Db	121	CCCAAGTGGAAACCACTTGTGCACAAATTCGTCAATTGGCCACTTAAAGGGTGCCTCTGCC	180
Qy	211	AsnTrpTrpAsnHisArgHisPheClnHisHisAlaLysProAsnIlePheHisLysAsp	230
Db	181	AACTGTGTGAATCATTCGGCACTTCAGCACCAACCCCAAGCTTAACATCTTCCCAAGGAT	240
Qy	231	ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTrpGly	250
Db	241	CCCGATGTGAACATGCTGCACGTGTTCTCTGGCGAATGGCAGCCATCGAGTAGCCGC	300
Qy	251	LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly	270
Db	301	AGAAGAGAGCTGAATATCTGCCCTACCAATCACCAGACGGAATACTTCTTCTGATGGG	360
Qy	271	ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis	290
Db	361	CGCGCGCTGCTCATCCCATGTATTTCAGGTACCAGATCATATGACCATGATCGTCCAT	420
Qy	291	LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr	310
Db	421	AGAAGCTGGTGGACTGGCTGGCCGTGAGCTACTACATCCGGTCTTTCATCACTCTAC	480
Qy	311	IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu	330
Db	481	ATCCCTTTCTACGGGATCTCTGGAGCCCTCTCTTTCTCAACTCATCAGGTTCTCTGGAG	540
Qy	331	SerHisTrpPheValTrpValThrClnMetAsnHisIleValMetGluIleAspGlnGlu	350
Db	541	AGCCACTGTTTTGTGTGGTACACAGATGAATCACATCTGTCATGGAGATTGACCAAGAG	600
Qy	351	AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe	370
Db	601	GCCTACCGTGACTGGTTTCAGTAGCCAGCTGACAGCCATCGAACGTGGAGCAGTCTCTTC	660
Qy	371	PheAsnAspTrpPheSerClyHisIleuAsnPheGlnIleGluHisIleLeuPheProThr	390
Db	661	TTTCAGACTGGTTTCAGTGGACACCTTAACTTTCAGATTGAGACCAACCTCTTCTCCCAAC	720
Qy	391	MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis	410
Db	721	ATGCCCGGGCACAACTTACACAAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT	780
Qy	411	GlyIleGluTyrClnGluLysProLeuLeuArgAlaLeuAspIleIleArgSerLeu	430
Db	781	GGCATTTGAATACAGAGAGAGCCGCTACTAGGGCCCTGTCTGGACATCATCAGGTCCCTG	840
Qy	431	LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys	444
Db	841	AGAAGCTCTGGGAAGCTGTGGCTGGACGCCCTACTCTTACAAA	882

RESULT 3

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1  US-10-102-806-232
2  Sequence 232, Application US/10102806
3  Publication No. US20030054421A1
4  GENERAL INFORMATION:
5  APPLICANT: Rosen et al.
6  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
7  FILE REFERENCE: PA103P1C1
8  CURRENT APPLICATION NUMBER: US/10/102,806
9  CURRENT FILING DATE: 2002-03-22
10 PRIOR APPLICATION NUMBER: 09/925,298
11 PRIOR FILING DATE: 2001-08-10
12 PRIOR APPLICATION NUMBER: PC3/US00/05881
13 PRIOR FILING DATE: 2000-03-08
14 PRIOR APPLICATION NUMBER: 60/124,270
15 PRIOR FILING DATE: 1999-03-12
16 NUMBER OF SEQ ID NOS: 846
17 SOFTWARE: Patent In Ver. 2.0
18 SEQ ID NO 232

```

QY 399 IleAlaProLeuValIysSerLeuCysAlaIysHisGlyIleGluTyrGlnGluYsPro 418
 DB 723 ATCGCCCGCTGGTGAAGTCTATGTGCGAAGCATGGCATGAATACCGAGAGCGG 782
 QY 419 LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeu 438
 DB 783 CTACTGAGGCGCTGCTGGACATCATCAGTCCCTGAAGAAGTCTGGGAAGCTGTGGCTG 842
 QY 439 AspAlaTyrLeuHisLys 444
 DB 843 GACGCTACCTTCACAAA 860

RESULT 4

US-10-262-617-2
 ; Sequence 2, Application US/10262617
 ; Publication No. US2003007747A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
 ; FILE REFERENCE: PP-0494-1 DIV
 ; CURRENT APPLICATION NUMBER: US/10/262,617
 ; CURRENT FILING DATE: 2002-09-30
 ; PRIOR APPLICATION NUMBER: 09/048,888
 ; PRIOR FILING DATE: 1998-03-26
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2
 ; LENGTH: 1717
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CB1
 US-10-262-617-2

Alignment Scores:

Pred. No.: 1.9e-172 Length: 1717
 Score: 1560.50 Matches: 278
 Percent Similarity: 76.23% Conservative: 62
 Best Local Similarity: 62.33% Mismatches: 103
 Query Match: 64.01% Indels: 3
 DB: 15 Gaps: 2

US-09-719-601-5 (1-444) x US-10-262-617-2 (1-1717)

QY 1 MetGlyLysGlyGlyAsnGlnGly-----GluGlyAlaAlaGluArgGluValSerVal 18
 DB 75 ATGGCGCGCTCGGGAGCGCGGACCGCGGAGGAGCGCGGCGCGCGCGCGCGCGCGCTG 134
 QY 19 ProThrPheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuVal 38
 DB 135 CCCACCTTCGTGGGAGAGATCCCGCGCGCACGACCGCGCGCGCGCGCGCGCGCGCTG 194
 QY 39 IleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlnArg 58
 DB 195 ATCGAGCGCGGTCTACGACATCAGCGCGTGGCGACGCGCGCGCGCGCGCGCGCGCG 254
 QY 59 ValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78
 DB 255 CTCATCGCGCACCGCGGTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 314
 QY 79 LeuGluPheValGlyLysPheLeuLeuProLeuLeuIleGlyGluLeuAlaProGluGlu 98
 DB 315 CTCATTTGTGCGCAAGTTCCTACAGCCCTGTGTGAGAGAGTGGCTCCGGAAGAA 374
 QY 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118
 DB 375 CCCAGCAGGATGGACCCCTGAATCGCGCATGGTTCGAGGACTCCGAGCCCTGCACCG 434
 QY 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla 138

DB 435 GCAGCGCGGACACATGAAGCTGTTGATGCGCAGTCCACACCTTCTTTGCTTCTACTGGGC 494
 QY 139 HisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrp 158
 DB 495 CACATCTCTGCGCATGGAGTGTGGCTGCTCTTATCTCTCTCTGCTGGTCTCTGCTGG 554
 QY 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178
 DB 555 GTGCCAGTGGCTGGCGGCTTCATCTTGGCCATCTCTCAGGCTCAGTCTGGTGTCTG 614
 QY 179 GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis 198
 DB 615 CAGCATGACCTGGCGCATGCTCTCAAGAGTCTCTGGTGGAAACACGCGGCGCCAG 674
 QY 199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218
 DB 675 AAGTTCGTGATGGCGGAGCTTCTCGGCCACTGGTGGAACTTCGCGCACTTC 734
 QY 219 GlnHisAlaLysProLysPheHisLysAspProAspValAsnMetLeuHisVal 238
 DB 735 CAGCACCGCCCAAGCCCAACATCTTCCAAAGACCCAGACGTGACGCGCGCGCGT 794
 QY 239 PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLysLysLysLys 258
 DB 795 TTCTCTCTGGGGAG--TCATCGTGGAGTATGGCAAGAGAAACGACATACCTACCC 851
 QY 259 TyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProLeuLeuLeuLeuProMetTyr 278
 DB 852 TACAACCGACGACGACCTGTACTTCTTCTGATCGCGCGCGCTGCTACCCCTGGTGAAC 911
 QY 279 PheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298
 DB 912 TTGAGTGGAAATCTGGCGTACTGTGTGTGATGTCAGTGGCGGAGTTGCTCTGG 971
 QY 299 AlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGly 318
 DB 972 GCGCGCAGCTTCTATGCGCGCTTCTTCTTATCTCTCTCTCTCTCTCTCTCTCTCTGG 1031
 QY 319 AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThr 338
 DB 1032 GTGCTGCTCTTCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1091
 QY 339 GlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSer 358
 DB 1092 CAGATGAACCACTCCCAAGGAGATCGGCGCACGAGAACGCGGAGTGGTCTCTCTCTCT 1151
 QY 359 GlnLeuThrAlaThrCysAsnValGluLysSerPhePheAsnAspTrpPheSerGlyHis 378
 DB 1152 CAGTGGCGCGCATCTGCAACGTTGGAGCCCTCTCTTTCACCACTGTTTACGCGGCGAC 1211
 QY 379 LeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLys 398
 DB 1212 CTCACCTTCAGATCGAGCACCACTCTTCCCGAGGATGCGGAGACACAACTACAGCGCG 1271
 QY 399 IleAlaProLeuValLysSerLeuCysAlaIysHisGlyIleGluTyrGlnGluYsPro 418
 DB 1272 GTGCGCGCGCTGGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1331
 QY 419 LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeu 438
 DB 1332 TTCCTCCTCCGCGCTGGTGGACATGTCAGGTCTCTGAAGAAGTCTGTGTGATCTGGCTG 1391
 QY 439 AspAlaTyrLeuHisLys 444
 DB 1392 GACGCTACCTCCATCAG 1409

RESULT 5

US-09-822-849A-485/c
 ; Sequence 485, Application US/09822849A
 ; Patent No. US20020045170A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wong, Gordon G.

; APPLICANT: Clark, Hilary
 ; APPLICANT: Fechtel, Kim
 ; APPLICANT: Agostino, Michael J.
 ; APPLICANT: Howes, Steven H.
 ; APPLICANT: Resnick, Richard J.
 ; APPLICANT: Gulukota, Kamalakara
 ; APPLICANT: Graham, James R.
 ; APPLICANT: Genetics Institute, Inc.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
 ; FILE REFERENCE: GIN 6403
 ; CURRENT APPLICATION NUMBER: US/09/822,849A
 ; CURRENT FILING DATE: 2001-09-04
 ; PRIOR APPLICATION NUMBER: 60/195,582
 ; PRIOR FILING DATE: 2000-04-06
 ; NUMBER OF SEQ ID NOS: 598
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 485
 ; LENGTH: 1972
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-822-849A-485

Alignment Scores:
 Pred. No.: 3,97e-167 Length: 1972
 Score: 1516.00 Matches: 272
 Percent Similarity: 76.08% Conservative: 62
 Best Local Similarity: 61.96% Mismatches: 99
 Query Match: 62.18% Indels: 6
 Gaps: 3

US-09-719-601-5 (1-444) x US-09-822-849A-485 (1-1972)

QY	11	AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluIleGln	27
DB	1864	CGCCGCGAGACCGCGGCTCAGGAGCTACCCGCGCTACCTCAGCTGGGAGGAGGCGCC	1805
QY	28	LyHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr	47
DB	1804	CAGCGCTCAGGTCGAGGAGCGGTGGCTAGTGTACCGCTAAGGTGTACATCAGC	1745
QY	48	LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp	67
DB	1744	GAGTTCCACCGCGGCATCCAGGGGCTCCCGGCTCATCAGCCACTACGCGGGCGGAGAT	1685
QY	68	AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys	87
DB	1684	GCCACGGATCCCTTTGTGGCTTCACATCAACAAGGCGCTTGTGAAGAAGTATATGAAC	1625
QY	88	ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer	107
DB	1624	TCTCTCTGATTTGGAGACTGTCTCCAGCAGCCAGCTTTGAGCCACCACCAAGATAA	1565
QY	108	LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys	127
DB	1564	GAGCTGACAGATAGTTCCCGGAGCTCGGGCCACAGTGGAGCGGATGGGCTCATGAAG	1505
QY	128	ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla	147
DB	1504	GCCACCAAGTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1445
QY	148	TrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal	167
DB	1444	TGGCTCAGCCCTTTGGGCTTTGGGAGCGTCTTTTGGCCCTTCTCTGCTGCTGCTGCTG	1385
QY	168	LeuAlaThrSerGlnAlaGluAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal	187
DB	1384	CTCAGTGAGTTTCAGCCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTG	1325
QY	188	TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly	207
DB	1324	TTACGACCTCAAGTGAACCATCTGCTACATCATTTTGTGATTTGGCCACTGAAGGGG	1265
QY	208	AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe	227

DB	1264	GCCTCCGCGAGTTGGTGAACCCATGTCATCTCCAGCACCATGCCAGCCCACTGCTTC	1205
QY	228	HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyValTrpGln	245
DB	1204	CGCAAAGACCCAGACATCAACATG---CATCCCTTCTTCTTCTTCTTCTTCTTCTTCTT	1148
QY	246	ProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys	265
DB	1147	TCGTGGAGCTTGGGAAACAGAAATAATATATATATATATATATATATATATATATATAT	1088
QY	266	PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMet	285
DB	1087	TTCTTCTTAATTGGGCGCCAGCTTGTGCTCTCTACTTCCAGGTATATTTCTAT	1028
QY	286	ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg	305
DB	1027	TTGTATTATCCAGCGAAAGAGTGGGTGGCTTGGCTGGATGATTAATTTCTACCTCCGC	968
QY	306	PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe	325
DB	967	TTCTTCTTCTTATGTGCTTATTTGGGCTGAAAGCTTCTCTGGGCTTTCTTCTTCTTCT	908
QY	326	IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet	345
DB	907	GTGAGTTTCTCGAAAGCAACTGGTTGTGTGGGTGACACAGATGAACCATATTTCCCATG	848
QY	346	GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn	365
DB	847	CACATTGATCATGACCGGAACATGCTGGTGGTTCACCCAGCTCCAGGCCACATGCAAT	788
QY	366	ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleLysHis	385
DB	787	GTCCCAAGTCTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	728
QY	386	HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer	405
DB	727	CATCTTTTCCACGATGCTCGACACATATACCAAGTGGCTCCCTGGTGGCTGCTGCTG	668
QY	406	LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp	425
DB	667	TTGTGTGCAAGCATGGCATAGTACCATGCTCAAGCCCTCTGCTGCTGCTGCTGCTGCTG	608
QY	426	IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys	444
DB	607	ATCATCCACTCTAAAGGAGTCAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	551

RESULT 6
 US-10-133-937-7
 ; Sequence 7, Application US/10133937
 ; Publication No. US20030207278A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Khan, Javed
 ; APPLICANT: Ringner, Markus
 ; APPLICANT: Peterson, Carsten
 ; APPLICANT: Meltzer, Paul
 ; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
 ; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
 ; TITLE OF INVENTION: OTHER BIOLOGICAL STATES
 ; FILE REFERENCE: 11613.56US01
 ; CURRENT APPLICATION NUMBER: US/10/133,937
 ; CURRENT FILING DATE: 2002-11-04
 ; NUMBER OF SEQ ID NOS: 99
 ; SOFTWARE: Patent In version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 4213
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-133-937-7

Alignment Scores:
 Pred. No.: 1,36e-166 Length: 4213
 Score: 1516.00 Matches: 272


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Percent Similarity: 76.08% Conservatives: 62
Best Local Similarity: 61.96% Mismatches: 99
Query Match: 62.18% Indels: 6
Db: 13 Gaps: 3

US-09-719-601-5 (1-444) x US-10-133-937-7 (1-4213)

QY 11 AlaAlaGluAArgGluValSerValProThr-----PheSerTrpGluGluIleGln 27
Db 99 GCCCGGAGACCGCGGCTCAGGACCTACCCGGGCTACTTCACTGGGACGAGGTGCC 158
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr 47
Db 159 CAGCCCTCAGGTGGCAGGACGGTGGTGTAGTACCGCTAAGGTGTACAAATCAGC 218
QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67
Db 219 GAGTTCACCCGGCGGCATCCAGGGGGCTCCCGGGTTCATCAGCCATCAGCCGGCAGGAT 278
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 279 GCCACGGATCCCTTTGTGGCTTCCACATCAACAAGGGCTTGTGAAGATATATGAAC 338
QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
Db 339 TCTCTCTGATTGGAGACTGTCTCCAGAGAGCCAGCTTTGAGCCACCAAGATATAA 398
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 399 GAGCTACAGATGAGTTCGGGAGCTGCGGGCCACAGTGGAGCGGATGGGCTCATGAAG 458
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleAlaLeuGluSerIleAla 147
Db 459 GCCACCACTGCTTCTCTGCTGTACCTGTGCACACTTCTCTCTGGTGGTGCAGCC 518
QY 148 TrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
Db 519 TGGCTCACCTTTGGGCTTTGGGAGCTCTTTTGGCTTCTCTCTCTCTCTCTCTCTCT 578
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187
Db 579 CTCAGTGCAGTTCAGGCCAGGCTGGCTGGCTGCAGCATGCTTTGGGACCTTCGGTC 638
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 639 TTCAGACCTCAAGTGGAACTCATCTGCTACATCTTTGTGATGGCCACCTGAAGGG 698
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePhe 227
Db 699 GCCCGGCGCATTTGGTGGAAACCATGCACTTCCAGCACCATGCCAAGCCCACTGCTTC 758
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 759 CGAAGACCCAGACATCAACATG---CATCCCTTCTTCTTCTTCTTCTTCTTCTTCT 815
QY 246 ProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyr 265
Db 816 TCTGTGAGCTTGGGAAACAGAAATAATATGCGGTACACCAACCAGCAGCAAAATAC 875
QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleMet 285
Db 876 TTCTTCTAATTGGGCCCCCAGGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 935
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg 305
Db 936 TTTGTTATCAGCGGAAAGAGTGGGTGAGTCTGGCTGGATGATTACCTTCTACGTCCGC 995
QY 306 PhePheLeuThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db 996 TTCTTCTCTCATGTATGCGCACTATTGGGCTGAAGCCCTTCTGGGCTTTTCTTCATA 1055
QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
Db 326 ILeArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345

1056 GTCAGGTTCTCTGGAAGCAACTGGTTTGTGGTGCACAGATGAACCATATTCCTCATG 1115
346 GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
1116 CACATTGATCATGACCGGAACATGACTGGGTTTCCACCCAGCTCCAGGCCACATGCAAT 1175
366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
1176 GTCCCAAGTCTGCTTCAATGACTGGTTCAGTGACACCTCACTTCAGATTGAGCAC 1235
386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
1236 CATCTTTTCCACGATGCTCGACACATTAACCAAAAGTGGCTCCCTGGTGGAGTCC 1295
406 LeuCysAlaLysHisGlyIleGlyTrpGlnGlyLysProLeuArgAlaLeuLeuAsp 425
1296 TTGTGTGCAAGCATGGCATGAGTACCAAGTCCAAAGCCCTCTGTCTGACCTTCCCGGAC 1355
426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaLysLeuHisLys 444
1356 ATCATCTCACTCAATAAGGAGTCAGGGCAGCTCTGGTAGATGCCTATCTTCAACCA 1412

RESULT 7
US-10-262-617-4
; Sequence 4, Application US/10262617
; Publication No. US2003007747A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
; FILE REFERENCE: PF-0494-1 DIV
; CURRENT APPLICATION NUMBER: US/10/262.617
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 09/048,888
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1928
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US2003007747A1 2056310CB1
US-10-262-617-4

Alignment Scores:
Pred. No.: 5 01e-167 Length: 1928
Score: 1515.00 Matches: 272
Percent Similarity: 76.08% Conservative: 62
Best Local Similarity: 61.96% Mismatches: 99
Query Match: 62.14% Indels: 6
Db: 15 Gaps: 3

US-09-719-601-5 (1-444) x US-10-262-617-4 (1-1928)
QY 11 AlaAlaGluAArgGluValSerValProThr-----PheSerTrpGluGluIleGln 27
Db 102 GCCCGGAGACCGCGGCTCAGGACCTACCCGGGCTACTTCACTGGGACGAGGTGCC 161
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr 47
Db 162 CAGCGCTCAGGTCCGAGGAGCGGTGCTAGTATGATCGACCGTAAGGTGTACACATCAGC 221
QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67
Db 222 GAGTTCACCCGGCGCATCCAGGGGGCTCCCGGGTCTATCAGCCACTACCGCGGCGAGAT 281
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 282 GCCACGGATCCCTTTGTGGCTTCCACATCAACAAGGGCTTGTGAAGATATATGAAC 341
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QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 559 TTCAGCACCCTCAAAGTGAACCATCTGCTCATCATATTTGTGATTTGGCCACCTGAAGGGG 618
QY 208 AlaserAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePhe 227
Db 619 GCGCCCGGCGTGTGGTGAACCATCATGCTTCAGCACCACCTGCAAGCCCACTGCTTC 678
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 679 CGCAAGACCCAGACATCAATG---CATCCCTTCCTTTTGGCTTTGGGGAAGATCCTC 735
QY 246 ProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys 265
Db 736 TCTGTGGAGCTTGGGAAACAGAAAGAAATATATGCGGTACAAACCCAGCAAAATAC 795
QY 266 PhePheLeuIleGlyProPheLeuLeuIleProMetTyrPheGlnTyrGlnIleMet 285
Db 796 TCTTCTCTCAATGTGGCCCGCCAGCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTAT 855
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg 305
Db 856 TTTGTATTACAGCGAAAGAGTGGGTGACCTGGCTGGATGATTAACCTTACGTCGCG 915
QY 306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db 916 TTTCTTCTCACTTATGTGCCACTATTGGGCTGAAAGCCTTCTTGGGCTTTTCTTCTA 975
QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
Db 976 GTCCAGCTTCTGAAAGCAACTGGTGTGTGTGGTGGACACAGATGAACCATATTCCCATG 1035
QY 346 GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
Db 1036 CACATTGATCATGACCGAATGAGTGGTGTGTGGTGGACACAGATGAACCATATTCCCATG 1095
QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
Db 1096 GTCCACAGCTGCTGCTCAATGACTGGTTCAGTGGGACACCTCACTTCCAGATTGAGCAC 1155
QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
Db 1156 CATCTTTTTCACGATGCTCGACACATTTACCAAAAGTGGCTTCCCTGGTGGAGTCC 1215
QY 406 LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
Db 1216 TTGTGTGCAAGCGTGGCATAGATACAGTACAGTCCAGCCCTGCTGTGAGCCTTCCCGAC 1275
QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 1276 ATCATCCACTCACTAAAGAGTCAAGGCGAGCTCTGGCTAGATGCTTATCTTCCACAA 1332
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RESULT 9

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US-10-191-513A-6
; Sequence 6, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US.D3
; CURRENT APPLICATION NUMBER: US/10191,513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
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; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
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; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-6
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Prod. No.: 1.61e-147 Length: 1686
Score: 1348.00 Matches: 241
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.23% Indels: 0
DB: 15 Gaps: 0
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US-09-719-601-5 (1-444) x US-10-191-513A-6 (1-1686)

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QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisLys 223
Db 3 CACTTAAAGGTTGCTCTGCAACTGTTGGAATCATCGCACTTCAGCACCACCCCAAG 62
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CTTAAACATCTTCCACAGGATCCCGATGTGAACATGCTGCACGTGTTGTTCTGGCGAA 122
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
Db 123 TGGCACCCTCGAGTACGGCAAGAGAGTGAATACCTGCTCTACAAATCACCAGCAC 182
QY 264 GluTyrPhePheLeuIleGlyProPheLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATACTCTTCTGATTTGGGCGCGCTGCTCATCTCCCATGTTATTTCCAGTACAGATC 242
QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 243 ATCATGACCATGATCTCCATAAGACTGGTGGACCTGGCTGGGCGCTAGCTACTAC 302
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
Db 303 ATCCGGTCTTTCATCATCTACCTACATCCCTTTCTACGGCATCTGGGAGCCCTCTTTCTC 362
QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACTTATCATGAGTTCTTGGAGACCACTGGTTTGTGGGTCCACACAGATGAATCACATC 422
QY 344 ValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThr 363
Db 423 GTCATGGAGATTGACCAGGAGGCGCTACCGTACTGTTTCTAGTACGAGCTGACAGCCACC 482
QY 364 CysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIle 383
Db 483 TGCACCTGGAGGAGTCTCTTTCACAGACTGGTTTCTAGTGGACACCTTAACITTCAGATT 542
QY 384 GluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuVal 403
Db 543 GAGCACCACCTCTTCCCAACCATGCCCCCGGCACAACTTACACAGATCGCCCCGCTGGTG 602
QY 404 LysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeu 423
Db 603 AAGTCTCTATGTGCCAAGCATGGCATTAATACAGGAGGAGCGCTACTGAGGCGCTG 662
QY 424 LeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHis 443
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RESULT 10

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US-09-981-876-63
; Sequence 63, Application US/09981876
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/ Patent No. US20020164669A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 70 Human Secreted Proteins
/ FILE REFERENCE: PZ001P1
/ CURRENT APPLICATION NUMBER: US/09/981,876
/ PRIOR FILING DATE: 2001-10-19
/ PRIOR APPLICATION NUMBER: 09/148,545
/ PRIOR FILING DATE: 1998-09-04
/ PRIOR APPLICATION NUMBER: 60/040,162
/ PRIOR FILING DATE: 1997-03-07
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 ; PRIOR APPLICATION NUMBER: 60/057,650
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/056,884
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 280
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 63
 ; LENGTH: 1478

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 Best Local Similarity: 64.72% Mismatches: 84
 Query Match: 53.32% Indels: 5
 DB: 10 Gaps: 1

US-09-719-601-5 (1-444) x US-09-981-876-63 (1-1478)

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 Db 16 ACGGATGCTTCCTGCTGCTTCCATCAAGATCTCAATTTTGCGGCAAGTTCTTACAGCCC 75
 Qy 89 LeuLeuIleGlyGluLeuAlaProGluProSerGlnAspHisGlyLysAsnSerLys 108
 Db 76 CTGTGTTGGAGAGCTGGCTCCGGAAGACCCAGCCAGGATGGACCCCTGATG--CGC 133
 Qy 109 IleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThr 128

RESULT 11

US-09-148-545-63
 ; Sequence 63, Application US/09148545
 ; Publication No. US20030027132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.

Db 134 ATGGTCGAGGACTTCGAGCCCTGCACCGAGCGGACATGAAGCTGTTTGATGCC 193
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 Db 194 AGTCCACACCTTCTTTGCTTCTTCTGAGCCACATCTGCGCATGAGGTGCTGGCTGG 253
 Qy 149 PheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIle-ThrAlaPheVal 168
 Db 254 CTCCTTATCTACCTCTCTGGGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 313
 Qy 168 uAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTy 188
 Db 314 GGCCATCTCTCAGCTCAGTCTGCTGGTGTCTGCAAGCATGACCTGGGCGATGC-TCCATCTT 372
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 Qy 208 aSerAlaAsnTrpTrpAsnHisIleArgHisPheGlnHisHisAlaValProAsnIlePheHi 228
 Db 433 CTCGCCCACTGGTGGAACTTCGCCCACTTCAGACACCGCCAGCCCAACATCTTCCA 492
 Qy 228 sLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGl 248
 Db 493 CAAAGACCCAGACGTGACGGTGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 549
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 Db 670 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729
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 Db 730 ATCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 789
 Qy 328 eLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAs 348
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 Qy 368 nSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPh 388
 Db 910 CTCACCTTTTCAACCACTGGTTACGGGGCACCTCACTTCAGATCAGACGACCACTCTT 969
 Qy 388 eProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAl 408
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 Qy 408 aLysHisGlyIleGluTyGlnGlnLysProLeuLeuArgAlaLeuLeuAspIleIleAr 428
 Db 1030 CAAGCACGCGCTCAGCTACGAATG-AAAGCCCTCTCTCAGCGCGCTGGTGGACATCGTCAG 1088
 Qy 428 gSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyIleuHisLys 444
 Db 1089 GTCCCTGAAGAAGTCTGGTGACATCTGGCTGGAGCGCTACTCTCCATCAG 1137

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3	FILE REFERENCE: P2001P1	4	EARLIER APPLICATION NUMBER: 60/043,311	5
5	CURRENT APPLICATION NUMBER: US/09/148,545	6	EARLIER FILING DATE: 1997-04-11	7
7	CURRENT FILING DATE: 1998-09-04	8	EARLIER APPLICATION NUMBER: 60/043,671	9
9	EARLIER APPLICATION NUMBER: PCT/US98/04482	10	EARLIER FILING DATE: 1997-04-11	11
11	EARLIER FILING DATE: 1998-03-06	12	EARLIER APPLICATION NUMBER: 60/043,674	13
13	EARLIER APPLICATION NUMBER: 60/040,162	14	EARLIER FILING DATE: 1997-04-11	15
15	EARLIER FILING DATE: 1997-03-07	16	EARLIER APPLICATION NUMBER: 60/043,669	17
17	EARLIER APPLICATION NUMBER: 60/040,333	18	EARLIER FILING DATE: 1997-04-11	19
19	EARLIER FILING DATE: 1997-03-07	20	EARLIER APPLICATION NUMBER: 60/043,312	21
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29	EARLIER APPLICATION NUMBER: 60/040,626	30	EARLIER FILING DATE: 1997-04-11	31
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51	EARLIER FILING DATE: 1997-05-23	52	EARLIER APPLICATION NUMBER: 60/056,893	53
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 1478

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Alignment Scores:
Pred. No.: 5,61e-142 Length: 1478
Score: 1300.00 Matches: 244
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Best Local Similarity: 64.72% Mismatches: 84
Query Match: 53.32% Indels: 5
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US-09-719-601-5 (1-444) x US-09-148-545-63 (1-1478)

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Qy 89 LeuLeuLleGlyLeuAlaProGluProSerGlnAspHisGlyLysAsnSerLys 108
Db 76 CTGTTGATGGAGAGCTGGCTCCGGAAGAACCCAGCAGGATGACCCCTGAATG--CGC 133

Qy 109 IleThrGluAspPheArgAlaLeuAlaGluAspMetAsnLeuPheLysThr 128
Db 134 ATGGTCGAGGACTTCGAGCCCTGACCCAGGACCGGAGGACATGAAGCTGTTTGATGCC 193

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Qy 129 AsnHisValPhePheLeuLeuLeuAlaHisLleLleAlaLeuLysLysLysLysLys 148
Db 194 AGTCCACACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 253
Qy 149 PheThrValPheThrPheGlyAsnGlyTrpLeuProThrLeuLle-ThrAlaPheVal 168
Db 254 CTCCTTATCTACCTCTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCT 313
Qy 168 uAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerVal 188
Db 314 GGCCATCTCTCAGGCTCAGTCTGGTGTCTGAGCATGACCTGGGCCATGCG--TCCATCT 372
Qy 188 xArgLysProLysTrpAsnHisValHisLysPheValLleGlyHisLeuLysGlyAl 208
Db 373 CAAGAAGWCCTGCTGGAACACAGTGGCCGAGGATTCGTGATGGGCGAGTAAAGGCTT 432
Qy 208 aSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnLysPhe 228
Db 433 CTCGCCCACTCTGGTGAACCTTCGCCACTTCCAGCACCCAGCCCAACATCTTCCA 492
Qy 228 sLysAspProAspValAsnMetLeuHisValPheValLeuGlyLysLysLysLysLys 248
Db 493 CAAGAAGCCAGAGCTGAGCGGCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 549
Qy 248 uTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 268
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Qy 348 pGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGlu 368
Db 850 CCAGAGAGACCCGAGCTGGTCTGCTCTCAGCTGGCAGCCACCTGCAAGCTGGAGCC 909
Qy 368 nSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnLleGluHisLeuPh 388
Db 910 CTCCTTTTCCAACTGTTTCCAGCGGCGACCTCAACTTCCAGATCAGACCCACCTCT 969
Qy 388 eProThrMetProArgHisAsnLeuHisLysLysLysLysLysLysLysLysLysLys 408
Db 970 CCCAGAGATGCGAGACACACTACAGCGGCTGGCGCGCTGGTCAAGTGGTGTGTC 1029
Qy 408 aLysHisGlyLleGluTyrGlnGlyLysProLeuLeuArgAlaLeuLeuLysLysLys 428
Db 1030 CAAGCACGCGCTCAGCTACGAATG--AAGCCCTTCTCTCACCGCGCTGGTGGACAT 1088
Qy 428 gSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
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RESULT 12
US-09-981-876-119
; Sequence 119, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876

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PRIOR APPLICATION NUMBER: 60/043,670
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PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,664
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PRIOR APPLICATION NUMBER: 60/056,876
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PRIOR APPLICATION NUMBER: 60/057,650
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 119
LENGTH: 2016

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US-09-719-601-5 (1-444) x US-09-981-876-119 (1-2016)

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QY 161 ThrLeuIle-ThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTyrLeuGlnHis 180
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EARLIER FILING DATE: 05-Sep-1997
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 119
LENGTH: 2016

Alignment Scores:
Pred. No.: 1,46e-125 Length: 2016
Score: 1162.00 Matches: 248
Percent Similarity: 54.88% Conservative: 50
Best Local Similarity: 45.67% Mismatches: 97
Query Match: 47.66% Indels: 153
DB: 11 Gaps: 3

US-09-719-601-5 (1-444) x US-09-148-545-119 (1-2016)

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DB 787 AAGTGGAAATCTGGCGTACATGCTGCTGTCATGTCAGTGGCGGAGTTTCTCTTGGGCGCG 846
QY 300 alserTyrTrpIleAcqPhePheIleThrTrpIleProPheTyrGlyIleLeuGlyAlaAl 320
DB 847 CCAGCTTCTATGCGCGCTTCTTCTTATCTTACCTACCTCCCTCTTACGCGGCTCCCTGGGGTGC 906

```

QY 320 euLeuPheLeuAsnPheIleArgPhe----- 328
|||
Db 907 TGCTCTCTTGTGCTGCTAGGTATGCGAGGATGGCGAGGTACACACAGCGGACAG 966
328 ----- 328
QY 967 GTGACCCCACTGACGCCCCCAACAGAGCTTCCCTTTCCGTCGTGAGNATGGGGCCA 1026
328 ----- 328
Db 1027 GTGGTACTGCTCCCTGCTGCTGGTGAATCACATAAACACAAAGYTTACAGAGCCAG 1086
328 ----- 328
QY 1087 GGTGCTGGGTTTAGGAGCGTGGCTGGCTTGTAAAGTGGCCGGTGGTGTGCGAGCTG 1146
328 ----- 328
Db 1147 CTCCTGACTCAGCTTCACAGTGGACAGCTGCTCCATTTCAGATTCTTTAAACACTGGCAAG 1206
328 ----- 328
QY 1207 GGGGATGGCCCAATCTATTGTACAGATAAGGAAGTCAAGGCCAYTTGGGGACAGYTG 1266
328 ----- 328
Db 1267 CTCCTCCAGCTCCACTCAGGTGCTTAAAGTGGTGAAGCTGAGCTAGGGCAGTGGCCGAG 1326
328 ----- 328
QY 1327 CTTCTCCAGCTCCACTCAGGTGCTTAAAGTGGTGAAGCTGAGCTAGGGCAGTGGCCGAG 1386
328 ----- 328
QY 1387 CCCAGGAGATGGCCACAGAGACCGGACTGGGTGAGTCTCAGCTGGCAGCCACC 1446
328 ----- 328
QY 1447 TGCAACGTTGGAGCCCTCACTTTTCAACCACTGGTTCAGCGGGCAGCTCAACTTCCAGATC 1506
328 ----- 328
QY 1507 GAGCACCACCTCTTCCAGATGCGGAGACACACTACAGCCGGGTGGCCCTGGTCTGTC 1566
328 ----- 328
QY 1567 AAGTCGCTGTGTGCCAAGCAGCGCTCAGCTACGAATG-AAGCCCTTCTCAGCGCGCTG 1625
328 ----- 328
QY 1626 GTGGACATGCTCAGTCTCCCTGAGGAAGTCTGTGACATCTGGTGGACGCTACCTCAT 1685
328 ----- 328

```

RESULT 14

```

US-10-191-513A-13
; Sequence 13, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08

```

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; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-191-513A-13

```

Alignment Scores:

```

Pred. No.: 3 12e-119 Length: 864
Score: 1103.00 Matches: 194
Percent Similarity: 77.93% Conservative: 32
Best Local Similarity: 66.90% Mismatches: 52
Query Match: 45.24% Indels: 12
DB: 15 Gaps: 3

```

```

US-09-719-601-5 (1-444) x US-10-191-513A-13 (1-864)

```

```

QY 157 GlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGly 176
|||
Db 22 GCGCGAATTCGCGCAGTT-----CAGCCCGAGGCTGGC 54
177 TrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeu 196
|||
Db 55 TGGCTGCAGCATGACTTTGGGCACCTGTGCGTCTTCAGCACCTCAAGTGGAAACCATCTG 114
197 ValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArg 216
|||
Db 115 CTACATCATTTTGTGATTGGCCACCTGAAGGGGGGGCCCGCCAGTGGTGGAAACCATG 174
217 HisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeu 236
|||
Db 175 CACTTCCAGCACCATGTCGAGCCCACTCTTCCGCAAGACCCAGACATCAACATG--- 231
237 His-----ValPheValLeuGlyLysTrpGlnProIleGlyTyrGlyLysLysLeu 254
|||
Db 232 CATCCCTCTCTTCTTGGCTGGGGAAGATCCCTCTCTGTGGAGCTTGGGAAACAGAGAAA 291
255 LysTyrLeuProTyrAsnHisGlnHisGlyTyrPhePheLeuIleGlyProLeuLeu 274
|||
Db 292 AATATATGCGGTACCAACCCAGCACAAATACTTCTTCTAATTTGGGCCCCAGCCTTG 351
275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294
|||
Db 352 CTGCTCTCTACTTCCAGTGGTATATTTCTATTGTTTATCCAGCGAAAGAGTGGGTG 411
295 AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314
|||
Db 412 GACTTGGCTGGATGATTACCTTTCAGTCCGCTTCTTCTCCTCACTATGTGCCATTATG 471
315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334
|||
Db 472 GGGCTGAAAGCCTTCTGCGGCTTTTCTTCATAGTCAGGTTCCTGGAAGCAACTGGTTT 531
335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlnAlaTyrArgAsp 354
|||
Db 532 GTGTGGGTGACACAGATGAACCATATTCCATGCACTATGATCATCGACGGAACATGGAC 591
355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374
|||
Db 592 TGGGTTTCCACCAGCTCCAGGCCACATGCAATGCCACAGTCTGCTTCAATGACTGG 651
375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHis 394
|||
Db 652 TTCACTGGGACCTCAACTTCCAGATTGAGCCACCATCTTTTCCACCGATGCTCGACAC 711
395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
|||
Db 712 AATTACCACAAGTGGCTCCCTCTGGTGGTGGTCTTGTGTGTGCCAAGCATGGCATAGATAC 771

```

QY 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleLeuAserLeuLysSerGly 434
 Db 772 CAGTCCAGCCCTGCTGCGACCTTCGCGACATCATCCACTCACTAAAGGAGTCAGG 831
 QY 435 LysLeuTrpLeuAspAlaTyrlleuHisLys 444
 Db 832 CAGCTCTGGCTAGATGCCTATCTTCCACAA 861

RESULT 15

US-10-191-513A-34
 ; Sequence 34, Application US/10191513A
 ; Publication No. US20030104596A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pardip
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Tapas, Das
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295.US.D3
 ; CURRENT APPLICATION NUMBER: US/10/191,513A
 ; CURRENT FILING DATE: 2002-09-25
 ; PRIOR APPLICATION NUMBER: US 09/227,613
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422
 ; PRIOR FILING DATE: 1998-04-10
 ; PRIOR APPLICATION NUMBER: US 08/833,610
 ; PRIOR FILING DATE: 1997-04-11
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 34
 ; LENGTH: 990
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-191-513A-34

Alignment Scores:
 Pred. No.: 2,37e-102 Length: 990
 Score: 960.00 Matches: 176
 Percent Similarity: 69.54% Conservative: 50
 Best Local Similarity: 54.15% Mismatches: 73
 Query Match: 39.38% Indels: 26
 DB: 15 Gaps: 4

US-09-719-601-5 (1-444) x US-10-191-513A-34 (1-990)

QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27
 Db 19 GCGCGCGAGACCGCGCTCAGGACCTACCCCGCTACTTCCACCTGGGACGAGTGGCC 78
 QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrlleuThr 47
 Db 79 CAGCGCTCAGGGTCCGAGGAGCGGTGCTAGTCATCGCGTAAAGTGTACACATCAGC 138
 QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrlleuGluAsp 67
 Db 139 GAGTTACCGCGCGCTCAGGGGCTCCGGGTCTATCAGCCACTACCGCGGCGAGGAT 198
 QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
 Db 199 GCCACGGATCCCTTTGTGGCTTCCATCAACAGGCGCTTGTGAAGAAGTATATGAAC 258
 QY 88 ProLeuLeuIleGlyGluLeuAlaProGluProSerGlnAspHisGlyLysAsnSer 107
 Db 259 TCCTCTCTGATGGAGAACTGTCTCCAGAGCAGCCCGAGCTTGAGCCCAAGATATAA 318
 QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
 Db 319 GAGCTGACAGATGAGTTCGCGAGCTCGCGCCACAGTCAGTGGCGGATGGCGCTCATGAAG 378
 QY 128 ThrAsnHisValPhePheLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147

Db 379 GCAACCATGCTCTTCTCTGCTGTACCTGTGCGACATCTTCTGCTGGATGGTCAGCC 438
 QY 148 TrpPheThrValPheTyrlleuGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
 Db 439 TGCTCACCTCTGGGCTCTTTGGGAGCTCTTTTGGGCTCTTCTCTCTGTCGGGTGCTG 498
 QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrlleuHisLeuSerVal 187
 Db 499 CTGAGTGCAGTTCAGGCCCGAGCTGGCTGGCTGCGACATGACTTTGGGACCTCTGCGTC 558
 QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
 Db 559 TTCAGCACCTCAAGTGAACCATCTGCTACATCATTTTGTGATTTGGCCACCTGAAGGG 618
 QY 208 AlaserAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
 Db 619 GCGCCCGCAGTTGGTGGAAACCATGCTCTCCAGCACCATGCCAGCCCACTGCTTC 678
 QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
 Db 679 CGCAAGACCCAGACATCAACATG---CATCCCTTCTTCTTGGCTTGGGGAAGATCCTC 735
 QY 246 ProIleGluTyrlleuLysLysLeuLysTyrlleuProTyrlleuAsnHisGlnHisGluTyrl 265
 Db 736 TCTGTGGAGCTTGGGAAACAGAAATAATATATGCTTACCAACCCAGCAAAATAC 795
 QY 266 PhePheLeuIleGly----- 270
 Db 796 TTCTTCTTAATTGGGCGCCCGAGCTTGTGCTCTCTTCTTCTTCTTCTTCTTCTTCTAT 855
 QY 271 -----ProProLeuLeuIleProMetTyrlleuGlnTyrlleuMet 285
 Db 856 TTTGTTATCCAGCGACCCCGAGCTTGTGCTCTCTTCTTCTTCTTCTTCTTCTTCTAT 915
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrlleuArg 305
 Db 916 TTTGTTATCCAGCGAAAGAGTGGTGGAGTGGCTTGGCTGGATGATTACCTTCTACGTCGC 975
 QY 306 PhePheIleThrTyrl 310
 Db 976 TTCTTCTCTCACTTAT 990
 RESULT 16
 US-10-191-513A-35
 ; Sequence 35, Application US/10191513A
 ; Publication No. US20030104596A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pardip
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Tapas, Das
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295.US.D3
 ; CURRENT APPLICATION NUMBER: US/10/191,513A
 ; CURRENT FILING DATE: 2002-09-25
 ; PRIOR APPLICATION NUMBER: US 09/227,613
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422
 ; PRIOR FILING DATE: 1998-04-10
 ; PRIOR APPLICATION NUMBER: US 08/833,610
 ; PRIOR FILING DATE: 1997-04-11
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 35
 ; LENGTH: 960
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-191-513A-35
 Alignment Scores:
 Pred. No.: 3,33e-99 Length: 960
 Score: 933.00 Matches: 170

Percent Similarity: 73.38%
Best Local Similarity: 58.02%
Query Match: 38.27%
DB: 15
Conservative: 45
Matches: 72
Indels: 6
Gaps: 3

US-09-719-601-5 (1-444) x US-10-191-513A-35 (1-960)

```
Qy 11 AlalaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27
Db 49 GCGCGAGAGCGCGGCTCAGGAGCTACCCGCGCTACTTACCTGGGAGGAGGTGGCC 108
Qy 28 LysHisLeuArgThrAspSerGlyLeuValleAspArgLysValTyAsnIleThr 47
Db 109 CAGCGCTCAGGTCGCGAGGCGGTGCTAGTATGACCGTAAGGTGTACAAATCAGC 168
Qy 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValleGlyHisTyAlaGlyGluAsp 67
Db 169 GAGTTCACCGCGGCTCAGGCGGCTCCCGGCTCATCAGCCACTACGCGCGGAGGAT 228
Qy 68 AlathrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 229 GCCAGGATCCCTTTGGGCTTCCACATCAACAGGCGCTTGTGAAGATATATGAAC 288
Qy 88 ProLeuLeuLeuGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
Db 289 TCTCTCTGATTGAGACTGTCTCCAGAGCGCGGCTTTCAGCCCAAGATATAA 348
Qy 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 349 GAGTGACATGATGTTCCGAGGCTCGGCGCCACAGTCAGGAGGATGGGCTCATGAAG 408
Qy 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
Db 409 GCCAACCATGCTTCTCTGCTGTACTGCTGCACATCTTGTGCTGAGTGTGAGCC 468
Qy 148 TrpPheThrValPheTyPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
Db 469 TGGCTCACCTTCTGGGCTTGGGAGCTCTTTTGGCTTCTCTCTCTCTCTCTCTCT 528
Qy 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyGlyHisLeuSerVal 187
Db 529 CTGAGTGAGTTCAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
Qy 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValleGlyHisLeuLysGly 207
Db 589 TTCAGCACTCAAGTGAACCATCTGCTACATCATTTTGTGATTTGCCACCTGAAGGG 648
Qy 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
Db 649 CCCCCCGCAGTTGGTGGAAACACATGCTCCAGCACCATGCGCAAGCCCAACTGCTC 708
Qy 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 709 CGCAAGACCCAGACATCAATG---CATCCCTTCTCTTTCCTTGGGAGATCTCTC 765
Qy 246 ProIleGluTyGlyLysLysLeuLysTyTrpLeuProTyTrpAsnHisGlnHisGluTy 285
Db 766 TCTGTGGAGCTTGGAAACAGAAAGAAATATATGCGGTACAAACCCAGCAAAATAC 825
Qy 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyPheGlnTyTrpGlnIleMet 285
Db 826 TCTCTCTTAATTTGGCCCCCGGCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTAT 885
Qy 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298
Db 886 TTTGTTATCCAGCAAGAAAGTGGGTGACATTGGCCTGG 924
```

RESULT 17

US-10-191-513A-5
; Sequence 5, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories

```
APPLICANT: Mukerji, Pardip  
APPLICANT: Leonard, Amanda E.  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Tapas, Das  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295.US.D3  
CURRENT APPLICATION NUMBER: US/10/191,513A  
CURRENT FILING DATE: 2002-09-25  
PRIOR APPLICATION NUMBER: US 09/227,613  
PRIOR FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: PCT/US98/07422  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: US 08/833,610  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 918  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (755)...(755)  
OTHER INFORMATION: r = g or a at position 755  
US-10-191-513A-5  
Alignment Scores:  
Pred. No.: 4.62e-98 Length: 918  
Score: 923.00 Matches: 167  
Percent Similarity: 74.04% Conservative: 44  
Best Local Similarity: 58.60% Mismatches: 68  
Query Match: 37.86% Indels: 6  
DB: 15 Gaps: 3  
US-09-719-601-5 (1-444) x US-10-191-513A-5 (1-918)  
Qy 19 ProThr-----PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSer 35  
Db 7 CCTACCCGCGGCTACTTCCCTGGAGCAGAGTGGCCAGCGCTCAGGCTGGCGAGGCGG 66  
Qy 36 GlyLeuValIleAspArgLysValTyAsnIleThrLysTrpSerIleGlnHisProGly 55  
Db 67 TGGCTAGTATGATCGCCGTAAGGTGTACAACTACAGAGTTCACCCGCGGCAATCCAGG 126  
Qy 56 GlyGlnArgValIleGlyHisTyAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75  
Db 127 GACTCCCGGCTCATCAGCCACTACGCGCGGAGGATGCCAGGATCCCTTTGTGGCTTC 186  
Qy 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95  
Db 187 CACATCAACAAAGGCGCTTGTGAAGAGTATATGAATCTCTCTCTGATTGGAGAACTGTCT 246  
Qy 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115  
Db 247 CCAGAGCAGCCAGCTTTGAGCCCAACCAAGATAAAGAGCTGACAGATGAGTTCGGGAG 306  
Qy 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPheLeuLeu 135  
Db 307 CTGCGGGCCACAGTGGAGCGGATGGGGCTCATGAAGGCCAACCACTGTCTTTCTTCGTGTG 366  
Qy 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyPheGly 155  
Db 367 TACCTGTGCACATTTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 426  
Qy 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAla 175  
Db 427 AGTCTCTTTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 486  
Qy 176 GlyTrpLeuGlnHisAspTyGlyHisLeuSerValTyArgLysProLysTrpAsnHis 195  
Db 487 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 546  
Qy 196 LeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHis 215
```

Db 547 CTGCTACATCTTTTGTGATTTGGCCACCTGAGGGGGCCCCCGCAGTTGGTGAACAC 606
Qy 216 ArgHisPheGlnHisHisAlaLysProAsnTlePheHisLysAspProAspValAsnMet 235
Db 607 ATGCACTTCCAGCACCATGCAAGCCCACTGCTTCCGCAAGAGCCAGACATCAACATG 666
Qy 236 LeuHis-----ValPheValLeuGlyGlnProLleGlnProLleGlyLysLys 253
Db 667 ---CACTCCTCTCTTTGCTTGGGGAAGATCCCTCTCTGGAAGCTTGGGAACAGAG 723
Qy 254 LeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuLleGlyProProLeu 273
Db 724 AAAAAATATATGCGGTACCAACACCAAGCAGACATCTCTCTCTAAATTTGGGCCCCAGCC 783
Qy 274 LeuLleProMetTyrPheGlnTyrGlnLlelleMetThrMetLleValHisLysAsnTyr 293
Db 784 TTGCTGCTCTCTACTTCCAGTGTATATTTCTATTTTGTATCCAGCGAAGAGTGG 843
Qy 294 ValAspLeuAlaTyr 298
Db 844 GTGGACTTGGCCTGG 858

RESULT 18

US-09-604-287A-425
; Sequence 425, Application US/09604287A
; Patent No. US20020064872A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaochun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-425

Alignment Scores:
Pred. No.: 4e-88 Length: 446
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 9 Gaps: 0

US-09-719-601-5 (1-444) x US-09-604-287A-425 (1-446)
Qy 204 HisLeuLysGlyAlaSerAlaAsnTyrTrpAsnHisArgHisPheGlnHisHisAlaLys 223
Db 2 CACTTAAAGGGTGCCTCTGCCAATCGGTGGAAATCATCGCACTTCCAGCACCAGCAAG 61
Qy 224 ProAsnLlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 62 CCTTAAATCTTCCACAAGATCCGATGTGAACATGCTGCAGTGTCTTCTGGGCGAA 121
Qy 244 TrpGlnProLleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
Db 122 TGGCAGCCCATCGATGAGCAAGAGAGTGAATACCTGCCTTACATCACCAGCAC 181
Qy 264 GluTyrPhePheLeuLleGlyProProLeuLleProMetTyrPheGlnTyrGlnLle 283
Db 182 GAATACTTCTCTGATTTGGGCCCGCGCTCATCCCATGATTTTCCAGTACCAGATC 241

Qy 284 IleMetThrMetLleValHisLysAsnTyrValAspLeuAlaTyrAlaValSerTyrTyr 303
Db 242 ATCATGACCATCATCGTCCATAGAACTGGGTGGACCTGGCTGGCGCGTCACTACTAC 301
Qy 304 IleArgPhePheLleThrTyrLleProPheTyrGlyLleLeuGlyAlaLeuLeuPheLeu 323
Db 302 ATCCGGTTCCTTCATCACCCTACATCCCTTCTACGGCATCCTGGGAGCCCTCTTTCCTC 361
Qy 324 AsnPheLleArgPheLeuGluSerHisTyrPheValTyrValThrGlnMetAsnHisLle 343
Db 362 AACTTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTACACACAGATGAATCACATC 421
Qy 344 ValMetGluLleAspGlnGlu 350
Db 422 GTCATGGAGATTGACCCAGGAG 442

RESULT 19

US-09-551-621-425
; Sequence 425, Application US/09551621
; Publication No. US20030104366A1
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaochun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C5
; CURRENT APPLICATION NUMBER: US/09/551,621
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-621-425

Alignment Scores:
Pred. No.: 4e-88 Length: 446
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 11 Gaps: 0

US-09-719-601-5 (1-444) x US-09-551-621-425 (1-446)
Qy 204 HisLeuLysGlyAlaSerAlaAsnTyrTrpAsnHisArgHisPheGlnHisHisAlaLys 223
Db 2 CACTTAAAGGGTGCCTCTGCCAATCGGTGGAAATCATCGCACTTCCAGCACCAGCAAG 61
Qy 224 ProAsnLlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 62 CCTTAAATCTTCCACAAGATCCGATGTGAACATGCTGCAGTGTCTTCTGGGCGAA 121
Qy 244 TrpGlnProLleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
Db 122 TGGCAGCCCATCGATGAGCAAGAGAGTGAATACCTGCCTTACATCACCAGCAC 181
Qy 264 GluTyrPhePheLeuLleGlyProProLeuLleProMetTyrPheGlnTyrGlnLle 283
Db 182 GAATACTTCTCTGATTTGGGCCCGCGCTCATCCCATGATTTTCCAGTACCAGATC 241
Qy 284 IleMetThrMetLleValHisLysAsnTyrValAspLeuAlaTyrAlaValSerTyrTyr 303
Db 242 ATCATGACCATCATCGTCCATAGAACTGGGTGGACCTGGCTGGCGCGTCACTACTAC 301
Qy 304 IleArgPhePheLleThrTyrLleProPheTyrGlyLleLeuGlyAlaLeuLeuPheLeu 323
Db 302 ATCCGGTTCCTTCATCACCCTACATCCCTTCTACGGCATCCTGGGAGCCCTCTTTCCTC 361

Qy 324 AsnPhelleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 362 AACTTCATCAGGTCTCTGGAGGCCACTGGTTGTGTGGGTCCACAGATCATCATC 421
Qy 344 ValMetGluIleAspGlnGlu 350
Db 422 GTCATGGAGATTGACAGGAG 442

RESULT 20

US-10-124-805-425
; Sequence 425, Application US/10124805
; Publication No. US2003016602A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10124.805
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-425

Alignment Scores:
Pred. No.: 4e-88 Length: 446
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 13 Gaps: 0

US-09-719-601-5 (1-444) x US-10-124-805-425 (1-446)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpAsnHisArgHisPheGlnHisAlaLys 223
Db 2 CACTTAAGGGTGCTCTGCCAATCTGGTGAATCATCGCCACTCCAGCACCAGCAAG 61
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlu 243
Db 62 CCTAACATCTCCACAGGATCCCGATGTGAACATGTGCACGTGTTTCTGGGGAA 121
Qy 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLys 263
Db 122 TGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAATCACCAGAC 181
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 182 GAATACTTCTCTGATGGCCCGCTGTCATCCCCATGTATTTCCAGTACCAGATC 241
Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 242 ATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGCGCTACTAC 301
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
Db 302 ATCCGGTCTTCATCACTACATCCCTTTCAGGGCATCTGGAGGCCCTCCCTTTCCCTC 361
Qy 324 AsnPhelleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 362 AACTTCATCAGGTCTCTGGAGGCCACTGGTTGTGTGGGTCCACAGATCATCATC 421
Qy 344 ValMetGluIleAspGlnGlu 350
Db 422 GTCATGGAGATTGACAGGAG 442

RESULT 21

US-10-007-805-425

; Sequence 425, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007.805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-425

Alignment Scores:
Pred. No.: 4e-88 Length: 446
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 14 Gaps: 0

US-09-719-601-5 (1-444) x US-10-007-805-425 (1-446)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpAsnHisArgHisPheGlnHisAlaLys 223
Db 2 CACTTAAGGGTGCTCTGCCAATCTGGTGAATCATCGCCACTCCAGCACCAGCAAG 61
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlu 243
Db 62 CCTAACATCTCCACAGGATCCCGATGTGAACATGTGCACGTGTTTCTGGGGAA 121
Qy 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLys 263
Db 122 TGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAATCACCAGAC 181
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 182 GAATACTTCTCTGATGGCCCGCTGTCATCCCCATGTATTTCCAGTACCAGATC 241
Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 242 ATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGCGCTACTAC 301
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
Db 302 ATCCGGTCTTCATCACTACATCCCTTTCAGGGCATCTGGAGGCCCTCCCTTTCCCTC 361
Qy 324 AsnPhelleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 362 AACTTCATCAGGTCTCTGGAGGCCACTGGTTGTGTGGGTCCACAGATCATCATC 421
Qy 344 ValMetGluIleAspGlnGlu 350
Db 422 GTCATGGAGATTGACAGGAG 442

RESULT 22

US-10-076-622-425
; Sequence 425, Application US/10076622
; Publication No. US20030023036A1


```
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-425

Alignment Scores:
Pred. No.: 48-88      Length: 446
Score: 834.00        Matches: 147
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 34.21%    Indels: 0
DB: 15               Gaps: 0

US-09-719-601-5 (1-444) x US-10-076-622-425 (1-446)
Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
Db 2 CACTTAAAGGGTCCCTCTGCAACTGGTGGATCATCGCACTTCAGCACCACCCCAAG 61
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 62 CCTAAACATCTTCACAGGATCCCGATGGAACATGCTGCACGTGTGTTCCTGGCGAA 121
Qy 244 TrpGlnProIleGlyLysLysLysLeuLysLeuLysLeuProTyrAsnHisGlnHis 263
Db 122 TGGCAGCCCATCGATCGCCAGAGAGAGCTGAAATACCTGCCCTTACATCACCAGCAC 181
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 182 GAATACCTCTCTGATGGCGCGCTGCTCATCCCATGATTTTCCAGTACCAGATC 241
Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 242 ATCATGACCATGATCGTCCATAAGAACTGGTGGACCTGGCCCTGGCGCTCAGTACTAC 301
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
Db 302 ATCCGGTTCATCATCACCTACATCCCTTTCTACGGCATCTCGGAGCCCTCTTTTCCTC 361
Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 362 AACTTCATCAGTTCTCGGAGAGCCACTGGTTTGTGTGGTCCACACAGATGAATCATCATC 421
Qy 344 ValMetGluIleAspGlnGlu 350
Db 422 GTCATGAGATTGACCCAGGAG 442

RESULT 23
US-09-604-287A-313
; Sequence 313, Application US/09604287A
; Patent No. US20020064872A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7

US-09-719-601-5 (1-444) x US-09-604-287A-313 (1-456)
Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
Db 3 CACTTAAAGGGTCCCTCTGCAACTGGTGGATCATCGCACTTCAGCACCACCCCAAG 62
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CCTAACATCTTCACAGGATCCCGATGGAACATGCTGCACGTGTGTTCCTGGCGAA 122
Qy 244 TrpGlnProIleGlyLysLysLysLeuLysLeuLysLeuProTyrAsnHisGlnHis 263
Db 123 TGGCAGCCCATCGATCGCCAGAGAGAGCTGAAATACCTGCCCTTACATCACCAGCAC 182
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATACCTCTCTGATGGCGCGCTGCTCATCCCATGATTTTCCAGTACCAGATC 242
Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 243 ATCATGACCATGATCGTCCATAAGAACTGGTGGACCTGGCCCTGGCGCTCAGTACTAC 302
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
Db 303 ATCCGGTTCATCATCACCTACATCCCTTTCTACGGCATCTCGGAGCCCTCTTTTCCTC 362
Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACTTCATCAGTTCTCGGAGAGCCACTGGTTTGTGTGGTCCACACAGATGAATCATCATC 422
Qy 344 ValMetGluIleAspGlnGlu 350
Db 423 GTCATGAGATTGACCCAGGAG 443

RESULT 24
US-09-339-338-313
; Sequence 313, Application US/09339338A
; Patent No. US20020102602A1
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-339-338-313
```

Alignment Scores:
 Pred. No.: 4,15e-88 Length: 456
 Score: 834.00 Matches: 147
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.21% Indels: 0
 DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x US-09-339-338-313 (1-456)

QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
 |||||
 Db 3 CACTTAAGGGTGCCTCTGCCAAGTGGTGGATCATCGCACTTCCAGCACCGCCAAAG 62
 |||||
 QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
 |||||
 Db 63 CCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTGTTTCTGGCGAA 122
 |||||
 QY 244 TrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
 |||||
 Db 123 TGGCAGCCCATCGATCGGCAAGAGCTGAATACCTGCCCTACATCACCAGCAC 182
 |||||
 QY 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
 |||||
 Db 183 GAATACCTTCTTCCATCACCTACATCCCTTCTACGGCATCTCGGAGCCCTCTTCTC 242
 |||||
 QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyr 303
 |||||
 Db 243 ATCATGACCATGATCGTCCATAAGAACTGGGGGACCTGGCGCTGGCGCTGAGTACTAC 302
 |||||
 QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
 |||||
 Db 303 ATCCGGTTCTTCCATCACCTACATCCCTTCTACGGCATCTCGGAGCCCTCTTCTC 362
 |||||
 QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
 |||||
 Db 363 AACCTTCATCAGTCTCTGGAGAGCCACTGGTTGTGTGGGTCCACACGATGAATCACATC 422
 |||||
 QY 344 ValMetGluIleAspGlnGlu 350
 |||||
 Db 423 GTCATGGAGATTGACCCAGGAG 443
 |||||

RESULT 25

US-09-551-621-313
 ; Sequence 313, Application US/09551621
 ; Publication No. US20030104366A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yuqi, Jiang
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 ; FILE REFERENCE: 210121.470C5
 ; CURRENT APPLICATION NUMBER: US/09/551,621
 ; CURRENT FILING DATE: 2000-04-17
 ; NUMBER OF SEQ ID NOS: 479
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 313
 ; LENGTH: 456
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-551-621-313

Alignment Scores:
 Pred. No.: 4,15e-88 Length: 456
 Score: 834.00 Matches: 147
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.21% Indels: 0
 DB: 11 Gaps: 0

US-09-719-601-5 (1-444) x US-09-551-621-313 (1-456)

QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
 |||||
 Db 3 CACTTAAGGGTGCCTCTGCCAAGTGGTGGATCATCGCACTTCCAGCACCGCCAAAG 62
 |||||
 QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
 |||||
 Db 63 CCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTGTTTCTGGCGAA 122
 |||||
 QY 244 TrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
 |||||
 Db 123 TGGCAGCCCATCGATCGGCAAGAGCTGAATACCTGCCCTACATCACCAGCAC 182
 |||||
 QY 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
 |||||
 Db 183 GAATACCTTCTTCCATCACCTACATCCCTTCTACGGCATCTCGGAGCCCTCTTCTC 242
 |||||
 QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyr 303
 |||||
 Db 243 ATCATGACCATGATCGTCCATAAGAACTGGGGGACCTGGCGCTGGCGCTGAGTACTAC 302
 |||||
 QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
 |||||
 Db 303 ATCCGGTTCTTCCATCACCTACATCCCTTCTACGGCATCTCGGAGCCCTCTTCTC 362
 |||||
 QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
 |||||
 Db 363 AACCTTCATCAGTCTCTGGAGAGCCACTGGTTGTGTGGGTCCACACGATGAATCACATC 422
 |||||
 QY 344 ValMetGluIleAspGlnGlu 350
 |||||
 Db 423 GTCATGGAGATTGACCCAGGAG 443
 |||||

RESULT 26

US-10-124-805-313
 ; Sequence 313, Application US/10124805
 ; Publication No. US20030166022A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Persing, David H.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.470C12
 ; CURRENT APPLICATION NUMBER: US/10/124,805
 ; CURRENT FILING DATE: 2002-04-15
 ; NUMBER OF SEQ ID NOS: 627
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 313
 ; LENGTH: 456
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-124-805-313

Alignment Scores:
 Pred. No.: 4,15e-88 Length: 456
 Score: 834.00 Matches: 147
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.21% Indels: 0
 DB: 13 Gaps: 0

US-09-719-601-5 (1-444) x US-10-124-805-313 (1-456)

QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
 |||||
 Db 3 CACTTAAGGGTGCCTCTGCCAAGTGGTGGATCATCGCACTTCCAGCACCGCCAAAG 62
 |||||
 QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
 |||||
 Db 63 CCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTGTTTCTGGCGAA 122
 |||||

QY 244 TrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
 DB 123 TGGCAGCCCATCGAGTACGGCAAGAAAGCTGAATACCTGCCCTACCAATCACCAGCAC 182
 QY 264 GluTyrPhePheLeuLeuGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIle 283
 DB 183 GAATACCTTCTTCCTGATTGGCGCGCGCTGCTCATCCCATGTATTTCAGTACCAGATC 242
 QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
 DB 243 ATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCTGGCGCTGAGTACTAC 302
 QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyLeuGlyAlaLeuLeuPheLeu 323
 DB 303 ATCCGGTTCTTCATCACCTACCTATCCCTTTCTAGGCACTCTGGAGCCCTCCTTTTCCTC 362
 QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
 DB 363 AACTTCATCAGGTTCTCGAGAGCCACTGGTTGTGGGTGCACACATGATCATCATC 422
 QY 344 ValMetGluIleAspGlnGlu 350
 DB 423 GTCATGGAGATTGACCAGGAG 443

RESULT 27

US-10-007-805-313

; Sequence 313, Application US/10007805

; Publication No. US20020150581A1

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yugu

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Durham, Margarita

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.470C10

; CURRENT APPLICATION NUMBER: US/10/007,805

; CURRENT FILING DATE: 2001-12-07

; NUMBER OF SEQ ID NOS: 593

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 313

; LENGTH: 456

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-007-805-313

Alignment Scores:

Pred. No.: 4,15e-88 Length: 456

Score: 834.00 Matches: 147

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 34.21% Indels: 0

DB: 14 Gaps: 0

US-09-719-601-5 (1-444) x US-10-007-805-313 (1-456)

QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLys 223
 DB 3 CACTTAAAGGGTGCCTCTGCAACTGGTGAATCATCGGCACCTCCAGCACCAGCAAG 62
 QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
 DB 63 CCTAACATCTTCACAGAGTCCGATGTGAACATGCTGCACGTGTGTCTGGGCGAA 122
 QY 244 TrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263

DB 123 TGGCAGCCCATCGAGTACGGCAAGAAAGCTGAATACCTGCCCTACCAATCACCAGCAC 182
 QY 264 GluTyrPhePheLeuLeuGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIle 283
 DB 183 GAATACCTTCTTCCTGATTGGCGCGCGCTGCTCATCCCATGTATTTCAGTACCAGATC 242
 QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
 DB 243 ATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCTGGCGCTGAGTACTAC 302
 QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyLeuGlyAlaLeuLeuPheLeu 323
 DB 303 ATCCGGTTCTTCATCACCTACCTATCCCTTTCTAGGCACTCTGGAGCCCTCCTTTTCCTC 362
 QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
 DB 363 AACTTCATCAGGTTCTCGAGAGCCACTGGTTGTGGGTGCACACATGATCATCATC 422
 QY 344 ValMetGluIleAspGlnGlu 350
 DB 423 GTCATGGAGATTGACCAGGAG 443

RESULT 28

US-10-076-622-313

; Sequence 313, Application US/10076622

; Publication No. US20030023036A1

; GENERAL INFORMATION:

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Sleath, Paul R.

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.470C11

; CURRENT APPLICATION NUMBER: US/10/076,622

; CURRENT FILING DATE: 2002-02-13

; NUMBER OF SEQ ID NOS: 627

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 313

; LENGTH: 456

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-076-622-313

Alignment Scores:

Pred. No.: 4,15e-88 Length: 456

Score: 834.00 Matches: 147

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 34.21% Indels: 0

DB: 15 Gaps: 0

US-09-719-601-5 (1-444) x US-10-076-622-313 (1-456)

QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLys 223
 DB 3 CACTTAAAGGGTGCCTCTGCAACTGGTGAATCATCGGCACCTCCAGCACCAGCAAG 62
 QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
 DB 63 CCTAACATCTTCACAGAGTCCGATGTGAACATGCTGCACGTGTGTCTGGGCGAA 122
 QY 244 TrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
 DB 123 TGGCAGCCCATCGAGTACGGCAAGAAAGCTGAATACCTGCCCTACCAATCACCAGCAC 182
 QY 264 GluTyrPhePheLeuLeuGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIle 283
 DB 183 GAATACCTTCTTCCTGATTGGCGCGCGCTGCTCATCCCATGTATTTCAGTACCAGATC 242
 QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
 DB 243 ATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCTGGCGCTGAGTACTAC 302

QY 304 ileArgPhePheIleThrTyrlleProPheTyrglyleLeuGlyAlaLeuLeuPheLeu 323
Db 303 ATCCGGTCTTTCATCACATCCCTTTCTAGCGCATCTGGGAGCCCTCTTTTCCTC 362
QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACCTTCATCAGGTCTCTGGAGGACCTGGTTTGTGTGGGTGCACACAGATGAATCATC 422
QY 344 ValMetGluIleAspGlnGlu 350
Db 423 GTCATGGAGATTGACCAGAG 443

RESULT 29

US-09-918-995-29095
; Sequence 29095, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29095
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(453)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-29095

Alignment Scores:
Pred. No.: 5,698-73 Length: 453
Score: 705.00 Matches: 127
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.92% Indels: 0
DB: 11 Gaps: 0

US-09-719-601-5 (1-444) x US-09-918-995-29095 (1-453)

QY 98 GluProSerGlnAspHisGlyIleAsnSerIleThrGluAspPheArgAlaLeuArg 117
Db 73 GAGCCAGCCAGGACACGCGAAGAACTCAAGATCACTGAGGACTTCGCGGCCCTGAGG 132
QY 118 LysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPheLeuLeuLeu 137
Db 133 AAGCGCTGAGGACATGAACCTGTTCAAGACCAACACGCTTCTTCTCTCTCTG 192
QY 138 AlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrglyAsnGly 157
Db 193 GCCCAACATCATCGCCCTGGAGAGCATTCATGCTTCTTACTTTGGCAATGCC 252
QY 158 TrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrp 177
Db 253 TGGATTCCTACCTCATACGCGCTTCTCTGTGTACTCTTCAGGCCCAAGCTGGATGG 312
QY 178 LeuGlnHisAspTyrglyHisLeuSerValTyrglyLysProLysTrpAsnHisLeuVal 197
Db 313 CTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAAACCAAGTGGAAACACCTTGT 372
QY 198 HisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHis 217
Db 373 CACAATTCGTATTGGCCACTTAAGGGTGCTCTGCCAACTGTGGAAATCATCGCCAC 432
QY 218 PheGlnHisAlaLysPro 224

Db 433 TTCCAGCACCAAGCCCAAGCCT 453

RESULT 30

US-10-191-513A-36
; Sequence 36, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US-D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-36

Alignment Scores:
Pred. No.: 5,798-63 Length: 473
Score: 620.00 Matches: 108
Percent Similarity: 81.17% Conservative: 17
Best Local Similarity: 70.13% Mismatches: 29
Query Match: 25.43% Indels: 0
DB: 15 Gaps: 0

US-09-719-601-5 (1-444) x US-10-191-513A-36 (1-473)

QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrlleArgPhePheIleThrTyrl 310
Db 9 AAGAAGTGGGTGGACTTGGCTGGATGATTACCTTCTAGCTCCGCTTCTCTCTACTTAT 68
QY 311 IleProPheTyrglyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
Db 69 GTCCCACTATTGGGCTGAAAGCCTTCTCGGGCCTTTCTTCATAGTCAGGTTCTGGAA 128
QY 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
Db 129 AGCAACTGTTTGTGTGGGTGCACAGATGAACCATATTTCCCATGCACATTGATGAC 188
QY 351 AlaTyrgArgAspTrpPheSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
Db 189 CGGAACATGAGCTGGGTTTCCACCCAGCTCTCGGCCACATGCAATGTCACCAAGTCTGC 248
QY 371 PheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThr 390
Db 249 TTCAATGACTGTTTCTAGTGACACCTCAACTTCCAGATTGAGCACCACCTCTTTTCCCACG 308
QY 391 MetProArgHisAsnLeuHisIleValAlaProLeuValLysSerLeuCysAlaLysHis 410
Db 309 ATGCTTCGACACATATTACCACAAAGGCTCCCTCGGTGGAGTCTCTTGTGTCCCAAGCCT 368
QY 411 GlyIleGlyTyrglnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430
Db 369 GGCATAGAGTACCAAGTCCCAAGCCCTCTGCTGTGTCAGCCTTCGCCGACATCATCCACTCACTA 428
QY 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrlleuHisLys 444
Db 429 AAGGAGTCAGGCGCTCTGGCTAGTATGCTATCTTCACCA 470

RESULT 31
US-10-191-513A-4
; Sequence 4, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-4
Alignment Scores:
Pred. No.: 304 Length: 3,63e-59
Score: 585.00 Matches: 101
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.00% Indels: 0
DB: 15 Gaps: 0
US-09-719-601-5 (1-444) x US-10-191-513A-4 (1-304)
QY 151 ValPheTyrPheGlyAsnGlyTrpLeuThrAlaPheValLeuAlaThr 170
Db 1 GCTTTTACTTTGGCAATGGCTGGATTCCTACCTCATCAGCCCTTTGCTGTACC 60
QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
Db 61 TTCAGGCCCAAGCTGGATGGTGGCAACATGATGATGAGCCCTCTGTCTACAGAAA 120
QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyValaSerAla 210
Db 121 CCCAAGTGGACCACTTGTCCACAAATTCGTCATGGCCACTTAAAGGTGCTCTGCC 180
QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
Db 181 AACTGGTGGAAATCATCGCCACTTCCAGCACCAAGCCCTAACATCTTCCACAAGGAT 240
QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250
Db 241 CCCGATGTGACATGCTGACCTGTTGTTCTGGGGGATGGCAGCCCATCGAGTACGCC 300
QY 251 Lys 251
Db 301 AAG 303
RESULT 32
US-10-191-513A-37
; Sequence 37, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

FILE REFERENCE: 6295 US D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)-(5)
; OTHER INFORMATION: k = g or t/u at position 5
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6)-(6)
; OTHER INFORMATION: m = a or c at position 6
US-10-191-513A-37
Alignment Scores:
Pred. No.: 1,16e-56 Length: 449
Score: 566.00 Matches: 102
Percent Similarity: 83.33% Conservative: 18
Best Local Similarity: 70.83% Mismatches: 24
Query Match: 23.22% Indels: 1
DB: 15 Gaps: 0
US-09-719-601-5 (1-444) x US-10-191-513A-37 (1-449)
QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyLeuGlyAlaLeu 320
Db 9 ACCTTCTAGCTCGCTTCTCTCTCACTATGTCCTACTATGGGCTGAAAGCTTCTCGG 68
QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
Db 69 GCCTTTCTTCATA-GTCAGGTTCTCTGGAAAGCACTGGTTTGTGGGTGACACAGATG 127
QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerGlnLeu 360
Db 128 AACCATATTCCTCATGACATGATGATGACCGGAACATGAGTGGTTTCCACCCAGCTC 187
QY 361 ThrAlaThrCysAsnValGlnGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
Db 188 CAGCCACATGCAATGTCACAGTCTGCCTTCAATGACTGGTTCAGTGGACACCTCAAC 247
QY 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
Db 248 TTCAGATTGAGCACCACATCTTTTCCACGATGCTCGACACAATTACCACAAAGTGCT 307
QY 401 ProLeuValLysSerLeuGlyAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db 308 CCCTGTGTGAGCCTCTGTGTGCGCAAGCATGGCATAGTACAGTCCAGGCCCTCTGTG 367
QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
Db 368 TCAGCCTTCGCCGACATCATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGTAGATGCC 427
QY 441 TyrIleHisLys 444
Db 428 TATCTTCACCAA 439
RESULT 33
US-10-191-513A-3
; Sequence 3, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories

; APPLICANT: Mukerji, Pardip
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Tapas, Das
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295.15.D3

```

, CURRENT_APPLICATION_NUMBER: US/10/191,513A
, CURRENT_FILING_DATE: 2002-09-25
, PRIOR_APPLICATION_NUMBER: US/09/227,613
, PRIOR_FILING_DATE: 1999-01-08
, PRIOR_APPLICATION_NUMBER: PCT/US98/07422
, PRIOR_FILING_DATE: 1998-04-10
, PRIOR_APPLICATION_NUMBER: US 08/833,610
, PRIOR_FILING_DATE: 1997-04-11
, NUMBER_OF_SEQ_ID NOS: 54
, SOFTWARE: FastSEQ for Windows Version 4.0

```

```
; SEQ ID NO 3
;
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-3
```

Alignment Scores:	
Pred. No.:	2,14e-56
Score:	566.00
Percent Similarity:	83.33%
Best Local Similarity:	70.83%
Query Match:	23.22%
DB:	15
	0
Length:	655
Matches:	102
Conservative:	18
Mismatches:	24
Indels:	1
Gaps:	0

US-09-719-601-5 (1-444) x US-10-191-513A-3 (1-655)

Qy	301	Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Hei	Leu	Thr	Tyr	Ile	Pro	Phe	Tyr	Gly	Ile	Leu	Gly	Ala	Leu	320
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Db	3	ACC	TTC	AGT	CCG	GTC	TTC	CCT	CACT	TAT	CGC	CACT	TAT	CGC	CACT	TAT	GGG	GGT	GAA	AGC	TTC	TGG	62

321 LeuPheLeuAsnPheIleAArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340

D _b	63	GCCTTTCTTCATA-GTCAGGTTCTGAAAGCAACTGGTTTGTFGGTGACACAGATG	121
Q _y	341	ASNHISIIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu	360

Db 122 AACCATATTCCTCATGCACATTGATCATGCCGGAACATGGACTGGGTTCCTCCACCCAGCTC 181
:::
Qy 361 ThrAlaIathCysAsnVal[GLUGI]nSerPheAenAsnTTPheSerGLuIstValVal 389

[illegible]

Qy PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnIeuHisLysIleAla 400
 |||||
Db TTCAGATTGAGCACCATTCTTTTCCCGATGCCTCGACACAATTACCAAAAGTGCGT 301
 |||||

[illegible]

DB 302 CCCCTGGTGCACTCCTTGTGTGCCAAGCATGGCATAGATACCAATCCAGCCCTGCTG 361

QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440

Db 362 TCAGCCTTCGCCGACATCATCCACTCACTAAAGAGTCAGGCGAGCTCTGGCTAGATGCC 421
QY 441 TyrLeuHisLys 444

427 444 444
|||||
422 TATCTTCACCA 433

RESULT 34
US-10-029-386-3070/c
; Sequence 3070, Application US/10029386

; Publication No. US20030194704A1
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Penn, Sharron G.
 ;
 ; APPLICANT: Penn, David B.
 ;
 ; APPLICANT: Penn, David B.

; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES US

```

: TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
: FILE REFERENCE: AEOMICA-X-2
: CURRENT APPLICATION NUMBER: US/0029,386
: CURRENT FILING DATE: 2001-12-20
: NUMBER OF SEQ ID NOS: 34288
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 3070
: LENGTH: 567
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO chr11.1
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.4
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.9
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.3
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.9
: OTHER INFORMATION: EST HUMAN HIT: BG696235.1, EVALUATE 1.00e-107
: OTHER INFORMATION: EST SPURD HIT: P32151, EVALUATE 3.20e+00
: OTHER INFORMATION: NT HIT: G14784594, EVALUATE 1.00e-108
: US-10-029-386-3070

```

Alignment Scores:	
Fred. No.:	1.245-48
Score:	499.00
Percent Similarity:	75.3%
Best Local Similarity:	74.63%
Query Match:	20.47%
DB:	13
	1
	13
	Gaps:
	1
	Indels:
	32
	Mismatches:
	2
	Conservative:
	1
	Matches:
	100
	Length:
	567

US-09-719-601-5 (1-444) x US-10-029-386-3070 (1-567)

Qy 104 GlyLysAsnSerIysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMet 123
:::
Db 518 GGTCAACAGCTCAAAGATCACTGAGGACTTCGGGCCCTTGAGGAGACCGCTGAGGACATG 459

QY 124 AsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIleLeuLeu 143

Db	AACCTGTTCAAGACCAACCACGTTGTCTTCCCTCCTCGGCCACATCATCGCCCTG	399
QY	GluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrIeuIle	163

Db	398	GAGAGCATTCGATGGTTCAC	TGCTCTTTACTTTGGCAATGGCTGGATTCTACCCCTCATC	339
Oy	164	ThrAlapheValIleuAlaThrSer	-----	171

171
 104 *mmAlarnev alveu al ih lse l*
 338 *ACGGCCTTTGTCTTGCTACCTC-TCAGGTAGGCGTGACACCTCACCTCCCTAGCTG* 280
 Db

QY 172 -----Gln 172
|||
Db 279 ACAGAGGCGTGCGCTGTTTCTGAGGCTGTGACAGCAGTGTGACCTCTCTCCCCAG 220

QY 173 AlaGlnAlaGlyTyrIleuGlnHisAspTyrGlyHisIleuSerValTyrArgLysProLys 192

DB 219 GCCCAAGCTGGATGGTGCACATGATTATATGGCCACCTGTCTCTCTACAGAAACCCCAAG 160

QY 193 TrpAsnHisLeuValHisLysPheValIleGlyHisLeuLys 206

Db 159 TGGACCACCTGTCTCCACAAATTCGTCATTGGCCACTTAAG 118

RESULT 35

US-09-967-477B-7
; Sequence 7, Application US/09967477B
; Patent No. US20020156254A1

	DATE	TIME	LOCATION
GENERAL INFORMATION:			
APPLICANT: Xiao Qiu			
APPLICANT: Haiping Hong			
TIME OF INTERVIEW	DATE	TIME	LOCATION

; TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
 ;
 ; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
 ; FILE REFERENCE: BNZ-001

```

; CURRENT APPLICATION NUMBER: US/09/967,477B
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/236,303
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/297,562
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Thraustochytrium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1380)
; US-09-967-477B-7

Alignment Scores:
Pred. No.: 96-48      Length: 1380
Score: 497.00      Matches: 132
Percent Similarity: 44.23%      Conservative: 79
Best Local Similarity: 27.67%      Mismatches: 176
Query Match: 20.39%      Indels: 90
DB: 10      Gaps: 16

US-09-719-601-5 (1-444) x US-09-967-477B-7 (1-1380)

QY 22 SerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAspArg 41
Db 37 ACTGGAAGAGATCGCGAGACCGGACCGCGCGCGCGCGGATCGTGAATTCACCAC 96
QY 42 LysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIleGly 61
Db 97 AAGGTCTACGACATCTCCAAAGTGGAC---TCGCACCGCGGTGGCTCC---GTGATGCTC 150
QY 62 HisTyrAlaGlyGluAspAlaThrAspAlaPheHisProAspLeuGluPhe 81
Db 151 AGCAGCGCGCGAGACGCCACGACGCTTCGCGGTCTCCACCCCTCTCCGCGGCTC 210
QY 82 ValGlyLysPheLeuLysProLeuLeuIleGlyGluLeu----- 94
Db 211 -----AAGCTGCTCGAGCAGTTCTACGTGGCGACGTGGACGAAACCTCCAAAGCCGAG 264
QY 95 AlaProGluLysProSerGlnAsp-----HisGlyLysAsnSerLysIleThrGlu--- 111
Db 265 ATCGAGGGGAGCGCGGACGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 324
QY 112 -----AspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsn 129
Db 325 ATCGCGTCTACCGTCTGTCGCGCTCAAGGTCAAGGCGATGGGCTCTACGACGCCAGC 384
QY 130 HisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPhe 149
Db 385 GCGCTCTACTACGCTGAGCTCTGAGCAGTTTCGCGCATCGCGGTGCTCTCGATGCGC 444
QY 150 ThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValIleAla 169
Db 445 ATCTGCTTCTTCTTC---AACAGTTTCGCATGTACATGGTCCGCGCGGTGATATGGG 501
QY 170 ThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArg 189
Db 502 CTCCTTCTACCAAGTCCGGATGGGTGGCGACGACTTCTTGCAACACCAAGCGTGGCGAG 561
QY 190 LysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSer 209
Db 562 AACCGCACGCTCGCAACCTTATCGCTGCTCGTGGGCAACGCTGGCAGGGGCTTCAGC 621
QY 210 AlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIle----- 226
Db 622 GTGCAGTGGTGAAGAACAAAGACAACTGTCACCAACCGCGGTGGCGAACTGCACAGCGCC 681
QY 227 -----PheHisLysAspProAspValAsnMetLeuHisValPheValIleGly 242

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Db 682 AAGGACGAGGGCTTCATCGCGCGACCGGACATCGACACCATG----- 723
QY 243 GluTrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGln 262
Db 724 -----CCGCTGCTGGCGTGTCTAAGGAGATGGCGGCAAGCGGTTCGAGTGGCG 774
QY 263 HisGluTyrPhe-----PheLeuIleGlyProProLeuLeuIlePro 276
Db 775 CACGCGCGGTTCTTCATCCGCAACCGAGCGTCTCTATCTCCCGCTGTGTGCTCGCG 834
QY 277 MetTyr-----PheGlnTyrGlnIle 283
Db 835 CGCCTGAGCTGCTCGCGCAGTCTTCTTCTAGCTGTTCCAGCAGTCTCTGTTGGCATC 894
QY 284 Ile-----MetThrMetIleValHisLysAsnTrp 293
Db 895 TTCGACAAGGTGAGTTCGACGCGGAGAGCGGGTCTGATCGTGACATACATCTCG 954
QY 294 ValAspLeuAlaTrpAlaValSerTyr-----11eArg 305
Db 955 -----CAGCTCGGATCCGTTACTTCTGCAACATGAGCTGTTTGGGGCGTGGCA 1005
QY 306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db 1006 TACTTCTCATGGCGCCAGCGCTCTCGCGCTTGTCTCTCGCGCTGTGTGTTTC----- 1056
QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
Db 1057 -----AGTATTGGCCACCAACGCGCATG 1077
QY 346 GluIle---AspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCys 364
Db 1078 TCGGTGTACGAGCGCGCAACCAAGCGGACTTCTTGGCAGCTGACGACGCGCGC 1137
QY 365 AsnValGluLysSerPheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGlu 384
Db 1138 ACATCCGCGCGTGGTATTTCAGTCTGTTCCCGCGGTGTTGAACTTACCAGATCGAC 1197
QY 385 HisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLys 404
Db 1198 CATCAGCTGTTCGCGTCTGTCGCGCCCAACTTGCCAAAGGTCAACGCTGCTCATCAAG 1257
QY 405 SerLeuCyAlaLysHisGlyIleGluTyrGlnGluLysPheLeuArgAlaLeuLeu 424
Db 1258 TCCTATGCAAGAGTTCGACATCCCGTTCACGAGACCGCGTTCGGAGGCGCATCTAC 1317
QY 425 AspIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyr 441
Db 1318 GAGGTGCTGGACCACTGCGCGGACATCAGCAAGGAATTCATCACCAGGTTTC 1368

RESULT 36
US-09-769-863-13
; Sequence 13, Application US/09769863
; Publication No. US20030157144A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DEGRADABLE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
; US-09-769-863-13

```

Alignment Scores:
 Pred. No.: 1,15e-46 Length: 1362
 Score: 487.50 Matches: 133
 Percent Similarity: 47.27% Conservatives: 92
 Best Local Similarity: 27.94% Mismatches: 164
 Query Match: 20.00% Indels: 87
 DB: 13 Gaps: 19

US-09-719-601-5 (1-444) x US-09-769-863-13 (1-1362)

QY 7 GlnGlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGluGluLe 26
 DB 7 CAGGGCCAAAGGCGGAGAG-----ATCTCGTGGCGGACCATC 45

QY 27 GlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyAsnIle 46
 DB 46 CGTGAGCAACACCGCAAGACACCGGTGGATCGTATCCACCAAGAGGTGTACGACATC 105

QY 47 ThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyAlaGlyGlu 66
 DB 106 TCGGCTTTGAG---GACCACCCGGGGCGGCTC---GTCATGTTTCACGCGGGCGGCGAA 159

QY 67 AspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeu 86
 DB 160 GACGCGACCGATGGTTCGCTCTTCACCCGAGCTCGGGCTC-----AGCTCCTC 213

QY 87 LysProLeuLeuIleGlyGluLeu-----AlaProGluGluProSerGln 101
 DB 214 GACGAGTACTACGTGGCGGACGTGACGACGAGTCGACGGCGGCGGACGATCTCG 273

QY 102 AsHisGlyLysAsnSerLys-----IleThrGluAspPheArgAlaLeuArgLysThr 119
 DB 274 GACGAGGTCAAGAGGACGACGACGCTTCATCTCGTCTGACCGCAAGCTCGGCTTGAA 333

QY 120 AlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHis 139
 DB 334 GTCAAGCCCTCGGCTTGTGACGCTCGAGCAAGCTCTACTACTCTCAAGTGGCGCTCG 393

QY 140 IleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyPheGlyAsnGlyTrpIle 159
 DB 394 ACCTGAGCATGGCTGTGTGCGGCGCCATTGGCTCCACTTT---GACTCGACGGCC 450

QY 160 ProThrLeuIleThrAlaPheValPheAlaThrSerGlnAlaGlnAlaGlyTrpLeuGln 179
 DB 451 ATGTACATGTCGGCGCTGTATCTTGGCTCTTTACCAGCAGTCGCGCTGGCTGCC 510

QY 180 HisAspTyGlyHisLeuSerValTyArgLysProLysTrpAsnHisLeuValHisLys 199
 DB 511 CATGACTTTCGACCAACCAAGTGTGAG-----AACCACTTGTGTGGCGAC 558

QY 200 PheVal-----IleGlyHisLeu---LysGlyAlaSerAlaAsnTrpTrpAsnHis 215
 DB 559 CTCGTGCGGTCATGTCGGCAACCTCTGGCAGGCTTCTCGGTGCAAGTGTGGAAGAC 618

QY 216 ArgHisPheGlnHisHisAlaLysProAsnIle-----PheHis 228
 DB 619 AAGCACAAACACGACCATTCGATCCCACTCCACCGCAGCCGCGGAGATCGCTTCCAC 678

QY 229 LysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGlu 248
 DB 679 GGCGACCGGACATGACACGATCGCATCTCGG-----TGG-----717

QY 249 TyrGlyLysLysLysLeuLysTyLeuProTyAsnHisGlnHisGluTyPhePheLeu 268
 DB 718 -----TCGCTCAAGATGGCG-----CAGCACGGGTCGACTCGGCC 753

QY 269 IleGlyProProLeuLeuIleProMetTyPheGlnTyGlnIleMetThrMetIle 288
 DB 754 GTCGGG-----CTCTTCTTCATGGCTTACCACCGTACTTCTTCCATCTTG 804

QY 289 ValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyTyTyTyTyTyTyTyTyTy 308
 DB 805 CTC-----TTTGGCGGTATCTCGTGGGTGATCCAGTCGGCCCATGTACGCGCTTCTAC 855

QY 309 ThrTyIlePro-----312

DB 856 AACGTTGGCCCGCGGCACCTTTGACAAAGTCCAGTACCCTGCTCGAGCGCCGCGC 915

QY 313 -----PheTyGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeu 329
 DB 916 CTCCTCTCTACTACGGCTGGAACTCGGCTTGTGTAGCGACCAACATGTCGCTGCTC 975

QY 330 GluSerHisTrpPheValTrpValThrGln-----339

DB 976 CAAGCGCTGCTCTCTCTTTGTGAGCCAGCGCTGTCGCGCTCTTCTCTCGCATGTCTC 1035

QY 340 -----MetAsnHisIleValMetGluIle---AspGlnGluAlaTyArgAspTrpPhe 356
 DB 1036 TTTAGCGTCGCCACAAACGGCATGGAGTCTTTGACAGGACAGCAAGCCGATTTTGG 1095

QY 357 SerSerGlnLeuLeuAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSer 376
 DB 1096 AAGCTGCAAGTCTCTCGACGCGCAACGTGACGTCTGCTGCTGCTGCTGCTGCTGCT 1155

QY 377 GlyHisLeuAsnPheGlnIleGluHisIleLeuPheProThrMetProArgHisAsnLeu 396
 DB 1156 GCGGCTCACTACATGATCGACCACTTGTTCCTGATGTCGTCGCGGCAACCTC 1215

QY 397 HisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyGlnGlu 416
 DB 1216 CCGGCGCTCAACGTCTCTCAAGTCTCTGCAAGCAGTACGACATCCCATACCAGCAG 1275

QY 417 LysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLys 432
 DB 1276 ACGGCTTCATCGCGGATGCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1323

RESULT 37
 US-10-054-534B-13
 ; Sequence 13, Application US/10054534B
 ; Publication No. US20030167525A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradip
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer M.
 ; APPLICANT: Persira, Suzette L.
 ; TITLE OF INVENTION: DSATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763.US.P1
 ; CURRENT APPLICATION NUMBER: US/10/054,534B
 ; PRIOR FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: US 09/769,863
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 1362
 ; TYPE: DNA
 ; ORGANISM: Saprolegnia diclina
 US-10-054-534B-13

Alignment Scores:
 Pred. No.: 1,15e-46 Length: 1362
 Score: 487.50 Matches: 133
 Percent Similarity: 47.27% Conservatives: 92
 Best Local Similarity: 27.94% Mismatches: 164
 Query Match: 20.00% Indels: 87
 DB: 13 Gaps: 19

US-09-719-601-5 (1-444) x US-10-054-534B-13 (1-1362)

QY 7 GlnGlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGluGluLe 26
 DB 7 CAGGGCCAAAGGCGGAGAG-----ATCTCGTGGCGGACCATC 45

QY 27 GlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyAsnIle 46
 DB 46 CGTGAGCAACACCGCAAGACACCGGTGGATCGTATCCACCAAGAGGTGTACGACATC 105

QY 47 ThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyAlaGlyGlu 66
 DB 106 TCGGCTTTGAG---GACCACCCGGGGCGGCTC---GTCATGTTTCACGCGGGCGGCGAA 159

QY 67 AspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeu 86
 DB 160 GACGCGACCGATGGTTCGCTCTTCACCCGAGCTCGGGCTC-----AGCTCCTC 213

QY 87 LysProLeuLeuIleGlyGluLeu-----AlaProGluGluProSerGln 101
 DB 214 GACGAGTACTACGTGGCGGACGTGACGACGAGTCGACGGCGGCGGACGATCTCG 273

QY 102 AsHisGlyLysAsnSerLys-----IleThrGluAspPheArgAlaLeuArgLysThr 119
 DB 274 GACGAGGTCAAGAGGACGACGACGCTTCATCTCGTCTGACCGCAAGCTCGGCTTGAA 333

QY 120 AlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHis 139
 DB 334 GTCAAGCCCTCGGCTTGTGACGCTCGAGCAAGCTCTACTACTCTCAAGTGGCGCTCG 393

QY 140 IleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyPheGlyAsnGlyTrpIle 159
 DB 394 ACCTGAGCATGGCTGTGTGCGGCGCCATTGGCTCCACTTT---GACTCGACGGCC 450

QY 160 ProThrLeuIleThrAlaPheValPheAlaThrSerGlnAlaGlnAlaGlyTrpLeuGln 179
 DB 451 ATGTACATGTCGGCGCTGTATCTTGGCTCTTTACCAGCAGTCGCGCTGGCTGCC 510

QY 180 HisAspTyGlyHisLeuSerValTyArgLysProLysTrpAsnHisLeuValHisLys 199
 DB 511 CATGACTTTCGACCAACCAAGTGTGAG-----AACCACTTGTGTGGCGAC 558

QY 200 PheVal-----IleGlyHisLeu---LysGlyAlaSerAlaAsnTrpTrpAsnHis 215
 DB 559 CTCGTGCGGTCATGTCGGCAACCTCTGGCAGGCTTCTCGGTGCAAGTGTGGAAGAC 618

QY 216 ArgHisPheGlnHisHisAlaLysProAsnIle-----PheHis 228
 DB 619 AAGCACAAACACGACCATTCGATCCCACTCCACCGCAGCCGCGGAGATCGCTTCCAC 678

QY 229 LysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGlu 248
 DB 679 GGCGACCGGACATGACACGATCGCATCTCGG-----TGG-----717

QY 249 TyrGlyLysLysLysLeuLysTyLeuProTyAsnHisGlnHisGluTyPhePheLeu 268
 DB 718 -----TCGCTCAAGATGGCG-----CAGCACGGGTCGACTCGGCC 753

QY 269 IleGlyProProLeuLeuIleProMetTyPheGlnTyGlnIleMetThrMetIle 288
 DB 754 GTCGGG-----CTCTTCTTCATGGCTTACCACCGTACTTCTTCCATCTTG 804

QY 289 ValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyTyTyTyTyTyTyTyTyTy 308
 DB 805 CTC-----TTTGGCGGTATCTCGTGGGTGATCCAGTCGGCCCATGTACGCGCTTCTAC 855


```
Db 46 CTGAGCAACCGCCAGACAAACGGTGGATCGTATCCACCACAAAGGTGTACGACATC 105
Qy 47 ThrLysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyAlaGlyGlu 66
Db 106 TCGGCTTTGAG--GACCACCGCGCGCGGCTC--GTCTGTTTACACGCGCGCGGAA 159
Qy 67 AspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeu 86
Db 160 GACGCGACCGATCGCTTCCTCTCCACCGAGCTCGGCGTC-----AGCTCTCTC 213
Qy 87 LysProLeuLeuIleGlyGluLeu-----AlaProGluGluProSerGln 101
Db 214 GACGAGTACTAGCTCGGCGACCTGACCAGTCGACGCGCGCGCTGACACGCTGCGATCTCG 273
Qy 102 AspHisGlyLysAsnSerLys-----IleThrGluAspPheArgAlaLeuArgLysThr 119
Db 274 GACGAGTCAAGAGAGCCAGTCGGACTTCATTGCTGCTACCGCAAGCTGCGCTTGA 333
Qy 120 AlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHis 139
Db 334 GTCACGCGCTCGGCTTGTACGACTCGAGCAAGCTCTACTACCTCTACAAGTGGCGCTCG 393
Qy 140 IleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyPheGlyAsnGlyTrpIle 159
Db 394 ACCTGAGCATTCGCGCTTGTGCGGCGCATTCGCTCCACTTT--GACTCAGCGGCC 450
Qy 160 ProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGln 179
Db 451 ATGTACATGTCGCGCTCTCATCTCTGCGCTCTTTTACCAGCATGCGGCTGGCTGCC 510
Qy 180 HisAspTyGlyHisLeuSerValTyArgLysProLysTyPheAsnHisLeuValHisLys 199
Db 511 CATGACTTCTGACCAACCAAGTGTGTAG-----AACCACTGTGTGGCGAC 558
Qy 200 PheVal-----IleGlyHisLeu--LysGlyAlaSerAlaAsnTrpTrpAsnHis 215
Db 559 CTCGTCGGGTGTCATGTCGCAACCTCTGCGAGGCTTCTCGTGCAGTGTGGAGAAC 618
Qy 216 ArgHisPheGlnHisAlaLysProAsnIle-----PheHis 228
Db 619 AAGCAACACGACCATGATGATCCCAACCTCCAGCGACGCGCGAGATCGCCTTCCAC 678
Qy 229 LysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGlu 248
Db 679 GCGACCGCGACATTGACACGATGCGGATTCGCG-----TGG----- 717
Qy 249 TyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 268
Db 718 -----TCGCTCAAGATGGCG-----CAGCAGCGGTGCTGACTCGGCC 753
Qy 269 IleGlyProProLeuLeuIleProMetTyPheGlnTyGlnIleIleMetThrMetIle 288
Db 754 GTCGGG-----CTCTTCTTCATGCGCTACCAAGCGTACCTGTACTTCCCATCTTG 804
Qy 289 ValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyTyRyleArgPhePheIle 308
Db 805 CTC-----TTTGGCGATATCTCGTGGGTGATCCAGTCGGCCATGTACGCTCTTAC 855
Qy 309 ThrTyRilePro----- 312
Db 856 AACGTTGGCGCGCGGCGACCTTTGACAGGTCCAGTACCCTGCTGCTGAGCGCGCGGC 915
Qy 313 -----PheTyGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeu 329
Db 916 CTCCTCTCTACTACGCTCGGAACCTCGGCTTGTGTACGACGCCAACATGTGCTGTCTC 975
Qy 330 GluSerHisTrpPheValTrpValThrGln----- 339
Db 976 CAAGCGGCTCGTTCCTCTTTGTGAGCCAGCGCTGTCGGCGCTCTCTCTCGCGATGTC 1035
Qy 340 -----MetAsnHisIleValMetGluIle--AspGlnGluAlaTyArgAspTrpPhe 356
Db 356 -----MetAsnHisIleValMetGluIle--AspGlnGluAlaTyArgAspTrpPhe 356
```

```
Db 1036 TTTAGCGTCGGCCACAAACGGCATGGAGGTCTTTTACAGGACAGCAAGCCGATTTTGG 1095
Qy 357 SerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSer 376
Db 1096 AAGCTCAAGTGTCTTCGACGCGCAACGAGTGCCTGCTGATCGCTGATCGCTGATCG 1155
Qy 377 GlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeu 396
Db 1156 GCGGCGCTCAACTTACAGTACGACCACTTGTTCCTGATGTCGCGCGCACCACTTC 1215
Qy 397 HisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyGlnGlu 416
Db 1216 CCGGCGCTCAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1275
Qy 417 LysProLeuLeuArgAlaLeuAspIleIleArgSerLeuLysLys 432
Db 1276 ACGGCTTTCATCGCGGCGCATGGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1323
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RESULT 38

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US-10-431-952-13
; Sequence 13, Application US/10431952
; Publication No. US2003019073A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/10/431,952
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US/09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
US-10-431-952-13
```

```
Alignment Scores:
Pred. No.: 1,15e-46 Length: 1362
Score: 487.50 Matches: 133
Percent Similarity: 47.27% Conservative: 92
Best Local Similarity: 27.94% Mismatches: 164
Query Match: 20.00% Indels: 87
DB: 13 Gaps: 19
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US-09-719-601-5 (1-444) x US-10-431-952-13 (1-1362)

```
Qy 7 GlnGlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGluGluIle 26
Db 7 CAGGGGCAAAAGCGCGAGAG-----ATCTCGTGGCGGACCATC 45
Qy 27 GlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyAsnIle 46
Db 46 CGTGAGCAACACCGCCCAAGCAACGCGTGTGATCCACCACCAAGGTGTACGACATC 105
Qy 47 ThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyAlaGlyGlu 66
Db 106 TCGGCTTTGAG---GACCACCGCGCGCGCTC---GTCTGTTTACGAGCGCGCGGAA 159
Qy 67 AspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeu 86
Db 160 GACGCGACCGATCGCTTCCTCTCCACCGAGCTCGGCGCTC-----AAGCTCTCTC 213
Qy 87 LysProLeuLeuIleGlyGluLeu-----AlaProGluGluProSerGln 101
Db 214 GACGAGTACTAGCTCGGCGACGCTGACCGAGTCCAGCGGCGCGCTGACAGCTGATCTCG 273
```

QY 102 AsphHisGlyLysAsnSerLys-----IleThrGluAspPheArgAlaLeuAArgLysThr 119
Db 274 GACGAGGTCAAGAGAGCCAGTCGGACTTCATTGCGTCGTACCGCAAGCTGGCCCTTGAA 333
QY 120 AlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHis 139
Db 334 GTCAGGCGCTCGGCTTGTACGACTGAGCAAGCTCTACTACCTCTACAGTCGCGCTCG 393
QY 140 IleIleAlaLeuGluSerIleAlaTrpPheThrValPheThrPheGlyAsnGlyTrpIle 159
Db 394 ACCTGAGCATTCGCTGTTGTCGGCGCCATTTCCTCCACTT---GACTCGAGGGCC 450
QY 160 ProThrIleuLeuThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGln 179
Db 451 ATGTACATGTCGGCTGTCATCTTCCTTGGCTCTTTTACAGCAGTCGCGCTCGCGC 510
QY 180 HisAspTyrrGlyHisLeuSerValTyrrArgLysProLysTrpAsnHisLeuValHisLys 199
Db 511 CATGACTTTCGCACCAACCAAGTGTGTAG-----AACCACTGTTTGGCGAC 558
QY 200 PheVal-----IleGlyHisLeu---LysGlyAlaSerAlaAsnTrpTrpAsnHis 215
Db 559 CTGTCGGCTCATGTCGCGCAACCTCTGCGAGGCTTCTCGGTGCAAGTGTGGAAGAAC 618
QY 216 ArgHisPheGlnHisHisAlaLysProAsnIle-----PheHis 228
Db 619 AAGCACAACAGCAGCATGTCATCCCACTCCAGCGAGCGCCGAGATCGCCTCCAC 678
QY 229 LysAspProAspValAsnMetLeuHisValPheValLeuGlyLutrpGlnProIleGlu 248
Db 679 GCGCAGCCGACATTGACAGATCGCGATTCTCGCG-----TGG----- 717
QY 249 TyrrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 268
Db 718 -----TCGCTCAAGATGGG-----CAGCAGCGGTGACTCGGCC 753
QY 269 IleGlyProProLeuLeuIleProMetTyrrPheGlnTyrrGlnIleMetThrMetIle 288
Db 754 GTGCGG-----CTCTCTCTCATGCGCTACCAAGCGTACCTGACTTCCACTTGG 804
QY 289 ValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrrTyrrIleArgPhePheIle 308
Db 805 CTC-----TTTGGCGTATCTCGTGGTGATCCAGTCGCGCCATGACGCTTCTAC 855
QY 309 ThrTyrrIlePro----- 312
Db 856 AACGTTGGCGCGCGCGCACCTTTGACAAGTCCAGTACCGCTGCTCGAGCGCGCGCGC 915
QY 313 -----PheTyrrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhelleArgPheLeu 329
Db 916 CTCTCTCTTACTACGCTGGAACCTCGGCTTGTGTACGACGCCAACATGTGCTGCTC 975
QY 330 GluSerHisTrpPheValTrpValThrGln----- 339
Db 976 CAAGCGCTCGCTTCTCTTTGTGAGCGAGGCTGTCGGGCTCTTCTCGCATGCTC 1035
QY 340 -----MetAsnHisIleValMetGluIle---AspGlnGluAlaTyrrArgAspTrpPhe 356
Db 1036 TTWAGCTGGCGGCACACCGCATGAGGTCTTTGACAAGCAGCAGCAAGCCGATTTTGG 1095
QY 357 SerSerGlnLeuThrAlaThrCysAsnValGlnInsPhePheAsnAspTrpPheSer 376
Db 1096 AACCTGCAAGTGTCTCGAGCGCCACAGTGCAGCTGCTGATCATCGATGTTTCATG 1155
QY 377 GlyHisLeuAsnPhedGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeu 396
Db 1156 GCGGCGCTCAACTACCAAGATCGACCACTTGTTCCTCCGATGTCGCGCGCACCACTC 1215
QY 397 HisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrrGlnGlu 416
Db 1216 CCGCGCTCAAGTGTCTGATAGTCTCTGCAAGCAGTACGATCCATCCATACCACGAG 1275
QY 417 LysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLys 432

Db 1276 ACGGCTTCATCGCGGGCATGCCGAGGTCGTGTGCACCTCGAGCGC 1323

RESULT 39

US-10-278-391-3
; Sequence 3, Application US/10278391
; Publication No. US20030159164A1
; GENERAL INFORMATION:
; APPLICANT: KOPCHIK, JOHN J.
; KELDER, BRUCE
; HUANG, YUNG-SHENG
; KIRCHNER, STEPHEN J.
; MUKERJI, PRADIP
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
; PRODUCTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,391
; FILING DATE: 23-Oct-2002
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,578
; FILING DATE: 29-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-03349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1374 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-278-391-3

Alignment Scores:
Pred. No.: 2,58e-43 Length: 1374
Score: 459.00 Matches: 118
Percent Similarity: 43.55% Conservative: 88
Best Local Similarity: 24.95% Mismatches: 183
Query Match: 18.83% Indels: 84
DB: 13 Gaps: 14

US-09-719-601-5 (1-444) x US-10-278-391-3 (1-1374)

QY 17 SerValProThrPheSerTrpGluGluIle-----GlnLys 28
Db 16 AGTGTGAGGACGTTTACTCGGCGCGAGGTTTGAATCCGAGGCTCTGATGAGGCAAG 75
QY 29 HisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThrLys 48
Db 76 AAGGATCCGAGGACCCCTTCTTGTATGATCATCGACACCAAGGTGTACGATGTCGCGAG 135
QY 49 TrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAspAla 68

136 TTGCTCCCTGATCATCCGGTGGAGTGTGATCTCAGGCAC---GTTGGCAAGGACGGC 192
 69 ThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysPro 88
 193 ACTGACGCTTTGACACTTTTACCC---GAGGCTGCTGGGAGACTCTTGCCAC 246
 89 LeuLeuIleGlyGluLeuAlaProGluProSerGlnAspHisGlyLysAsnSerLys 108
 247 TTTTACGTTGTGATAT---GACGAGAGCAGCCGATATC---AGATATGATC 297
 109 IleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThr 128
 298 TTTGGGCGGAGTCCGACGCTGATCTGTTTCCAGCTCTCTGCTTACTACGATCT 357
 129 AsnHisValPhePheLeuLeuAlaHisIleLeuLeuGluSerIleAlaTrp 148
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 US-10-029-756-4
 Sequence 4, Application US/10029756
 Publication No. US20020108147A1
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 APPLICANT: Thomas, Terry L.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESS: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/029,756
 FILING DATE: 21-Dec-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/934,254
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 8383ZYXWVU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1685 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
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 US-10-029-756-4
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 Best Local Similarity: 29.02% Mismatches: 182
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Search completed: December 10, 2003, 21:04:18
Job time : 367 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2003, 12:23:27 ; Search time 7608 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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DEFINITION Homo sapiens fatty acid desaturase 2 (FADS2) mRNA, complete cds.
ACCESSION AF084559
VERSION AF084559.1
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3149)
AUTHORS Marquardt A., Stohr H., White K. and Weber B.H.
TITLE cDNA cloning, genomic structure, and chromosomal localization of three members of the human fatty acid desaturase family

JOURNAL Genomics 66 (2), 175-183 (2000).
 MEDLINE 20318619
 PUBMED 10860662
 REFERENCE 2 (bases 1 to 3149)
 AUTHORS Marquardt A., Stoeck H., Passmore, L.A., Kraemer, P., Rivera, A. and Weber, B.H.F.
 TITLE Direct Submission
 JOURNAL Submitted (05-AUG-1998) Institute of Human Genetics, University of Wuerzburg, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany
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Qy	2430	CAGCCAACTCCCTGGCCATTGGCCCCAGGGGACGTGGGCCCTGCAGGCTGTCAGAGGGC	2489
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Qy	2490	ACTGGAGCTGGGAGGTCTCGTCCAGGCCCTCCCCCATCTCGGGGCTGTGTGTGACAGCGCG	2549
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Query Match 96.2%; Score 3064; DB 6; Length 3083;		
Best Local Similarity 99.8%; Pred. No. 0;		
Matches 3078; Conservative 0; Mismatches 5; Indels 1; Gaps 1;		
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DEFINITIONACCESSION
VERSIONKEYWORDS
SOURCE

ORGANISM

REFERENCE
AUTHORSTITLE
JOURNALREFERENCE
AUTHORSTITLE
JOURNAL

COMMENT

FEATURES
source

CDS

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AK074939
AK074939.1 GI:22760711
oligo capping: fis (full insert sequence).
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1

Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S.,
Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,
Kojima, S., Nagahara, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y.,
Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.

NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3083)
Isogai, T. and Otsuki, T.
Direct Submission

Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 252-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- and 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).

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DEFINITION Sequence 2 from Patent EP1035207.
ACCESSION AX035941
VERSION AX035941.1 GI:11191483
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
Marquardt, A. and Weber, B. H.
Cdna molecules of the members of gene family encoding human fatty
acid desaturases and their use in diagnosis and therapy
Patent: EP 1035207-A 2 13-SEP-2000;
JOURNAL

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BASE COUNT 875 a 1230 c 1136 g 848 t
ORIGIN

Query Match 94.2%; Score 2998.2; DB 6; Length 4089;
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Db 1 GGTCAACATCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
QY 220 GCGAGGTCTCGGTGCTCCACCTTCAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 279
Db 61 GCGAGGTCTCGGTGCTCCACCTTCAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
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RESULT 5

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QY	710	GCTGCAACATGATTAGCCACCTGCTGCTCTACAGAAACCCCAAGTGGACACACCTTGT	769		
DB	133	GCTGCAACATGATTAGCCACCTGCTGCTCTACAGAAACCCCAAGTGGACACACCTTGT	192		
QY	770	CCACAAATTCGTCAATTTGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATGCCCA	829		
DB	193	CCACAAATTCGTCAATTTGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATGCCCA	252		
QY	830	CTTCCAGCACACCGCCAGCCCTAAACATCTTCCACAGGATCCCGATGCTGACATGCTGCA	889		
DB	253	CTTCCAGCACACCGCCAGCCCTAAACATCTTCCACAGGATCCCGATGCTGACATGCTGCA	312		
QY	890	CGTGTGTTCTTGGGGAAATGCGACCCATCGAGTACGGCAAGAAAGCTGAATAACCT	949		
DB	313	CGTGTGTTCTTGGGGAAATGCGACCCATCGAGTACGGCAAGAAAGCTGAATAACCT	372		
QY	950	GCCTCAACATCACCGACAGAACTCTTCTCTGATTTGGCGCGCGCTGCTCATCCCCAT	1009		
DB	373	GCCTCAACATCACCGACAGAACTCTTCTCTGATTTGGCGCGCGCTGCTCATCCCCAT	432		
QY	1010	GTAATTTCCAGTACAGATCATCATGACCAATGCTCCATGAACTGGGTGGACCTGGC	1069		
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DB	493	CTGGGCGGTGAGCTACTACATCCGGTCTTTCATCACTTACCTTCTTACGGCATCCT	552		
QY	1130	GGAGGCCCTCTTTCTCTCAAATTCATAGGTTCTGTGAGAGCCACTGGTTGTGGGT	1189		
DB	553	GGAGGCCCTCTTTCTCTCAAATTCATAGGTTCTGTGAGAGCCACTGGTTGTGGGT	612		
QY	1190	CACACAGATGAATCATCGTATGAGATTGACACAGGAGCCCTACCGTACTGGTTTACG	1249		
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DB	673	TAGCCAGCTGACAGCCACTGCGAAGTGGAGAGCTCTTCTTCAACGACTGGTTTACGTTG	732		
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DB	793	CAAGATGCCCCCTGGTGAAGTCTATGTGCGAAGCATGGCATTTGATACAGAGAGAA	852		
QY	1430	GCGGCTACTGAGGGCCCTGCTGACATCATCAGGTCCCTGGAAGAGTCTGGGAAGCTGTG	1489		
DB	853	GCGGCTACTGAGGGCCCTGCTGACATCATCAGGAGACCTGATGAAGTCTGGGAAGCTGTG	912		
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QY	1670	CTCTTCACATCTCCCATAGCACCTGCGCTCATGGACCTGCGCTCCTCCTCAGCCGCA	1729		
DB	1093	CTCTTCACATCTCCCATAGCACCTGCGCTCATGGACCTGCGCTCCTCCTCAGCCGCA	1152		
QY	1730	GCCATCAGCCATGGCCCTCCACGTGCTCTAGCCCTTCTTCCAAAGAGACAGAGGTG	1789		
DB	1153	GCCATCAGCCATGGCCCTCCACGTGCTCTAGCCCTTCTTCCAAAGAGACAGAGGTG	1212		
QY	1790	GCCACCGGGGTGCTCTGCTTACCTCACTCTCTGCCCCCTAAAGATGGGAGGAGACCA	1849		
DB	1213	GCCACCGGGGTGCTCTGCTTACCTCACTCTCTGCCCCCTAAAGATGGGAGGAGACCA	1272		
QY	1850	GCGGTCCATGGGTCTGCGCTGTGAGTCTCCCTTTCAGCTCGGTCTAGGCAATCACCCC	1909		
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DB	1393	CCTGACCCCTCCGGCTTGGCTTCACTCTCCCTGACCGGTGCCATTTGGTCCACCTTTCT	1452		
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DB	1453	AGAGAGGCTGCTTTTGTACAAAGCTCGGTCTCCCTCTGAGCTCGGTAAAGTACCGG	1512		
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DB	1513	AGGCTCTCTTAAAGTCTCCAGGGCCCGGCGGAGACAGCCAGCCGCAACCTTGG	1572		
QY	2150	GCCCTGGAAGAGTCTCTCACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCA	2209		
DB	1573	GCCCTGGAAGAGTCTCTCACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCA	1632		
QY	2210	CCATTCACCGCTCCCAACTTGAGCCTGTGACCTTGGGACCAAGAGGGGAGTCCCTCG	2269		
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DB	1693	TCTCTTGTGACTCAGCAGAGAGCGAGTGGCCACGTTTCAAGGAGGGGCGCGCTGGAGG	1752		
QY	2330	CTCAGCCCAACCTCCAGCTTTCTCAGGGGTGCTGAGGTCCAAGATTCAGAGCAATC	2389		
DB	1753	CTCAGCCCAACCTCCAGCTTTCTCAGGGGTGCTGAGGTCCAAGATTCAGAGCAATC	1812		
QY	2390	TGACCCCTTCTCCAAAGGCTCTGTTATCAGCTGGGCACTGACAGCCAAATCCCTGGCCATTT	2449		
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QY	2450	GGCCCCAGGGGAGCTGGGCCCTGACAGCTGACAGAGGGGCACTGGAGCTGGGAGGTCTCG	2509		
DB	1873	GGCCCCAAGGGGAGCTGGGCCCTGACAGCTGACAGAGGGGCACTGGAGCTGGGAGGTCTCG	1931		
QY	2510	TCCAGGCCCTCCCATCTCGGGGCTGTGTGTGGAAGGGGCTGCCCTCAGGCACTCTCTCTG	2569		
DB	1932	TCCAGGCCCTCCCATCTCGGGGCTGTGTGTGGAAGGGGCTGCCCTCAGGCACTCTCTCTG	1991		
QY	2570	TCTGAACCTGCGCCTTACTGTGTTTAACTGTGTCTCAGGATGCATTTCTATAGGAGGGG	2629		
DB	1992	TCTGAACCTGCGCCTTACTGTGTTTAACTGTGTCTCAGGATGCATTTCTATAGGAGGGG	2051		
QY	2630	GCGGAGGGCTGGGCTTTGTGCAAAATCTGCTTTTACCAATGCGCTTGCCTCGGTGGCC	2689		
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[illegible]

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Qy	2715	GC	AGCGGG	GAGGAG	GTCTC	CAGAGG	AGGCTG	CCCTC	GAGGGG	TGGGGG	AGGGGTAC	27774
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Qy	2835	AG	GGGAC	GGGCA	AGT	TGAGCG	GAGGAG	GGAAGT	CTCTGG	GAGGAT	CTCTCAG	28944
Db	2220	AG	GGGAC	GGGCA	AGT	TGAGCG	GAGGAG	GGAAGT	CTCTGG	GAGGAT	CTCTCAG	22799
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Qy	2955	AA	TGGGGG	CTTT	CGGGG	AGGGCG	CGCTAG	TCCCCC	CAAGCT	CTAA	GCA	30114
Db	2340	AA	TGGGGG	CTTT	CGGGG	AGGGCG	CGCTAG	TCCCCC	CAAGCT	CTAA	GCA	23999
Qy	3015	GC	ATCT	TAAGCAT	TGGGTT	TGCCAT	TGGCAAT	TGGCAAT	TGCCCC	CCAGCT	ACTGTAT	30744
Db	2400	GC	ATCT	TAAGCAT	TGGGTT	TGCCAT	TGGCAAT	TGGCAAT	TGCCCC	CCAGCT	ACTGTAT	24599
Qy	3075	AC	CCCCC	CGAGG	CAGAA	TGAA	CCCA	TAGGG	AGCTG	ATCTCG	TATGTTT	31344
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Db	2520	CCCC	ACCCCT	TACAT	TTTTT	TGAAAT	TAATAA	TAAGGA	ATTTT			2558

RESULT 11

AK074925	AK074925	2558 bp	mrna	linear	PRI 03-SEP-2002
LOCUS	AK074925				
DEFINITION	Homo sapiens cDNA FLJ90444 fis, clone NT2RP3001159.				
ACCESSION	AK074925				
VERSION	AK074925.1	GI:22750689			
KEYWORDS	oligo capping; fis (full insert sequence).				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				

REFERENCE
AUTHORS
1 Isogami, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Cno, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2558)

AUTHORS
Isogai, T. and Otsuki, T.

TITLE Direct Submission

JOURNAL
Submitted (23-MAR-2002)
Genomics Laboratory: 15

genomics@hri.ri.ih.gov
(E-mail:genomics@hri.ri.ih.gov)

COMMENT	NEDO human cDNA sequence

Economy, Trade and Indu

Research Association for

Institute of Medical Sciences
Genetics and Biotechnology Division


```

Db      1920 GCTGTGTGGAGCGCGCTGCCTCAGGCACCTCTCCCTGTCTGAACCTGCCTTACTGTGTGA 1979
Qy      2595 ACCTGTGCTCCAGATGCACTTCTGATAGAGGGGGGGGCGAGGGCTGGGCTTGTGACAA 2654
Db      1980 ACCTGTGCTCCAGATGCACTTCTGATAGAGGGGGGGGCGAGGGCTGGGCTTGTGACAA 2039
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Db      2160 ATGAGGACCGAGGCTGAGAGGAGGAGGAGGCTGGGAGGCTGAGGAGGCTGAGGAGGCTG 2219
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Db      2520 CCCACCCCTACATTTTGTGAATTAATAAGGAATTTT 2558

RESULT 12
LOCUS   BD158110
DEFINITION
Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD158110
VERSION     BD158110.1  GI:27863868
KEYWORDS   JP 2002191363-A/12953.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2190)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 12953 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/12953
PD 09-JUL-2002
PF 28-JUL-2000  JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/00 CC
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PC C12P21/02, C12Q1/68, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC

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Primer for synthesizing full-length cDNA and use thereof FH Key
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ORIGIN

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Db 121 CACCTACATCCCTTTCTACGGCATCTCTGGAGCCCTCCTTTTCTCAACTTCATCAGGTT 180
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AK027513

LOCUS AK027513 2165 bp mRNA linear PRI 01-AUG-2002

DEFINITION Homo sapiens cDNA FLJ14607 f1s, clone NT2RP1000609.

ACCESSION AK027513

VERSION AK027513.1 GI:14042243

KEYWORDS oligo capping; f1s (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Shiratori, A., Sudo, H., Nishikawa, T., Nagai, K., Sugano, S., Kodaira, H., Kondo, H., Wagatsuma, M., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.

TITLE NED0 human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2165)

AUTHORS Isogai, T. and Otsuki, T.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yano, Kisarazu, Chiba 292-0812, Japan

(E-mail: genomics@ri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NED0 human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: 5'- & 3'- end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES

Location/Qualifiers

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BASE COUNT 410 a 655 c 629 g 471 t

ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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RESULT 16
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LOCUS
DEFINITION
Primer for synthesizing full-length cDNA and use thereof.
ACCESSION
BD157807
VERSION
BD157807.1 GI:27863565
KEYWORDS
JP 2002191363-A/12650.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2146)
Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof.
Patent: JP 2002191363-A 12650 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/12650
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12P1/68, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
FT CDS Location/Qualifiers
1. 2146

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BASE COUNT	403 a	651 c	626 g	466 t																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
ORIGIN																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
Query Match	66.9%;	Score	2130.2;	DB 6;	Length	2146;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
Best Local Similarity	99.8%;	Pred. No.	0;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
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QY	1027	T	A	T	C	A	T	G	A	C	T	G	C	T	A	A	A	A	C	T	G	G	T	G	G	A	C	T	G	G	C	T	G	G	C	T	G	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A	C	T	A

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QY	2947	C	A	A	T	C	A	T	C	3006
DB	1920	C	A	A	T	C	A	T	C	1979
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LOCUS Homo sapiens cDNA FLJ14553 f1s, clone NT2RM2001785, highly similar
DEFINITION to Homo sapiens delta-6 fatty acid desaturase mRNA.
ACCESSION AK027459
VERSION AK027459.1 GI:14042148
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Aotsuka,S., Yoshikawa,Y.,
Matsumura,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Makamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Sasaki,N.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2146)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(B-mail:genomics@hri.co.jp, Tel.81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.
FEATURES
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neuronal precursor cells."
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ORIGIN

Query Match 66.9%; Score 2130.2; DB 9; Length 2146;
Best Local Similarity 99.8%; Pred. No. 0;
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QY 2827 GGTACCTCATGAGGAGGAGGAGGCTGAGGAGGAGGAGGAGGCTGGGAGGCTGGGAGG 2886
Db 1800 GGTACCTCATGAGGAGGAGGAGGCTGAGGAGGAGGAGGAGGCTGGGAGGCTGGGAGG 1859
QY 2887 GTGCTGTGAGTCTAACCCCTAATCAGTCTTCTAGATTCAGGGGAGGAGGAGGAGGAGG 2946
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Db 1920 CAATCTCAGAGTGGGCTTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1979
QY 3007 AGGAGCTGCTATCAGGATCTGGGTTGGCATGGCAATGGCATGCCCCCAGGCTACTGTA 3066
Db 1980 AGGAGCTGCTATCAGGATCTGGGTTGGCATGGCAATGGCATGCCCCCAGGCTACTGTA 2039
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AR221960 LOCUS 2257 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 8 from patent US 6428990.
ACCESSION AR221960
VERSION AR221960.1 GI:23329263
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2257)

Mukerji, P., Leonard, A. E. Y., Huang, Y.-S. and Parker-Barnes, J. M.
TITLE Human desaturase gene and uses thereof
JOURNAL Patent: US 6428990-A 9 06-AUG-2002;
LOCATION/Qualifiers

source 1..2257
BASE COUNT 438 a 719 c 504 t
ORIGIN

Query Match 60.9%; Score 1937.6; DB 6; Length 2257;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;

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1970 QY CTTGACCTCCCGGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2029
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RESULT 19
BD082640
LOCUS

DEFINITION 2257 bp DNA linear PAT 27-AUG-2002
Methods and compositions for synthesis of long chain
poly-unsaturated fatty acids.

ACCESSION BD082640
VERSION BD082640.1 GI:22628250
KEYWORDS JP 2001523091-A/20.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE

1. (bases 1 to 2257)
Knutzon, D.; Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and
Loenard, A.E.Y.

TITLE

Methods and compositions for synthesis of long chain

poly-unsaturated fatty acids

Patent: JP 2001523091-A 20 20-NOV-2001;

CALGENE LLC, ABBOTT LABORATORIES

PN JP 2001523091-A/20

PD 20-NOV-2001

PF 10-APR-1998 JP 1998544053

PR 11-APR-1997 US 08/834655

PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI

THURMOND,

PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD

PC C12N15/53, C12N15/81, C12N9/02, C12N5/10, C12N1/19, C12P7/64 PC

, C11B1/00, A61K31/20,

PC A23L1/30

CC Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers.

Location/Qualifiers

1. 2257

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/mol_type="genomic DNA"

/db_xref="taxon:32644"

BASE COUNT 438 a 719 c 596 g 504 t

ORIGIN

FEATURES

source

Query Match

Best Local Similarity

Matches 2066; Conservative

60.9%; Score 1937.6; DB 6; Length 2257;

92.1%; Pred. No. 0;

Mismatches 174; Indels 4; Gaps 2;

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15 GCGCTACTTCACTTCCCTGGGAGCGAGGTGGCCAGCGCTCAGGGTGGGAGGCGGTGGCTAGT 74

293 CATTGACCGCAGGTTTACACATCACCAATGGTCCATCCAGACCCGGGGGGCCAGCG 352

75 GATCGACCGTAAGGTGTACACATCAGCGAGTTTACCCCGCGGCATCCAGGGGCTCCCG 134

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413 CTTGGAATTTGTTGGGCAAGTCTTTGAAACCCCTGCTGATTGGTGAACCTGCCCGGAGGA 472

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Qy	533	GACGGCTGAGGACATGAACCTGTTCAAGACCAACACGCTGTTCTTCTCTCTCTCTCTGCG	592
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Qy	890	CGTGTTTGTTCTGGCGCAATGGCAGCCCATCGAGTACGGCAAGAGAAGCTGAAATACCT	949
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Qy	1490	GCTTGGAGCCTTACTTTCACAAATGAAGCCACAGCCCCGGGACACCTGTGGGGAAGGGGTG	1549
Db	1275	GCTTGGAGCCTTACTTTCACAAATGAAGCCACAGCCCCGGGACACCTGTGGGGAAGGGGTG	1334

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QY	1610	GGTGTATGCACCTGCTCAGCGACCCCATGTTGGATCTTTTCTCCCTTTCTCTCTCTCTTTT	1669
DB	1395	GGTGTATGCACCTGCTCAGCGACCCCATGTTGGATCTTTTCTCCCTTTCTCTCTCTCTTTT	1454
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DB	1695	CGCTTGGTTCCTCAGATGCTCTTGGGGTTCATAGGGGCGAGTCTAGTCGGGCGAGGCC	1754
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DB	1815	AGAGAGCCCTGCTTTGTATCAAAGCTCGGGTCTCCCTCTGSCAGCTCGGTAAAGTACCCG	1874
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DB	1875	AGGCTCTCTTAAGATGTCAGAGGCCCCAGGCCCGCGGGGCACAGCCAGCCCAACCTTGG	1934
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DB	1935	GCCTGGAAGAGTCTCCACCCCATCACTAGAGTGTCTCTGACCTGGGCTTTCACGGGCC	1994
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RESULT 20	ACCESSION
BD082655	VERSION
LOCUS	
DEFINITION	

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KEYWORDS      JP 2001523092-A/15.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 2257)
AUTHORS        Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and
                Leonard,A.E.Y.
TITLE          Methods and compositions for synthesis of long chain
                polyunsaturated fatty acids
JOURNAL        CALGENE LLC,ABBOTT LABORATORIES
COMMENT        PN JP 2001523092-A/15
                PD 20-NOV-2001
                PF 10-APR-1998 JP 1998544176
                PR 11-APR-1997 US 08/833610
                PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
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ORIGIN

Query Match      60.9%; Score 1937.6; DB 6; Length 2257;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;

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QY 293 CATTGACCGCAGGTTTACAACTACCAATGGTTCATCCAGCACCCCGGGGGCCAGCG 352
DB 75 GATCGACCGTAAAGGTGTACAACTCAGCGATTACCGCGCGCATCCAGGGGGTCCCG 134

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BD092934 2257 bp DNA linear PAT 27-AUG-2002
 LOCUS Methods and compositions for synthesis of long chain
 DEFINITION polyunsaturated fatty acids in plants.
 ACCESSION BD092934
 VERSION BD092934
 KEYWORDS JP 2001527395-A/21
 SOURCE JP 2001527395-A/21
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 2257)
 AUTHORS Knutson, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Leonard, A.E.Y.
 TITLE Methods and compositions for synthesis of long chain
 JOURNAL polyunsaturated fatty acids in plants
 PATENT: JP 2001527395-A 21 25-DEC-2001;
 CALGENE LLC, ABBOTT LABORATORIES
 COMMENT PN JP 2001527395-A/21
 PD 25-DEC-2001
 PF 10-APR-1998 JP 1998544175
 PR 11-APR-1997 US 08/833610, 11-APR-1997 US 08/834033 PR
 11-APR-1997 US 08/834655, 24-OCT-1997 US 08/956985 PI
 DEBORAH KNUTSON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
 THURMOND,
 PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
 PC
 C12N15/53, C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
 30, A23K1/00
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CC Topology: Linear; Location/Qualifiers.
 FH Key Location/Qualifiers
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 BASE COUNT 438 a 719 c 596 g 504 t
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 Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;

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DEFINITION Sequence 7 from patent US 6428990.
ACCESSION AR221959
VERSION AR221959.1 GI:23329262
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1843)
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.
TITLE Human desaturase gene and uses thereof
JOURNAL Patent: US 6428990-A 7 06-AUG-2002;
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BASE COUNT 356 a 598 c 466 g 423 t
ORIGIN

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RESULT 24

BD082654
LOCUS

DEFINITION

ACCESSION

VERSION
KEYWORDS

KEYWORDS
SOURCE

ORGANISMS

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

11

BD082654
1947 Jan
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Methods and compositions for synthesis of long chain

polyunsaturated fatty acids.
BD082654

BD082654.1 GI:22628264

JP 2001523092-A/14.
unidentified

unclassified
unclassified

1 (bases 1 to 1843)

Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Leonard, A.E.Y.

Methods and compositions for synthesis of long chain

polyunsaturated fatty acids
Patent: JP 2001523092-A 14 20-NOV-2001;

CALGENE LLC, ABBOTT LABORATORIES
PN JP 2001523092-2/14

PD 20-NOV-2001

FF 10-APR-1998 JP 1998544176
PR 11-APR-1997 US 08/833610

PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THIRUMON

PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD

PC
C12N15/53.C12N15/83.C12N5/10.C12P7/64.C11B1/00.A61K31/20.A23L1/00

RECEIVED: 1967-01-10

ACCESSION	BD092933
VERSION	BD092933.1 GI:22638544
KEYWORDS	JP 2001527395-A/20.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	1 (bases 1 to 1843).
AUTHORS	Knutson,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Leonard,A.E.Y.
TITLE	Methods and compositions for synthesis of long chain polyunsaturated fatty acids in plants
JOURNAL	Patent: JP 2001527395-A 20-DEC-2001;
COMMENT	CALGENE LLC, ABBOTT LABORATORIES
	PN JP 2001527395-A/20
	PD 25-DEC-2001
	PF 10-APR-1998 JP 1998544175
	PR 11-APR-1997 US 08/833610,11-APR-1997 US 08/834033 PR
	11-APR-1997 US 08/834655,24-OCT-1997 US 08/956985 PI
	DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
	THURMOND,
	PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
	PC
	C12N15/53, C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/30, A23K1/00
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QY	990 CGCGCGCTGCTCATCCCCCATGATTTCAGTACCATCATATGACCATGATCGTCCAT 1049
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Db 1681 GGGGCGGCGTGGCTGGAGGCTCAGCCACCTCCAGCTTTTCTTCAGGAGTGTCTCAGG 1740
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RESULT 26
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DEFINITION Homo sapiens chromosome 11 clone CTD-3231N5 map 11, WORKING DRAFT
AC084857
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Biren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone CTD-3231N5
Unpublished
2 (bases 1 to 133683)
Biren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavsky,L.,
Boukhalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepe,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,
Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
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Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G.,
Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
O'Donnell,P., O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
Sougnex,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Travers,M., Triglio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-NOV-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: l11038
Center clone name: 3231.N.5
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

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Consensus quality: 126761 bases at least Q40
 Consensus quality: 129952 bases at least Q30
 Consensus quality: 131351 bases at least Q20
 Insert size: 128000; agarose-1p
 Insert size: 132483; sum-of-contigs
 Quality coverage: 6.1 in Q20 bases; agarose-1p
 Quality coverage: 5.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 13 contigs. the true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 * 1460 1559: gap of 100 bp
 * 1560 2520: contig of 961 bp in length
 * 2521 2620: gap of 100 bp
 * 2621 6334: contig of 3714 bp in length
 * 6335 6434: gap of 100 bp
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 * 11914 12013: gap of 100 bp
 * 12014 20756: contig of 8743 bp in length
 * 20757 29735: contig of 8879 bp in length
 * 29736 29835: gap of 100 bp
 * 29836 38645: contig of 8810 bp in length
 * 38646 38745: gap of 100 bp
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 * 52194 52293: gap of 100 bp
 * 52294 65209: contig of 12916 bp in length
 * 65210 65309: gap of 100 bp
 * 65310 79796: contig of 14487 bp in length
 * 79797 79896: gap of 100 bp
 * 79897 95896: contig of 16000 bp in length
 * 95897 113419: contig of 17423 bp in length
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 * 113520 133683: contig of 20164 bp in length.

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Matches 1721; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

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VERSION AF139813.1 GI:4633837
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 142092)
AUTHORS Petukhin,K., Koisman,M.J., Bakall,B., Li,W., Xie,G., Marknell,T.,
Sandgren,O., Forsman,K., Holmgren,G., Andreasson,S., Vujic,M.,
Bergen,A.A., McGarty-Dugan,V., Figueroa,D., Austin,C.P.,
Metzker,M.L., Caskey,C.T. and Wadelius,C.
IDENTIFICATION of the gene responsible for Best macular dystrophy
Nat. Genet. 19 (3), 241-247 (1998)
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MEDLINE 98324772
PUBMED 9662395
REFERENCE 2 (bases 1 to 142092)
AUTHORS McGarty-Dugan,V.A., Hammond,H.A., Clement,M.K., Larson,D.R.,
Liu,X., Soderman,A.R., McGowan,J.M., DeAngelis,D.M., Lin,C.,
Fitzpatrick,E.S., Harrison,K.M., Petrukhin,K., Caskey,C.T. and
Metzker,M.L.
TITLE Direct Submision
JOURNAL Submitted (01-APR-1999) Department of Human Genetics, Merck & Co.,
Inc., Summeytown Pike, West Point, PA 19486, USA
REMARK IMPORTANT: This submission contains the entire insert of clone
PDJ759j12 which comes from a PAC library constructed at the Roswell
Park Cancer Institute by the Pieter de Jong group. This clone has
been finished according to strict quality criteria and attempts
have been made to resolve all base calling problems such as
compressions and repetitive elements. This sequence has been
finished such that all consensus base calls consist of two or more
separate clones with double-stranded coverage or two or more
separate clones with two types of sequencing chemistry. The
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VERSION AC004770
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 185035)
AUTHORS Lamerdin,J.E., McCreedy,P.M., Coleman,M., Skowronski,E., Adamson,A.W., Burkhardt-Schultz,K., Gordon,L., Kyle,A., Ramirez,M., Stilwagen,S., Phan,H., Velasco,N., Do,L., Regala,W., Terry,A., Gaines,J., Danganan,L., Poundstone,P., Christensen,M., Georgescu,A., Avila,J., Liu,S., Attix,C., Andreise,T., Trankheim,M., Amico-Keller,G., Coefield,J., Duarte,S., Lucas,S., Bruce,R., Thomas,P., Quan,G., Kronmiller,B., Arellano,A., Montgomery,M., Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S. and Carrano,A.V.
SEQUENCE ANALYSIS of a human BAC containing the FEN1 DNA repair gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 185035)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
REFERENCE 3 (bases 1 to 185035)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
COMMENT On Jun 12, 1998 this sequence version replaced gi:3169154.
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
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Direct Submission
Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
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AUTHORS				
Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,				
Totoki,Y., Watanabe,H. and Sakaki,Y.				
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JOURNAL				
Published Only in Database (2003)				
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AUTHORS				
Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,				
Totoki,Y., Watanabe,H. and Sakaki,Y.				
TITLE				
Direct Submission				
JOURNAL				
Submitted (27-FEB-2003) Masahira Hattori, The Institute of Physical				
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);				
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan				
[E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,				
Tel:81-45-503-9111, Fax:81-45-503-9170]				
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Quality coverage: 4.0ix in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

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68000 74526 contig of 6428 bp in length
74527 81299 contig of 6673 bp in length
81300 87316 contig of 5917 bp in length
87317 91541 contig of 4125 bp in length
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104949 105048 contig of 1109 bp in length
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Sequence updated (20-Oct-1999)

NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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Qy	1442	GGCCCTGCTGGGACATCATCAGGTCCTCTGAAGAAAGTCTGGGAAGCTGTGGCTGGAGCGCTTA	1501
Db	38909	GGTCCATCCCAACTTTTGAGGTCCTCTGAAGAAAGTCTGGGAAGCTGTGGCTGGAGCGCTTA	38850
Qy	1502	CCTTCACAAATGAAGCCACAGACCCCGGACACCGTGGGGGAAGGGTGACAGTGGGGTGA	1561
Db	38849	CCTTCACAAATGAAGCCACAGACCCCGGACACTGTGGGAAGGGTGACAGTGGGGTGA	38790
Qy	1562	TGGCCAGAGGAATGATGGGCTTTTGTCTTGAGGGGTGTCGAGAGGCTGGTGTATGCACT	1621
Db	38789	TGGCCAGAGGAATGATGGGCTTTTGTCTTGAGGGGTGCCGAGAGGCTGGTGTATGCACT	38730
Qy	1622	GCTCAGGGACCCCATGTTGGATCTTTCTCCCTTTCCTCTCTCTCTCTCTCTCTCTCTCTCACT	1681
Db	38729	GCTCAGGGACCCCATGTTGGATCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCACT	38670
Qy	1682	CCCCATAGCACCCCTGCCCTCATGGACCTGCGCTCCCTCAGCCCTCAGCCATCAGCCAT	1741
Db	38669	CCCCATAGCACCCCTGCCCTCATGGACCTGCGCTCCCTCAGCCCTCAGCCATCAGCCAT	38610
Qy	1742	GGCCCTCCAGTGCCTCTAGGCCCTTTCTCAAGAGCAGAGAGGTGGCCACCGGGGT	1801
Db	38609	GGCCCTCCAGTGCCTCTAGGCCCTTTCTCAAGAGCAGAGAGGTGGCCACCGGGGT	38550
Qy	1802	GGCTCTGTCTACTCCACTCTCTGCGCCCTTAAAGATGGAGAGACACGCGTCCATGGG	1861
Db	38549	GGCTCTGTCTACTCCACTCTCTGCGCCCTTAAAGATGGAGAGACACGCGTCCATGGG	38490
Qy	1862	CTTGGCCTGTGAGTCTCCCTTTGCAGCCTGTGCTACTAGGCATCAGCCCGCTTTGGTTCT	1921
Db	38489	CTTGGCCTGTGAGTCTCCCTTTGCAGCCTGGTCACTAGGCATCAGCCCGCTTTGGTTCT	38430
Qy	1922	TCAGATGCTCTTGGGGTTTCATAGGGCAGGTCGTAGTGGGGCAGGGCCCTGACCTGCC	1981
Db	38429	TCAGATGCTCTTGGGGTTTCATAGGGCAGGTCGTAGTGGGGCAGGGCCCTGACCTGCC	38370
Qy	1982	GGCCTGGCTTCACTCTCCCTGACGGTGCATTTGTCACCTTTCATAGAGAGGCCCTGC	2041
Db	38369	GGCCTGGCTTCACTCTCCCTGACGGTGCATTTGTCACCTTTCATAGAGAGGCCCTGC	38310
Qy	2042	TTTGTTCACAAAGCTCGGGTCTCCCTCTCAGCTGGTTAAGTACCCGAGGCTCTCTTA	2101
Db	38309	TTTGTTCACAAAGCTCGGGTCTCCCTCTCAGCTGGTTAAGTACCCGAGGCTCTCTTA	38250
Qy	2102	AGATGTCCAGGGCCCCAGGCCCGGGGCACAGCCAGCCCAAACCTTGGCCCTGGAAGAG	2161
Db	38249	AGATGTCCAGGGCCCCAGGCCCGGGGCACAGCCAGCCCAAACCTTGGCCCTGGAAGAG	38190
Qy	2162	TCCTCCACCCCATCACTAGAGTCTCTGACCTTGGGCTTTCACGGGCCCATTCACCGC	2221
Db	38189	TCCTCCACCCCATCACTAGAGTCTCTGACCTTGGGCTTTCACGGGCCCATTCACCGC	38131
Qy	2222	CTCCCAACTTGAGCCTGTGACCTTGGGACCAAGGGGAGTCCCTGCTCTCTTGTGACT	2281
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TITLE Human desaturase gene and uses thereof
JOURNAL Patent: US 6428990-A 6 06-AUG-2002;
FEATURES Location/Qualifiers
1. 1686
source /organism="unknown"

BASE COUNT 322 a 551 c 435 g 378 t
ORIGIN

Query Match 52.6%; Score 1675; DB 6; Length 1686;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 967 ACGAATATCTTCTCTGATTTGGCGCGCTGCTCATCCCATGTATTTCCAGTACAGCA 1026
DB 181 ACGAATATCTTCTCTGATTTGGCGCGCTGCTCATCCCATGTATTTCCAGTACAGCA 240
QY 1027 TCATCATGACCATGATCGTCCATGAAGAACTGGGTGAGACCTGGCGCTGAGCTACT 1086
DB 241 TCATCATGACCATGATCGTCCATGAAGAACTGGGTGAGACCTGGCGCTGAGCTACT 300
QY 1087 ACATCCGGTCTTTCATCACCTPACATCCCTTTACGGCATCTCTGGAGCCCTCTTTTC 1146
DB 301 ACATCCGGTCTTTCATCACCTPACATCCCTTTACGGCATCTCTGGAGCCCTCTTTTC 360
QY 1147 TCAACTTCATCAGGTTCTTGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCA 1206
DB 361 TCAACTTCATCAGGTTCTTGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCA 420
QY 1207 TCGTCATGGAGATGACGAGAGCCCTACCGTACCTGGTTCAGTACGAGCTGACAGCA 1266
DB 421 TCGTCATGGAGATGACGAGAGCCCTACCGTACCTGGTTCAGTACGAGCTGACAGCA 480
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DB 481 CTTGCAACGTGGAGCAGTCTCTTCAACAGCTGGTTCACTGACACCTTAACCTTCCAGA 540
QY 1327 TTGAGCACCACTTCTCCCAACATGCCCCGAGCAACTTACAAAGATCGCCCCGCTGG 1386
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DB 601 TGAAGTCTATGTGCAAGCAGTGGATTTGAATACCAAGAGAGCGCTACTGAGGGCCC 660
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QY 1567 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGGTGTATGACCTGCTCA 1626
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DB 841 CGGACCCCATGTTGGATCTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
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DB 1321 TCCAGGGCCCCCAGGGCCCCGGGCGCACAGCCAGCCCAACCTTTGGGCTTGGAGAGTCTCTC 1380
QY 2167 CACCCCATCATAGAGTCTGCTGAGCTGGGCTTTCAGGGCCCCCATTCACCGGCTCCC 2226
DB 1381 CACCCCATCATAGAGTCTGCTGAGCTGGGCTTTCAGGGCCCCCATTCACCGGCTCCC 1440
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DB 1441 CAACTTGAAGCTGTGACCTTGGGACCAAGGGGAGTCCCTGCTCTCTGTGACTCAGCA 1500
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QY 2467 GGCCTGT 2473
DB 1680 GGCCTGT 1686

RESULT 34
BD082638

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

BD082638 1686 bp DNA linear PAT 27-AUG-2002
Methods and compositions for synthesis of long chain
poly-unsaturated fatty acids.

BD082638

BD082638.1 GI:22628248

JP 2001523091-A/18.

unidentified

unclassified.

1 (bases 1 to 1686)

Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and

Loenard, A.E.Y.

Methods and compositions for synthesis of long chain

poly-unsaturated fatty acids

Patent: JP 2001523091-A 18 20-NOV-2001;

COMMENT		CALGENE LLC, ABBOTT LABORATORIES	
PN	JP 2001523091-A/18	PN	JP 2001523091-A/18
PD	20-NOV-2001	PD	20-NOV-2001
PF	10-APR-1998 JP 1998544053	PF	10-APR-1998 JP 1998544053
PI	11-APR-1997 US 08/834655	PI	11-APR-1997 US 08/834655
THURMOND,		THURMOND,	
PI	SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD	PI	SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD
PC	C12N15/53, C12N15/81, C12N9/02, C12N5/10, C12N1/19, C12P7/64 PC	PC	C12N15/53, C12N15/81, C12N9/02, C12N5/10, C12N1/19, C12P7/64 PC
PC	, C11B1/00, A61K31/20,	PC	, C11B1/00, A61K31/20,
CC	A23L1/30	CC	A23L1/30
CC	Strandedness: Single;	CC	Strandedness: Single;
CC	Topology: Linear;	CC	Topology: Linear;
EH	Key	EH	Key
FEATURES		FEATURES	
source	Location/Qualifiers.	source	Location/Qualifiers.
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BASE COUNT	322 a 551 c 435 g 378 t	BASE COUNT	322 a 551 c 435 g 378 t
ORIGIN		ORIGIN	
Query Match		Query Match	
Best Local Similarity 99.9%; Pred. No. 0;		Best Local Similarity 99.9%; Pred. No. 0;	
Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;		Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
QY	787 GCACCTTAAGAGTGGCTTGCACACTGGTGAATCATCGGCACATTCAGCACACGCGCA 846	QY	787 GCACCTTAAGAGTGGCTTGCACACTGGTGAATCATCGGCACATTCAGCACACGCGCA 846
DB	1 GCACCTTAAGAGTGGCTTGCACACTGGTGAATCATCGGCACATTCAGCACACGCGCA 60	DB	1 GCACCTTAAGAGTGGCTTGCACACTGGTGAATCATCGGCACATTCAGCACACGCGCA 60
QY	847 AGCCTAACATCTTCCACAGGATCCGATGTGAACATGTGCACATGTTTGTCTGGGCG 906	QY	847 AGCCTAACATCTTCCACAGGATCCGATGTGAACATGTGCACATGTTTGTCTGGGCG 906
DB	61 AGCCTAACATCTTCCACAGGATCCGATGTGAACATGTGCACATGTTTGTCTGGGCG 120	DB	61 AGCCTAACATCTTCCACAGGATCCGATGTGAACATGTGCACATGTTTGTCTGGGCG 120
QY	907 AATGGAGCCATCATGATAGCGCAGAGAGAGCTGAATACCTGCGCTTACATCAACACGAGC 966	QY	907 AATGGAGCCATCATGATAGCGCAGAGAGAGCTGAATACCTGCGCTTACATCAACACGAGC 966
DB	121 AATGGAGCCATCATGATAGCGCAGAGAGAGCTGAATACCTGCGCTTACATCAACACGAGC 180	DB	121 AATGGAGCCATCATGATAGCGCAGAGAGAGCTGAATACCTGCGCTTACATCAACACGAGC 180
QY	967 AGCAATACCTTCTTCTGATGGGCGCGCGCTCTCATCCCATGTATTTTCAGTACCAGA 1026	QY	967 AGCAATACCTTCTTCTGATGGGCGCGCGCTCTCATCCCATGTATTTTCAGTACCAGA 1026
DB	181 AGCAATACCTTCTTCTGATGGGCGCGCGCTCTCATCCCATGTATTTTCAGTACCAGA 240	DB	181 AGCAATACCTTCTTCTGATGGGCGCGCGCTCTCATCCCATGTATTTTCAGTACCAGA 240
QY	1027 TCATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCGCGCGCTGAGCTACT 1086	QY	1027 TCATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCGCGCGCTGAGCTACT 1086
DB	241 TCATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCGCGCGCTGAGCTACT 300	DB	241 TCATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCGCGCGCTGAGCTACT 300
QY	1087 ACATCGGGTCTTTCATCACTACATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTCC 1146	QY	1087 ACATCGGGTCTTTCATCACTACATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTCC 1146
DB	301 ACATCGGGTCTTTCATCACTACATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTCC 360	DB	301 ACATCGGGTCTTTCATCACTACATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTCC 360
QY	1147 TCACTTCATCAAGTTCCTGGAGAGCCACTGGTTTGTGGGTCAACAGATGAATCACA 1206	QY	1147 TCACTTCATCAAGTTCCTGGAGAGCCACTGGTTTGTGGGTCAACAGATGAATCACA 1206
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QY	1207 TCGTCATGAGATTGACACAGAGGCGCTACCGTGAATCGTTTGTGGGTCAACAGATGAATCACA 1266	QY	1207 TCGTCATGAGATTGACACAGAGGCGCTACCGTGAATCGTTTGTGGGTCAACAGATGAATCACA 1266
DB	421 TCGTCATGAGATTGACACAGAGGCGCTACCGTGAATCGTTTGTGGGTCAACAGATGAATCACA 480	DB	421 TCGTCATGAGATTGACACAGAGGCGCTACCGTGAATCGTTTGTGGGTCAACAGATGAATCACA 480
QY	1267 CTGCAACGTGGAGCAGTCTTCTTCAACGACTGGTTTGTGGGTCAACAGATGAATCACA 1326	QY	1267 CTGCAACGTGGAGCAGTCTTCTTCAACGACTGGTTTGTGGGTCAACAGATGAATCACA 1326
DB	481 CTGCAACGTGGAGCAGTCTTCTTCAACGACTGGTTTGTGGGTCAACAGATGAATCACA 540	DB	481 CTGCAACGTGGAGCAGTCTTCTTCAACGACTGGTTTGTGGGTCAACAGATGAATCACA 540
QY	1327 TTGAGCACACCTCTTTCCCAACATGCGCCGCGCAACTTACACAGATTCGCCCGCTGG 1386	QY	1327 TTGAGCACACCTCTTTCCCAACATGCGCCGCGCAACTTACACAGATTCGCCCGCTGG 1386
DB	541 TTGAGCACACCTCTTTCCCAACATGCGCCGCGCAACTTACACAGATTCGCCCGCTGG 600	DB	541 TTGAGCACACCTCTTTCCCAACATGCGCCGCGCAACTTACACAGATTCGCCCGCTGG 600
QY	1387 TGAAGTCTCTATGTGCCAAGCATGGCAATGAATACAGGAGAGCGGCTACTGAGGGGCC 1446	QY	1387 TGAAGTCTCTATGTGCCAAGCATGGCAATGAATACAGGAGAGCGGCTACTGAGGGGCC 1446
DB	601 TGAAGTCTCTATGTGCCAAGCATGGCAATGAATACAGGAGAGCGGCTACTGAGGGGCC 660	DB	601 TGAAGTCTCTATGTGCCAAGCATGGCAATGAATACAGGAGAGCGGCTACTGAGGGGCC 660
QY	1447 TGCTGGACATCATGAGTCCCTTGAGAGAGTCTGGAGAGCTGTGGTGGAGCGCTTACCTTC 1506	QY	1447 TGCTGGACATCATGAGTCCCTTGAGAGAGTCTGGAGAGCTGTGGTGGAGCGCTTACCTTC 1506
DB	661 TGCTGGACATCATGAGTCCCTTGAGAGAGTCTGGAGAGCTGTGGTGGAGCGCTTACCTTC 720	DB	661 TGCTGGACATCATGAGTCCCTTGAGAGAGTCTGGAGAGCTGTGGTGGAGCGCTTACCTTC 720

RESULT 35
BD082653
LOCUS

BD082653 1686 bp DNA linear PAT 27-AUG-2002

DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids.
ACCESSION BD082653
VERSION BD082653.1 GI:22628263
KEYWORDS JP 2001523092-A/13.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1. (bases 1 to 1686)
AUTHORS Knutzen, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Leonard, A.E.Y.
TITLE Methods and compositions for synthesis of long chain
JOURNAL polyunsaturated fatty acids
COMMENT Patent: JP 2001523092-A 13 20-NOV-2001;
CALGENE LLC, ABBOTT LABORATORIES
FN JP 2001523092-A/13
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544176
PR 11-APR-1997 US 08/833610
PI DEBORAH KNUZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND,
PI SUNITA CHAUDHARY, AVANDA EUN YEONG LEONARD
PC
C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/PC
30, A23K1/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
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1..1686
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/db_xref="taxon:32644"
BASE COUNT 322 a 551 c 435 g 378 t
ORIGIN
Query Match 52.6%; Score 1675; DB 6; Length 1686;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 787 GCCACTTAAGGGTGCCCTCCCAACTGGTGGATCATGCCACTTCCAGCACACGCCA 846
DB 1 GCCCTTAAGGGTGCCCTCCCAACTGGTGGATCATGCCACTTCCAGCACACGCCA 60
QY 847 AGCCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGCAGCTGTTGTCTGGCG 906
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Db      1621  CTCCTGTATCAGTGGGAGTGGCAGCCAAATCCCTGGCCATTTGGCCCGGAGGAGCTG 1679
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RESULT 36
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LOCUS   BD092932 1686 bp DNA linear PAT 27-AUG-2002
DEFINITION
Methods and compositions for synthesis of long chain
polyunsaturated fatty acids in plants.
ACCESSION
BD092932
VERSION
BD092932.1 GI:22638543
KEYWORDS
JP 2001527395-A/19.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 1686)
AUTHORS
Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and
Leonard,A.E.Y.
TITLE
Methods and compositions for synthesis of long chain
polyunsaturated fatty acids in plants
JOURNAL
Patent: JP 2001527395-A 19 25-DEC-2001;
CARGENE LLC,ABBOTT LABORATORIES
COMMENT
PN JP 2001527395-A/19
PD 25-DEC-2001
PF 10-APR-1998 JP 1998544175
PR 11-APR-1997 US 08/833610,11-APR-1997 US 08/834033 PR
11-APR-1997 US 08/834655,24-OCT-1997 US 08/956985 PI
DEBORAH KNUZON, PRADIP MUKERJI, YONG SHENG HUANG, JENNIFER PI
THURMOND,
PI SONITA CHAUDHARY, AVANDA EUN YEONG LEONARD
PC
C12N15/53,C12N15/82,C12N5/10,C12P7/64,C11B1/00,A61K31/20,A23L1/ PC
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CC Topology: Linear;
FH Key Location/Qualifiers.
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ORIGIN
Query Match 52.6%; Score 1675; DB 6; Length 1686;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 GCCACTTAAAGGTGCTCGCCAACTGGTGGATCATCGCCACTTCACGACACACGCCA 60
QY 847 AGCCTAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCACGTGTTTCTGGCG 906
Db 61 AGCCTAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCACGTGTTTCTGGCG 120
QY 907 AATGCGACCCATCGAGTACGGCAGAGAGAGTGAATACCTCCCTACATCACCAGC 966
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QY 967 ACGAATACTCTTCTGATTGGCGCGCGCTGCCTCATCCCCCATGATTTCAGTACCAGA 1026
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DEFINITION Sequence 4 from Patent WO0170993.
ACCESSION AX253298
VERSION AX253298.1 GI:16073842
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Winther,M.D., Smith,H.L., Allen,S.J., Ponton,A. and de Antueno,R.J.
TITLE Polynucleotides that control delta-6-desaturase genes and methods
for identifying compounds for modulating delta-6-desaturase
JOURNAL Patent: WO 0170993-A 4 27-SEP-2001;
Scotia Holdings plc (GB)
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VERSION	BC009011.1	GI:14290485			
KEYWORDS	MGC.				
SOURCE	BC009011.1	GI:14290485			
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
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JOURNAL	Strausberg, R.				
	Direct Submission				
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	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,				
	USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk				
	Email: cgabs@mail.nih.gov				
	Tissue Procurement: David N. Louis, M.D.				
	cDNA Library Preparation: Life Technologies, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
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	Sequencing Center				
	Center code: BCM-HGSC				
	Web site: http://www.hgsc.bcm.tmc.edu/cdna/				
	Contact: villalon@bcm.tmc.edu				
	Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,				
	A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,				
	Muzny, D.M., Gibbs, R.A.				
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source	through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov				
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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
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; Sequence 9, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
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; PRIOR FILING DATE: 1999-01-08
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Best Local Similarity		81.8%	Pred. No. 1.2e+207;		
Matches		351;	Conservative 31;	Mismatches 44;	Indels 3; Gaps 1;
Qy	19	PT---	FSWEEIOKHNRU	TSGLVIDRKVYNTKWSIQHPGQORVICHVAGEDATDAFRAF	75
Db	3	PTPRYFTDEVAQRSGCEERWLVIDRKVYNTSEFTRRHFGGSRVISHYAGQDATDPFVAF	62		
Qy	76	HPDLRFVGKFLPGLLIGELAPEEPSODHGKSKITEDFRALRKTAE	DMNLPKTNHVFLL	135	
Db	63	HINKGLVKYMSLLIGELSPQPSPEPTKNTKELTDEFRELATVERMGLMKA	NHVFLL	122	
Qy	136	LLAHIIALBSIAWFTVYFGNGWIP	PLTIPAFVLATSQAQAGWLQHDYGHLSVYRKPKWNH	195	
Db	123	YLLHILLDGAAWLTWVFGTSLPFLLC	AVLSAQAGWLQHDYGHLSVYRKPKWNH	182	
Qy	196	LVHKFVIGHLKASANWNHRHFOHAKENI	PHKOPDVMNLHVFLGEWQPLEYGGKKLK	255	
Db	183	LVHKFVIGHLKASANWNHRHFOHAKENI	PHKOPDVMNLHVFLGEWQPLEYGGKKLK	242	

QY 256 YLPYNHQHEFFLIGPPLIPMFYQOIIMTIVHKWVDLAWAVSYIRFFIIPFYG 315
DB 243 YLPYNHQHEFFLIGPPLIPMFYQOIIMTIVHKWVDLAWAVSYIRFFIIPFYG 302
QY 316 ILGALLFLNFIRESHFVWVTQNMHI VMEIDQAYRDWFSQLTATCNVEQSFNDWF 375
DB 303 ILGALLFLNFIRESHFVWVTQNMHI VMEIDQAYRDWFSQLTATCNVEQSFNDWF 362
QY 376 SGHLNFQIEHLPFTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGK 435
DB 363 SGHLNFQIEHLPFTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGK 422
QY 436 LWLDAYLHK 444
DB 423 LWLDAYLHK 431

RESULT 2

US-09-227-613-9
; Sequence 9, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295, US P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: Xaa at position 432 is unknown or other.
US-09-227-613-9

Query Match 79.6%; Score 1940.5; DB 4; Length 432;
Best Local Similarity 81.8%; Pred. No. 1.2e-207;
Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;

QY 19 PT---FSWEEIQKLNLTDSGLVIDRKVYNIKWSIQHFGQGVIGHYAGEDATDAFRAF 75
DB 3 PTPRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHFGGSRVISHYAGQDATDPFVAF 62
QY 76 HPDLFEYGVKFLKLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNLFKTNHVPFLL 135
DB 63 HINKGLVKYWNLSLIGELSPQSPFPTKNKELTDEFRELATVERMGLMKANHVFFLL 122
QY 136 LLAHIIALESTAMFTVYFGNGWIPTLITAFVLATSAQAQAGWLQHDYGHLSVYRKPKNH 195
DB 123 YLLHILLDGAAMLTLWVFGTSFLPFLCAVLSAQAQAGWLQHDYGHLSVYRKPKNH 182
QY 196 LVHKFVIGHLKGSANWNNHRHFOHAKPNI FHKDPDVMNMLHVFLGEMOPIEYGGKKLK 255
DB 183 LVHKFVIGHLKGSANWNNHRHFOHAKPNI FHKDPDVMNMLHVFLGEMOPIEYGGKKLK 242
QY 256 YLPYNHQHEFFLIGPPLIPMFYQOIIMTIVHKWVDLAWAVSYIRFFIIPFYG 315
DB 243 YLPYNHQHEFFLIGPPLIPMFYQOIIMTIVHKWVDLAWAVSYIRFFIIPFYG 302
QY 316 ILGALLFLNFIRESHFVWVTQNMHI VMEIDQAYRDWFSQLTATCNVEQSFNDWF 375
DB 303 ILGALLFLNFIRESHFVWVTQNMHI VMEIDQAYRDWFSQLTATCNVEQSFNDWF 362
QY 376 SGHLNFQIEHLPFTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGK 435
DB 363 SGHLNFQIEHLPFTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGK 422

QY 436 LWLDAYLHK 444
DB 423 LWLDAYLHK 431
RESULT 3
US-09-439-261-40
; Sequence 40, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295, US P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (432)...(432)
; OTHER INFORMATION: Xaa = Unknown or other at position 432
; NAME/KEY: VARIANT
; LOCATION: (459)...(459)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
US-09-439-261-40

Query Match 79.6%; Score 1940.5; DB 4; Length 465;
Best Local Similarity 81.8%; Pred. No. 1.3e-207;
Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;

QY 19 PT---FSWEEIQKLNLTDSGLVIDRKVYNIKWSIQHFGQGVIGHYAGEDATDAFRAF 75
DB 3 PTPRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHFGGSRVISHYAGQDATDPFVAF 62
QY 76 HPDLFEYGVKFLKLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNLFKTNHVPFLL 135
DB 63 HINKGLVKYWNLSLIGELSPQSPFPTKNKELTDEFRELATVERMGLMKANHVFFLL 122
QY 136 LLAHIIALESTAMFTVYFGNGWIPTLITAFVLATSAQAQAGWLQHDYGHLSVYRKPKNH 195
DB 123 YLLHILLDGAAMLTLWVFGTSFLPFLCAVLSAQAQAGWLQHDYGHLSVYRKPKNH 182
QY 196 LVHKFVIGHLKGSANWNNHRHFOHAKPNI FHKDPDVMNMLHVFLGEMOPIEYGGKKLK 255
DB 183 LVHKFVIGHLKGSANWNNHRHFOHAKPNI FHKDPDVMNMLHVFLGEMOPIEYGGKKLK 242
QY 256 YLPYNHQHEFFLIGPPLIPMFYQOIIMTIVHKWVDLAWAVSYIRFFIIPFYG 315
DB 243 YLPYNHQHEFFLIGPPLIPMFYQOIIMTIVHKWVDLAWAVSYIRFFIIPFYG 302
QY 316 ILGALLFLNFIRESHFVWVTQNMHI VMEIDQAYRDWFSQLTATCNVEQSFNDWF 375
DB 303 ILGALLFLNFIRESHFVWVTQNMHI VMEIDQAYRDWFSQLTATCNVEQSFNDWF 362
QY 376 SGHLNFQIEHLPFTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGK 435
DB 363 SGHLNFQIEHLPFTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGK 422
QY 436 LWLDAYLHK 444

OTHER INFORMATION: Xaa at position 320 is unknown or other.
US-09-227-613-18

Query Match 66.8%; Score 1628.5; DB 4; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.6e-173;
Matches 293; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 151 VFVFGNGMPTLITAFVLATSAQAAGWLGQHDYGLSVYRKPNHVLVHKFVIGHLKGASA 210
DB 1 VFVFGNGMPTLITAFVLATSAQAAGWLGQHDYGLSVYRKPNHVLVHKFVIGHLKGASA 60
QY 211 NWNHRRHFQHAHPNI FHKPDVNNMLHVFLGEMQPIEYGGKKLKYLPYNHQQHYFFFLIG 270
DB 61 NWNHRRHFQHAHPNI FHKPDVNNMLHVFLGEMQPIEYGGKKLKYLPYNHQQHYFFFLIG 120
QY 271 PLLIPMVFQYQIIMTMIVHKNWDLAWAVSYIRFFIT-IPFYGILGALLFLNFIHFLE 330
DB 121 PLLIPMVFQYQIIMTMIVHKNWDLAWAVSYIRFFIT-IPFYGILGALLFLNFIHFLE 179
QY 331 SHWFVMTOMNHVMEIDQAYRDWFSSQLTATCNVEQSFNDWFSGLNFIQIEHHLPPT 390
DB 180 SHWFVMTOMNHVMEIDQAYRDWFSSQLTATCNVEQSFNDWFSGLNFIQIEHHLPPT 239
QY 391 MPRHNLKTAIPLVKSICAKHGIEYQEKPLLRALLDIIRSLKSGKGLMDAYLHK 444
DB 240 MPRHNLKTAIPLVKSICAKHGIEYQEKPLLRALLDIIRSLKSGKGLMDAYLHK 293

RESULT 7
US-09-048-888-1
Sequence 1, Application US/09048888
Patent No. 6492108
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,888
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0494 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: ENDANOT01

CLONE: 2451043
US-09-048-888-1

Query Match 64.0%; Score 1560.5; DB 4; Length 445;
Best Local Similarity 62.3%; Pred. No. 3e-165;
Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;
QY 1 MGGKGNQG--EAGAAREVSVPTFSWBEIQKNLRLDGLVIDRKVYNITKNSIQHPGGOR 58
DB 1 MGGVGFPGREGAQPAGPLTFCEWQIRAHQDPGDKWLVIERVVDISRWAQRHGGSR 60
QY 59 VIGHYAGEDATDAFRAHPDLEFVGKFLKPLIGELABEPPSODHGKSKITEDRALAK 118
DB 61 LIGHGAEDATDAFRAHQDLNFKFLQPLIGELABEPPSODGFLNAQLVEDFRAHQ 120
QY 119 TADNMLFKTNHVFVLLLAHIALESIAWFTVFVFGNGWIPTLITAFVLATSAQAAGWL 178
DB 121 AEDMKLPASPTFFAFLGHILAMEVLAWLLIYLLGPGWPSALAAFIASQAQSWCL 180
QY 179 QHDYGLSVYRKPNHVLVHKFVIGHLKGASANNHRRHFQHAHPNI FHKPDVNNMLHV 238
DB 181 QHDLGHASIFKKSNNHVAQKFMGQKGFSAHNNFRHFQHAHPNI FHKPDVNVAPV 240
QY 239 FVLGEQPIEYGGKKLKYLPYNHQQHYFFFLIGPPLIPMYFOVQIIMTMIVHKNWVDLAW 298
DB 241 FLIGE--SSVEYGGKKRKYLPYNQOHLFYFLIGPPLLTLYNFEVENLAYMLVCWQADLLW 299
QY 299 AVSYIRFFITYIPFYGILGALLFLNFIHFSSHFWVTOMNHVMEIDQAYRDWFSS 358
DB 300 AASFYARFFLSYLPFYGVFGLLFFVAVRVLESHFWVTOMNHIPKEIGHKRDWSS 359
QY 359 QLTATCNVEQSFNDWFSGLNFIQIEHHLPPTMPRHNLKTAIPLVKSICAKHGIEYQEK 418
DB 360 QLAATCNVPSLFTNWFSGHLNFIQIEHHLPFPMPRNYSRVAPLVKSLCAKGLSVEVKP 419
QY 419 LRLALLDIIRSLKSGKGLMDAYLHK 444
DB 420 FLTALVDIVRSLKSGDILWDAYLHQ 445

RESULT 8
US-09-048-888-3
Sequence 3, Application US/09048888
Patent No. 6492108
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,888
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132

```
/ REFERENCE/DOCKET NUMBER: PF-0494 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 444 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: BIPINOT01
/ CLONE: 2056310
US-09-048-889-3

Query Match
Best Local Similarity 62.1%; Score 1515; DB 4; Length 444;
Matches 272; Conservative 62; Mismatches 99; Indels 6; Gaps 3;

QY 11 AAEREVSVP---FSWEEIQKNNLRDTSGLVIDRKVYNTKWSIQHPGQQRVIGHYAGED 67
Db 7 AAETAAQGPTRYFTWDEVAQRSGCEERWLVIDRKVYNTSEFTRRHPGGSRVISHYAGD 66

QY 68 ATDAFRAPDLEFVGKFLKPLLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNMLFK 127
Db 67 ATDPFVAFHINKLVKYNNSLLIGELSPQSFPEFTKKNELTDEPRELRATVERMGLMK 126

QY 128 TNHVFFLLLAHIIALESIAWTFVYFGNGWIPTLITAFVLATSQAQAGWLQHDYGHLSV 187
Db 127 ANHVFFLLYLLHLLDGAALTLWVFGTSFLPFLCAVLLSAVQAQAGWLQHDYGHLSV 186

QY 188 YRKPKNHVLVHKFVIGHLKAGASANNWNRHFOHAKPNIFHKDPDVNMLH--VFVLGEWQ 245
Db 187 FSTSKNNHLLHFEVIGHLKAGASANNWNRHFOHAKPNCFRKDPDINN-HPFSFALGKIL 245

QY 246 PIYKGGKKLYLPYNHQHYFFLIGPPLLIPIFYQYQIIMTWIHKWVDLAWAVSYIIR 305
Db 246 SVELGKQKKYMPYNHQHYFFLIGPPLLIPIFYQYQIIMTWIHKWVDLAWAVSYIIR 305

QY 306 FIITYIPFGILGALLFLNFIPLSHFWVWVWQNNHIVMEIDQAYRDWFSQLTATCN 365
Db 306 FIITYVPLLGKAFGLFFIVFPLESNWVWVWQNNHIVMEIDQAYRDWFSQLTATCN 365

QY 366 VEQSFNDWFSGLNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQKPLLRALLD 425
Db 366 VHKSAFNDWFSGLNFQIEHLLFPTMPRNLHKAIPLVQSLCAKHGIEYQKPLLSAFAD 425

QY 426 IIRSLKSKGLMDAYLHK 444
Db 426 IIRSLKESQGLMDAYLHQ 444

RESULT 9
US-09-439-261-11
/ Sequence 11, Application US/09439261
/ Patent No. 6428990
/ GENERAL INFORMATION:
/ APPLICANT: Abbott Laboratories
/ APPLICANT: Mukerji, Pardip
/ APPLICANT: Leonard, Ananda E.
/ APPLICANT: Huang, Yung-Sheng
/ TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
/ FILE REFERENCE: 6295.US.P1
/ CURRENT APPLICATION NUMBER: US/09/439,261
/ CURRENT FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: US 08/833,610
/ PRIOR FILING DATE: 1997-04-11
/ PRIOR APPLICATION NUMBER: PCT/US98/07422
/ PRIOR FILING DATE: 1998-04-10
/ PRIOR APPLICATION NUMBER: US 09/227,613
/ PRIOR FILING DATE: 1999-01-08
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: FastSEQ for Windows Version 4.0

/ SEQ ID NO 11
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-439-261-11

Query Match
Best Local Similarity 61.9%; Score 1508; DB 4; Length 444;
Matches 271; Conservative 62; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAEREVSVP---FSWEEIQKNNLRDTSGLVIDRKVYNTKWSIQHPGQQRVIGHYAGED 67
Db 7 AAETAAQGPTRYFTWDEVAQRSGCEERWLVIDRKVYNTSEFTRRHPGGSRVISHYAGD 66

QY 68 ATDAFRAPDLEFVGKFLKPLLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNMLFK 127
Db 67 ATDPFVAFHINKLVKYNNSLLIGELSPQSFPEFTKKNELTDEPRELRATVERMGLMK 126

QY 128 TNHVFFLLLAHIIALESIAWTFVYFGNGWIPTLITAFVLATSQAQAGWLQHDYGHLSV 187
Db 127 ANHVFFLLYLLHLLDGAALTLWVFGTSFLPFLCAVLLSAVQAQAGWLQHDYGHLSV 186

QY 188 YRKPKNHVLVHKFVIGHLKAGASANNWNRHFOHAKPNIFHKDPDVNMLH--VFVLGEWQ 245
Db 187 FSTSKNNHLLHFEVIGHLKAGASANNWNRHFOHAKPNCFRKDPDINN-HPFSFALGKIL 245

QY 246 PIYKGGKKLYLPYNHQHYFFLIGPPLLIPIFYQYQIIMTWIHKWVDLAWAVSYIIR 305
Db 246 SVELGKQKKYMPYNHQHYFFLIGPPLLIPIFYQYQIIMTWIHKWVDLAWAVSYIIR 305

QY 306 FIITYIPFGILGALLFLNFIPLSHFWVWVWQNNHIVMEIDQAYRDWFSQLTATCN 365
Db 306 FIITYVPLLGKAFGLFFIVFPLESNWVWVWQNNHIVMEIDQAYRDWFSQLTATCN 365

QY 366 VEQSFNDWFSGLNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQKPLLRALLD 425
Db 366 VHKSAFNDWFSGLNFQIEHLLFPTMPRNLHKAIPLVQSLCAKHGIEYQKPLLSAFAD 425

QY 426 IIRSLKSKGLMDAYLHK 444
Db 426 IIRSLKESQGLMDAYLHQ 444

RESULT 10
US-09-227-613-12
/ Sequence 12, Application US/09227613A
/ Patent No. 6432684
/ GENERAL INFORMATION:
/ APPLICANT: Mukerji, Pradip
/ APPLICANT: LEONARD, Amanda E.
/ APPLICANT: HUANG, Yung-Sheng
/ TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
/ FILE REFERENCE: 6295.US.P1
/ CURRENT APPLICATION NUMBER: US/09/227,613A
/ CURRENT FILING DATE: 1999-01-08
/ PRIOR APPLICATION NUMBER: 08/833,610
/ PRIOR FILING DATE: 1997-04-11
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: FastSEQ for Windows Version 3.0
/ SEQ ID NO 12
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-227-613-12

Query Match
Best Local Similarity 61.7%; Pred. No. 2.2e-159;
Matches 271; Conservative 62; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAEREVSVP---FSWEEIQKNNLRDTSGLVIDRKVYNTKWSIQHPGQQRVIGHYAGED 67
Db 7 AAETAAQGPTRYFTWDEVAQRSGCEERWLVIDRKVYNTSEFTRRHPGGSRVISHYAGD 66
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Qy	68	ATDAFRAPHDLEFVGKFLKPLLIGELAPBEPSSODHGKSNKIITDEFPAUKRKTAEDMNLFK	127
Db	67	ATDPFVAFHINKGLVKKYMNNLLIGELSPQSPETKNKELTDFELRATVERMGLMK	126
Qy	128	TNHFVPLLALAHIALESIAFTVFYFCNGWIPTLITAFVLATSOAQAGWLQHDYGHLSV	187
Db	127	ANHVPFLLYLLHLLDGAAMUTLVFTSPFLCAVLLSAVQAQAGWLQHDGFHLSV	186
Qy	188	YRKPKNWHLVHKFVIGHLKGSANWNNHRHFQHHAKPNIFFHKDPVNNLH--VFVLGEWQ	245
Db	187	FSTSXWNLHLHFVIGHLKGPASWNNHWHFQHHAKPNCFRKPDINN-HPPEFFALGKIL	245
Qy	246	PTEYGGKKUYLPYNHQHHEYFLIPDPLLIIPMYQYQIINTMIVHKQWDLAWAVSYIIR	305
Db	246	SVELGQKKYMPYNHQHKEYFFLIPGALLFLYFQWIFFYVIOKKQWDLAWNITFYVR	305
Qy	306	FFITYTPFYGILGALLFLNFIRFLESHWFWVTQNNHIVMEIDOEAYRDMFSSQLATCN	365
Db	306	FFUTYVPLIGLKAFGLFTTPIRVLESSNFWVTQNNHIDPHIDHRNDNWSTQLLATCN	365
Qy	366	VEOSFNDWFSGHNLNFIIEHLLFPTWPRHNLHKIAPLVKSLCAKHGIEYQKPLLRALLD	425
Db	366	VHKSANDWFSGHNLNFIIEHLLFPTWPRHNVHKVAPLVQSLCAKHGIEYQKPLLSAFAD	425
Qy	426	IIRSLKSGKMLMDAYLHK	444
Db	426	IHSLSKESGOLWLDAYLHO	444

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RESULT 11
US-09-439-261-39
; Sequence 39, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (445)...(445)
; OTHER INFORMATION: Xaa = Unknown or other at position 445
US-09-439-261-39

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Db      127  ANHVPELLYLHLLDGAWLTVFGTSFPLFLCAVLLSAVQAQWLOHQDFGLSV 186
      188  YRKPKWNHLVHKFVIGHLKGAASANNWNRHHRFQHQHAKNPFIHKDPDVNMLH--VPVLGEWQ 245
      187  FSTSKWNHLHHRFVIGHLKGAFAASWNNHMHFQHQHAKPNCFKDPDINN-HPFFFAFGKIL 245
      246  PLEYGKKLKLYLPYNEOHEVFFLIGPPLIIPMYFOYCIIMTIVHKWVDLANAVSYIIR 305
      246  SVELGQKKKMYNEQHKIFFLIGPALLPLFYQWIFYFVLRQKKWVDLANWITFYVR 305
      306  FFITYIPFYGILGALLFLNFIRELESWFVWVMTQNMHIVMEIDOEAYRDWFFSOLTATCN 365
      306  FLTYVVELLGLKAFGLFFTVRELSNWFVWVQNMHPHMHIDHRDNDWVSTQLLATCN 365
      366  VEOGFENDAFSGHLNFIQIEHLEFPTPRNHLKTIAPLVKSLCAKHGIEYOEKPLLRALD 425
      366  VHSAFNDWFSGLNFIQIEHLEFPTPRNHYHKVAPLVQSLCAKRGIEYOSKPLLSAFAD 425
      426  IIRSLKSKGLWLDAYLHK 444
      426  IHSLESQGLWLDAYLHQ 444

RESULT 12
US-09-439-261-45
; Sequence 45, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295, US, P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (445)...(445)
; OTHER INFORMATION: Xaa = Unknown or other at position 445
US-09-439-261-45

```

	Query Match	61.9%	Score 1508;	DB 4;	Length 445;	
	Best Local Similarity	61.7%;	Pred. No. 2.2e-159;			
	Matches 271; Conservative	62;	Mismatches 100;	Indels	6;	Gaps 3
Qy	11 AAEREVSVPT---FSWEEIQKHLNRITDGLVIDRKVNITKWSIQHPGQRGVIGHYAED	67				
	: : : : : : : : : : : : : : : : : : : : : : : :					
Dd	7 AETAQAQGTPRYFTWDVEAQRSGCEERLWIDIRKVNISEFTRRPGSGRVISHYAQGD	66				
	: : : : : : : : : : : : : : : : : : : : : : : :					
Qy	68 ATDAFRAPHPLEFGVKFLKLIIIGELAPEPSODHGKNSKITEDFRALRKTAEDMNLFK	127				
	: : : : : : : : : : : : : : : : : : : : : : : :					
Dd	67 ATDPFAFHINKLVKKYNSLLIGELSPESPEPTKNKELTDEFRELRAETVERBMLWK	126				
	: : : : : : : : : : : : : : : : : : : : : : : :					
Qy	128 TNHVFPLLALLHAIIATALESIAINFVTFFYGNGMIPLTIATFVLATSQAQAGWLQHDYGHLSV	187				
	: : : : : : : : : : : : : : : : : : : : : : : :					
Dd	127 ANHVFFLLYLHIILLDDGAAMTLTWFGTSFPFLLCVALISAVOQAQGNLQHDYGHLSV	186				
	: : : : : : : : : : : : : : : : : : : : : : : :					
Qy	188 YRKPKWNHLVHKFVIGHLIKGASANNWHRRHTQHAKPNI FHKPDVVNMLH--VFVIGEWQ	245				
	: : : : : : : : : : : : : : : : : : : : : : : :					

Db 187 FSTSKWNLHLLHFFVIGLKGAPASWNNHMFQHHAKNCPKDPDINN-HPFFALGKIL 245
Qy 246 PIEYGGKKLKYLPYNHHEYFELGPPILLIPMYFOYQIIMTMIVHKWVDLAWAVSYIR 305
Db 246 SVELGKQKKYMPYNHGHYFELGPPALLPLFYFQWIFYFVIOQKKWVDLAWMITFYR 305
Qy 306 FFITYIPPYGILGALLFLNFIRESHFWVVTQNNHIVMEIDQAYRDWPSQLTATCN 365
Db 306 FFITYVPLLLGLKAFGLFFIVRLESNFWVVTQNNHIVMEIDHNRNDWVSTQLLATCN 365
Qy 366 VEQSFNDWFSGHLNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLD 425
Db 366 VKSAFNDWFSGHLNFQIEHLLFPTMPRNLHKAIPLVQSLCAKRGIEYQSKPLLSAFAD 425
Qy 426 IIRSLKSKGLWLDAYLHK 444
Db 426 IIRSLKSKGLWLDAYLHQ 444

RESULT 13

US-09-439-261-43
; Sequence 43, Application US/09439261
; Patent No. 6426930

GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (444)...(444)
; OTHER INFORMATION: Xaa = Unknown or other at position 444

US-09-439-261-43

Query Match 61.3%; Score 1493.5; DB 4; Length 444;
Best Local Similarity 61.5%; Pred. No. 98-158;
Matches 270; Conservative 62; Mismatches 100; Indels 7; Gaps 4;

Qy 11 AAREVSVPT---FSWEEIQKNLRDSDGLVIDRKYNTKWSIQHPGQQRVIGHYAGED 67
Db 7 AAEATAAGTPTPYFTWDEVAQRSGCEERWLVIDRKYNISFTRRHPGGSRVISHYAGD 66
Qy 68 ATDAFAPFDLEFVCKFLKPLLIGELAPEEPOHGNKSKITEDPRALRKTAEADNLFK 127
Db 67 ATDPFVAFHINKGLVKYNNLSLIGELSPQSPFPTKNEKLTDBFE-LRATVERMGLMK 125
Qy 128 TNHVFLLLLAHIIALESIAFWTFVFGNGWPTLTITAFVLATSAQAQAGLQHDYGLSV 187
Db 126 ANHVFFLLYLLHLLDGAALTLWVFGTSPFLPCLCAVLSAVQAQAGLQHDYGLSV 185
Qy 188 YRKPKNHLVHKFVIGHLKGASANNWNRHFOHAKNPNI FHKDPDNNMLH--VFVLGEWQ 245
Db 186 FSTSKWNLHLLHFFVIGLKGAPASWNNHMFQHHAKNCPKDPDINN-HPFFALGKIL 244
Qy 246 PIEYGGKKLKYLPYNHHEYFELGPPILLIPMYFOYQIIMTMIVHKWVDLAWAVSYIR 305
Db 245 SVELGKQKKYMPYNHGHYFELGPPALLPLFYFQWIFYFVIOQKKWVDLAWMITFYR 304
Qy 306 FFITYIPPYGILGALLFLNFIRESHFWVVTQNNHIVMEIDQAYRDWPSQLTATCN 365
Db 306 FFITYVPLLLGLKAFGLFFIVRLESNFWVVTQNNHIVMEIDHNRNDWVSTQLLATCN 365
Qy 426 IIRSLKSKGLWLDAYLHK 444
Db 426 IIRSLKSKGLWLDAYLHQ 444

Qy 306 FFITYIPPYGILGALLFLNFIRESHFWVVTQNNHIVMEIDQAYRDWPSQLTATCN 365
Db 306 FFITYVPLLLGLKAFGLFFIVRLESNFWVVTQNNHIVMEIDHNRNDWVSTQLLATCN 364
Qy 366 VEQSFNDWFSGHLNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLD 425
Db 366 VKSAFNDWFSGHLNFQIEHLLFPTMPRNLHKAIPLVQSLCAKRGIEYQSKPLLSAFAD 424
Qy 426 IIRSLKSKGLWLDAYLHK 444
Db 426 IIRSLKSKGLWLDAYLHQ 444

RESULT 14

US-09-227-613-42
; Sequence 42, Application US/09227613A
; Patent No. 6432684

GENERAL INFORMATION:

; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: Xaa at position 444 is unknown or other.
US-09-227-613-42

Query Match 61.3%; Score 1493.5; DB 4; Length 444;
Best Local Similarity 61.5%; Pred. No. 98-159;
Matches 270; Conservative 62; Mismatches 100; Indels 7; Gaps 4;

Qy 11 AAREVSVPT---FSWEEIQKNLRDSDGLVIDRKYNTKWSIQHPGQQRVIGHYAGED 67
Db 7 AAEATAAGTPTPYFTWDEVAQRSGCEERWLVIDRKYNISFTRRHPGGSRVISHYAGD 66
Qy 68 ATDAFAPFDLEFVCKFLKPLLIGELAPEEPOHGNKSKITEDPRALRKTAEADNLFK 127
Db 67 ATDPFVAFHINKGLVKYNNLSLIGELSPQSPFPTKNEKLTDBFE-LRATVERMGLMK 125
Qy 128 TNHVFLLLLAHIIALESIAFWTFVFGNGWPTLTITAFVLATSAQAQAGLQHDYGLSV 187
Db 126 ANHVFFLLYLLHLLDGAALTLWVFGTSPFLPCLCAVLSAVQAQAGLQHDYGLSV 185
Qy 188 YRKPKNHLVHKFVIGHLKGASANNWNRHFOHAKNPNI FHKDPDNNMLH--VFVLGEWQ 245
Db 186 FSTSKWNLHLLHFFVIGLKGAPASWNNHMFQHHAKNCPKDPDINN-HPFFALGKIL 244
Qy 246 PIEYGGKKLKYLPYNHHEYFELGPPILLIPMYFOYQIIMTMIVHKWVDLAWAVSYIR 305
Db 245 SVELGKQKKYMPYNHGHYFELGPPALLPLFYFQWIFYFVIOQKKWVDLAWMITFYR 304
Qy 306 FFITYIPPYGILGALLFLNFIRESHFWVVTQNNHIVMEIDQAYRDWPSQLTATCN 365
Db 306 FFITYVPLLLGLKAFGLFFIVRLESNFWVVTQNNHIVMEIDHNRNDWVSTQLLATCN 364
Qy 366 VEQSFNDWFSGHLNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLD 425
Db 366 VKSAFNDWFSGHLNFQIEHLLFPTMPRNLHKAIPLVQSLCAKRGIEYQSKPLLSAFAD 424
Qy 426 IIRSLKSKGLWLDAYLHK 444
Db 426 IIRSLKSKGLWLDAYLHQ 444

RESULT 15
US-09-439-261-41
; Sequence 41, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-439-261-41

Query Match 46.3%; Score 1128; DB 4; Length 360;
Best Local Similarity 57.2%; Pred. No. 3.8e-117;
Matches 203; Conservative 56; Mismatches 90; Indels 6; Gaps 3;
QY 11 AAREVSVPT---FSWEEIOXNLRDTSGLVDRKYNITKMSIQHPGQGVIGHYAGD 67
DB 7 AATAAAGCTPRYFTWDEVAQRSGCEERWLVDRKYNISEFTRRHPGGSRVISHYAGD 66
QY 68 ATDAFRAFPDLFVGKFLKPLLIGELAPEPSQDHCKSKITEDFRALRKTAEADNMLFK 127
DB 67 ATDPFVAFHINKGLVKYKNSLLIGELSPQSPFETPKNKLDELFRERATVERMGLMK 126
QY 128 TNHVFLLLAHIALESIAWTFVFGNGWITLITAFVLATSOAAGWLQHDYGHLSV 187
DB 127 ANHVFLLYLLHLLDGAALTLWVFGTSLFPLLCVALLSAVQAQAGWLQHDYGHLSV 186
QY 188 YRKEPKWNHLVHKFVIGHLKASANNWNRHFFQHHAKENIFHKDPDVNMLH--VFVLGEWQ 245
DB 187 PSTSKWNHLLHFFVIGHLKGPASWNNHMFQHHAKENCFRKPDPDINN-HPFFALGKIL 245
QY 246 PIEYKKKKLYLPYNHGHYFFLIGPPELLIPMYFQYQIINTMIVHKWVDLAWAVSYIR 305
DB 246 SVELGKQKKYMPYNHGHYFFLIGPPELLIPMYFQYFVYFVIOQRKQWDLAWMITFYR 305
QY 306 FFITYIPYGLGALLFLNFRPLESHWVWVTOMNHVMEIDQEAAYRDWFSOL 360
DB 306 FFITYVPLLGKAFGLFFIVRFLESNFWVWVTOMNHIPMHIDHRNDWVSTQL 360

RESULT 16
US-09-227-613-39
; Sequence 39, Application US/09227613A
; Patent No. 6432884
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-613-39

Query Match 46.3%; Score 1128; DB 4; Length 360;
Best Local Similarity 57.2%; Pred. No. 3.8e-117;
Matches 203; Conservative 56; Mismatches 90; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEEIOXNLRDTSGLVDRKYNITKMSIQHPGQGVIGHYAGD 67
DB 7 AATAAAGCTPRYFTWDEVAQRSGCEERWLVDRKYNISEFTRRHPGGSRVISHYAGD 66
QY 68 ATDAFRAFPDLFVGKFLKPLLIGELAPEPSQDHCKSKITEDFRALRKTAEADNMLFK 127
DB 67 ATDPFVAFHINKGLVKYKNSLLIGELSPQSPFETPKNKLDELFRERATVERMGLMK 126
QY 128 TNHVFLLLAHIALESIAWTFVFGNGWITLITAFVLATSOAAGWLQHDYGHLSV 187
DB 127 ANHVFLLYLLHLLDGAALTLWVFGTSLFPLLCVALLSAVQAQAGWLQHDYGHLSV 186
QY 188 YRKEPKWNHLVHKFVIGHLKASANNWNRHFFQHHAKENIFHKDPDVNMLH--VFVLGEWQ 245
DB 187 PSTSKWNHLLHFFVIGHLKGPASWNNHMFQHHAKENCFRKPDPDINN-HPFFALGKIL 245
QY 246 PIEYKKKKLYLPYNHGHYFFLIGPPELLIPMYFQYQIINTMIVHKWVDLAWAVSYIR 305
DB 246 SVELGKQKKYMPYNHGHYFFLIGPPELLIPMYFQYFVYFVIOQRKQWDLAWMITFYR 305
QY 306 FFITYIPYGLGALLFLNFRPLESHWVWVTOMNHVMEIDQEAAYRDWFSOL 360
DB 306 FFITYVPLLGKAFGLFFIVRFLESNFWVWVTOMNHIPMHIDHRNDWVSTQL 360

RESULT 17
US-09-439-261-13
; Sequence 13, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-439-261-13

Query Match 45.2%; Score 1103; DB 4; Length 287;
Best Local Similarity 66.9%; Pred. No. 1.6e-114;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;
QY 157 GWIPTLITAFVLATSOAAGWLQHDYGHLSVYRKPKNHVLVHKFVIGHLKASANNWNRH 216
DB 8 GGIPAV-----QAQAGWLQHDYGHLSVFSKWNHLLHFFVIGHLKGPASWNNHM 58
QY 217 HFQHHAKENIFHKDPDVNMLH--VFVLGEWQPIEGKKKLYLPYNHGHYFFLIGPULL 274

Db 59 HFQHAKNPCFRKPDINN--HPFFALGKILSVLGGKQKKYMPYNNHQHYFFLIGPPAL 117
QY 275 IPMYFOYQIIMTMIVHKNWVDLAWAVSYIRFFITVYIPYIGLALLFLNFIRESHWF 334
Db 118 LPLYFQWYIFVYIQRKKWVDLAWMITFVVRFFLTVPLGLKAFGLFFIVRFLSNWF 177
QY 335 VVWVTQNNHIVMEIDQAYRDWFSQSQTATCNVQSFNDWFSGLNFQIEHHLFPTMPRH 394
Db 178 VVWVTQNNHIVMEIDQAYRDWFSQSQTATCNVQSFNDWFSGLNFQIEHHLFPTMPRH 237
QY 395 NLHKAIPVLSLCAKHGIEYQSKPLLRALLDIIRSLKSGKLWLDAYLHK 444
Db 238 NYHKVAPLVQSLCAKHGIEYQSKPLLRALLDIIRSLKSGKLWLDAYLHK 287

RESULT 18

US-09-227-613-14
; Sequence 14, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-227-613-14

Query Match 45.2%; Score 1103; DB 4; Length 287;
Best Local Similarity 66.9%; Pred. No. 1.6e-114; Indels 12; Gaps 3;
Matches 194; Conservative 32; Mismatches 52

QY 157 GMIPTLITAFVLATSOAQAQWLOHDYGHLSVYRKPKNHVLHVKFVIGHLKGASANNWNR 216
Db 8 GGIPAV-----QAQAGWLOHDYGHLSVYRKPKNHVLHVKFVIGHLKGASANNWNR 58
QY 217 HFQHAKNPCFRKPDINN--HPFFALGKILSVLGGKQKKYMPYNNHQHYFFLIGPPAL 274
Db 59 HFQHAKNPCFRKPDINN--HPFFALGKILSVLGGKQKKYMPYNNHQHYFFLIGPPAL 117
QY 275 IPMYFOYQIIMTMIVHKNWVDLAWAVSYIRFFITVYIPYIGLALLFLNFIRESHWF 334
Db 118 LPLYFQWYIFVYIQRKKWVDLAWMITFVVRFFLTVPLGLKAFGLFFIVRFLSNWF 177
QY 335 VVWVTQNNHIVMEIDQAYRDWFSQSQTATCNVQSFNDWFSGLNFQIEHHLFPTMPRH 394
Db 178 VVWVTQNNHIVMEIDQAYRDWFSQSQTATCNVQSFNDWFSGLNFQIEHHLFPTMPRH 237
QY 395 NLHKAIPVLSLCAKHGIEYQSKPLLRALLDIIRSLKSGKLWLDAYLHK 444
Db 238 NYHKVAPLVQSLCAKHGIEYQSKPLLRALLDIIRSLKSGKLWLDAYLHK 287

RESULT 19

US-09-439-261-16
; Sequence 14, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2

; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (288)...(288)
; OTHER INFORMATION: Xaa = Unknown or other at position 288
US-09-439-261-14

Query Match 45.2%; Score 1103; DB 4; Length 288;
Best Local Similarity 66.9%; Pred. No. 1.7e-114;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;
QY 157 GMIPTLITAFVLATSOAQAQWLOHDYGHLSVYRKPKNHVLHVKFVIGHLKGASANNWNR 216
Db 8 GGIPAV-----QAQAGWLOHDYGHLSVYRKPKNHVLHVKFVIGHLKGASANNWNR 58
QY 217 HFQHAKNPCFRKPDINN--HPFFALGKILSVLGGKQKKYMPYNNHQHYFFLIGPPAL 274
Db 59 HFQHAKNPCFRKPDINN--HPFFALGKILSVLGGKQKKYMPYNNHQHYFFLIGPPAL 117
QY 275 IPMYFOYQIIMTMIVHKNWVDLAWAVSYIRFFITVYIPYIGLALLFLNFIRESHWF 334
Db 118 LPLYFQWYIFVYIQRKKWVDLAWMITFVVRFFLTVPLGLKAFGLFFIVRFLSNWF 177
QY 335 VVWVTQNNHIVMEIDQAYRDWFSQSQTATCNVQSFNDWFSGLNFQIEHHLFPTMPRH 394
Db 178 VVWVTQNNHIVMEIDQAYRDWFSQSQTATCNVQSFNDWFSGLNFQIEHHLFPTMPRH 237
QY 395 NLHKAIPVLSLCAKHGIEYQSKPLLRALLDIIRSLKSGKLWLDAYLHK 444
Db 238 NYHKVAPLVQSLCAKHGIEYQSKPLLRALLDIIRSLKSGKLWLDAYLHK 287

RESULT 20

US-09-439-261-16
; Sequence 16, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (288)...(288)


```

; OTHER INFORMATION: Xaa = Unknown or other at position 288
US-09-439-261-16

Query Match      45.2%; Score 1103; DB 4; Length 288;
Best Local Similarity 66.9%; Pred. No. 1.7e-114;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GWIPTLITAFVLATSAQAGWLDHGYHLSVYRKPKNHLVHKFVIGHLKGASANNWNRH 216
DB 8 GGIPAV-----QAQAGWLQDHFGLSVFSTSKNHLHHPVIGHLKGAPASANNW 58

QY 217 HFQHAKEPIFHKDPDNNMLH--VFVLGEWQPIEYGGKKLKYLPYNHGHYFFLIGPPLL 274
DB 59 HFQHAKEPNCFRKPDINN-HPFFALGKILSVELGKQKKYMPYNHGHYFFLIGPPLL 117

QY 275 IPMYFOYQIIMTVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRESHW 334
DB 118 LPLYEQWYIFVFIQKQKVDLAWMITFYVRFFLTVPLGLKAFGLFFIVRFLSNWF 177

QY 335 VVVTQNMHIHVEIDQAYRDWFSQLTATCNVEQSFNDWFSGLNFQIEHLLFPTMPRH 394
DB 178 VVVTQNMHIHVEIDQAYRDWFSQLTATCNVEQSFNDWFSGLNFQIEHLLFPTMPRH 237

QY 395 NLHKAIPLVKSLCAKGIYQKPELRLALDIIRSLKSGKGLWLDAYLHK 444
DB 238 NYHKVAPLVQSLCAKGIYQKPELRLALDIIRSLKSGKGLWLDAYLHK 287

; OTHER INFORMATION: Xaa = Unknown or other at position 288
US-09-439-261-17

Query Match      45.2%; Score 1103; DB 4; Length 288;
Best Local Similarity 66.9%; Pred. No. 1.7e-114;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GWIPTLITAFVLATSAQAGWLDHGYHLSVYRKPKNHLVHKFVIGHLKGASANNWNRH 216
DB 8 GGIPAV-----QAQAGWLQDHFGLSVFSTSKNHLHHPVIGHLKGAPASANNW 58

QY 217 HFQHAKEPIFHKDPDNNMLH--VFVLGEWQPIEYGGKKLKYLPYNHGHYFFLIGPPLL 274
DB 59 HFQHAKEPNCFRKPDINN-HPFFALGKILSVELGKQKKYMPYNHGHYFFLIGPPLL 117

QY 275 IPMYFOYQIIMTVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRESHW 334
DB 118 LPLYEQWYIFVFIQKQKVDLAWMITFYVRFFLTVPLGLKAFGLFFIVRFLSNWF 177

QY 335 VVVTQNMHIHVEIDQAYRDWFSQLTATCNVEQSFNDWFSGLNFQIEHLLFPTMPRH 394
DB 178 VVVTQNMHIHVEIDQAYRDWFSQLTATCNVEQSFNDWFSGLNFQIEHLLFPTMPRH 237

QY 395 NLHKAIPLVKSLCAKGIYQKPELRLALDIIRSLKSGKGLWLDAYLHK 444
DB 238 NYHKVAPLVQSLCAKGIYQKPELRLALDIIRSLKSGKGLWLDAYLHK 287

```

```

RESULT 21
US-09-439-261-18
; Sequence 18, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paradi
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US-P2
; CURRENT FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (288)...(288)
; OTHER INFORMATION: Xaa = Unknown or other at position 288
US-09-439-261-18

Query Match      45.2%; Score 1103; DB 4; Length 288;
Best Local Similarity 66.9%; Pred. No. 1.7e-114;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GWIPTLITAFVLATSAQAGWLDHGYHLSVYRKPKNHLVHKFVIGHLKGASANNWNRH 216
DB 8 GGIPAV-----QAQAGWLQDHFGLSVFSTSKNHLHHPVIGHLKGAPASANNW 58

QY 217 HFQHAKEPIFHKDPDNNMLH--VFVLGEWQPIEYGGKKLKYLPYNHGHYFFLIGPPLL 274
DB 59 HFQHAKEPNCFRKPDINN-HPFFALGKILSVELGKQKKYMPYNHGHYFFLIGPPLL 117

QY 275 IPMYFOYQIIMTVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRESHW 334
DB 118 LPLYEQWYIFVFIQKQKVDLAWMITFYVRFFLTVPLGLKAFGLFFIVRFLSNWF 177

QY 335 VVVTQNMHIHVEIDQAYRDWFSQLTATCNVEQSFNDWFSGLNFQIEHLLFPTMPRH 394
DB 178 VVVTQNMHIHVEIDQAYRDWFSQLTATCNVEQSFNDWFSGLNFQIEHLLFPTMPRH 237

QY 395 NLHKAIPLVKSLCAKGIYQKPELRLALDIIRSLKSGKGLWLDAYLHK 444
DB 238 NYHKVAPLVQSLCAKGIYQKPELRLALDIIRSLKSGKGLWLDAYLHK 287

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RESULT 23
US-09-439-261-42
; Sequence 42, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paradi
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US-P2
; CURRENT FILING DATE: 1999-11-12
US-09-439-261-42

Query Match      45.2%; Score 1103; DB 4; Length 288;
Best Local Similarity 66.9%; Pred. No. 1.7e-114;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GWIPTLITAFVLATSAQAGWLDHGYHLSVYRKPKNHLVHKFVIGHLKGASANNWNRH 216
DB 8 GGIPAV-----QAQAGWLQDHFGLSVFSTSKNHLHHPVIGHLKGAPASANNW 58

QY 217 HFQHAKEPIFHKDPDNNMLH--VFVLGEWQPIEYGGKKLKYLPYNHGHYFFLIGPPLL 274
DB 59 HFQHAKEPNCFRKPDINN-HPFFALGKILSVELGKQKKYMPYNHGHYFFLIGPPLL 117

QY 275 IPMYFOYQIIMTVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRESHW 334
DB 118 LPLYEQWYIFVFIQKQKVDLAWMITFYVRFFLTVPLGLKAFGLFFIVRFLSNWF 177

QY 335 VVVTQNMHIHVEIDQAYRDWFSQLTATCNVEQSFNDWFSGLNFQIEHLLFPTMPRH 394
DB 178 VVVTQNMHIHVEIDQAYRDWFSQLTATCNVEQSFNDWFSGLNFQIEHLLFPTMPRH 237

QY 395 NLHKAIPLVKSLCAKGIYQKPELRLALDIIRSLKSGKGLWLDAYLHK 444
DB 238 NYHKVAPLVQSLCAKGIYQKPELRLALDIIRSLKSGKGLWLDAYLHK 287

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; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (251)...(251)
; OTHER INFORMATION: Xaa = Unknown or other at position 251
; NAME/KEY: VARIANT
; LOCATION: (329)...(330)
; OTHER INFORMATION: Xaa = Unknown or other at these positions
US-09-439-261-42
Query Match 37.3%; Score 909.5; DB 4; Length 347;
Best Local Similarity 58.6%; Pred. No. 8.4e-93;
Matches 167; Conservative 43; Mismatches 68; Indels 7; Gaps 4;
QY 19 PT---FSWEEIOKHNLRDTSGLVIDRKVYNTKWSIQHPGGORVIGHYAGSDATDAFRAP 75
DB 3 PTPRIFTWDEVAQRSCCERWLVIDRKVYNISEFTRRHPGGSRVISHYAGQDATDPFVAF 62
QY 76 HPDLFVGVKFLKPLIGELAPEEPSQDHGKNSKITEDFRALKTAEDNMFLKTNHVPFLL 135
DB 63 HINKGLVKYMNLSLIGLSPEQSPFPTKNELTDFEFLRATVVERMGLMKAHVFPFL 122
QY 136 LLAHIIALESIAWFTVFEVNGWIPTLITAFVLATSOAQAGWLQHDYGHLSVYRKPKWNH 195
DB 123 YLHLLLDGAARWLTVFGTSFLPFLCAVLSSAVQAQAGWLQHD-GHLSVFTSKWNH 181
QY 196 LVHKEVIGHLKGASANNWNRHFQHAKENIFHKDPDVMNLH--VFVLGEMQPIEYGGKK 253
DB 182 LLHHEVIGHLKGAPASANNWNRHFQHAKENCFKDPDINN-HPPFFALGKILSVELGKQK 240
QY 254 LKYLPNYHCHYEFLIGPPLIPMYFOYQIIMTIVHKNWVDLAW 298
DB 241 KKYMPYHCHYEFLIGPPLIPMYFOYQIIMTIVHKNWVDLAW 285
RESULT 24
US-09-227-613-40
; Sequence 40, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: Xaa at position 251 is unknown or other.
; OTHER INFORMATION: Xaa at position 329 is unknown or other.
; OTHER INFORMATION: Xaa at position 330 is unknown or other.
US-09-227-613-40
Query Match 37.3%; Score 909.5; DB 4; Length 347;
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (251)...(251)
; OTHER INFORMATION: Xaa = Unknown or other at position 251
; NAME/KEY: VARIANT
; LOCATION: (329)...(330)
; OTHER INFORMATION: Xaa = Unknown or other at these positions
US-09-439-261-42
Query Match 37.3%; Score 909.5; DB 4; Length 347;
Best Local Similarity 58.6%; Pred. No. 8.4e-93;
Matches 167; Conservative 43; Mismatches 68; Indels 7; Gaps 4;
QY 19 PT---FSWEEIOKHNLRDTSGLVIDRKVYNTKWSIQHPGGORVIGHYAGSDATDAFRAP 75
DB 3 PTPRIFTWDEVAQRSCCERWLVIDRKVYNISEFTRRHPGGSRVISHYAGQDATDPFVAF 62
QY 76 HPDLFVGVKFLKPLIGELAPEEPSQDHGKNSKITEDFRALKTAEDNMFLKTNHVPFLL 135
DB 63 HINKGLVKYMNLSLIGLSPEQSPFPTKNELTDFEFLRATVVERMGLMKAHVFPFL 122
QY 136 LLAHIIALESIAWFTVFEVNGWIPTLITAFVLATSOAQAGWLQHDYGHLSVYRKPKWNH 195
DB 123 YLHLLLDGAARWLTVFGTSFLPFLCAVLSSAVQAQAGWLQHD-GHLSVFTSKWNH 181
QY 196 LVHKEVIGHLKGASANNWNRHFQHAKENIFHKDPDVMNLH--VFVLGEMQPIEYGGKK 253
DB 182 LLHHEVIGHLKGAPASANNWNRHFQHAKENCFKDPDINN-HPPFFALGKILSVELGKQK 240
QY 254 LKYLPNYHCHYEFLIGPPLIPMYFOYQIIMTIVHKNWVDLAW 298
DB 241 KKYMPYHCHYEFLIGPPLIPMYFOYQIIMTIVHKNWVDLAW 285
RESULT 25
US-09-439-261-20
; Sequence 20, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-439-261-20
Query Match 32.2%; Score 784; DB 4; Length 219;
Best Local Similarity 61.7%; Pred. No. 4.1e-79;
Matches 137; Conservative 27; Mismatches 46; Indels 12; Gaps 3;
QY 157 GWIPTLITAFVLATSOAQAGWLQHDYGHLSVYRKPKWNHVLHVKFVIGHLKGASANNWNR 216
DB 8 GGIPAV-----QAQAGWLQHDYGHLSVFTSKWNHLLHFFVIGHLKGAPASANNW 58
QY 217 HFQHAKENIFHKDPDVMNLH--VFVLGEMQPIEYGGKKLKYLPYNHCHYEFLIGPPL 274
DB 59 HFQHAKENCFKDPDINN-HPPFFALGKILSVELGKQKKNYPYNHCHYEFLIGPPL 117
QY 275 IPMYFOYQIIMTIVHKNWVDLAWVSYVYRPTTYIPFYGLGALLFLNFIREFLESHWF 334
DB 118 LPFYFOYTYFYVYQIRKKWVDLAWMTTYFYRFFLTYPVLLGLKAFGLGFLTYVRFLESNWF 177
QY 335 VVYTMNHHVMEIDQRAYRDWFSQSQTATCNVEQSFNDWFS 376
DB 178 VVYTMNHHVMEIDQRAYRDWFSQSQTATCNVEQSFNDWFS 219
RESULT 26
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US-09-227-613-19
; Sequence 19, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradiip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-227-613-19

Query Match 32.2%; Score 784; DB 4; Length 219;
Best Local Similarity 61.7%; Pred. No. 4.1e-79;
Matches 137; Conservative 27; Mismatches 46; Indels 12; Gaps 3;

QY 157 GMIPTLITAFVLATSAQAQAGWLQHDYGHLSVYRKPKXNHLVHKFVIGHLKGASANWNNHR 216
DB 8 GGIPAV-----QAQAGWLQHDYGHLSVSTSKWNHLJHHFVIGHLKGASANWNNHM 58

QY 217 HFQHAKPNIFHKDPDNNMLH--VFVLGSEWQPIEYKQKLLKYLPNYHQHEYFFLIGPPLL 274
DB 59 HFQHAKPNCFKDPDNNM--HPFFALGKILSVLQKQKXMPYNNHQHYFFLIGPPAL 117

QY 275 IPMYFQYQIIMTVHKNWDLAWAVSYIRFIYIPYIGLQALLFNIRFLESHPF 334
DB 118 LPLFYQWYIFFYFIQKRWKVDLAWMITFYVRFLTYVPLGLKAFGLFFIVRFLESNWF 177

QY 335 VVYTMNHVMEIDQAYDWFSSQLTATCNVEQSFNDWFS 376
DB 178 VVYTMNHVPMHIDBNDWDSVTLQATCNVHKSAFNDWFS 219

RESULT 27
US-09-439-261-21
; Sequence 21, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradiip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1997-04-11
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (128)...(128)
; OTHER INFORMATION: Xaa = Unknown or other at position 128
US-09-439-261-21

US-09-227-613-19
; Sequence 19, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradiip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-227-613-19

Query Match 32.2%; Score 784; DB 4; Length 219;
Best Local Similarity 61.7%; Pred. No. 4.1e-79;
Matches 137; Conservative 27; Mismatches 46; Indels 12; Gaps 3;

QY 157 GMIPTLITAFVLATSAQAQAGWLQHDYGHLSVYRKPKXNHLVHKFVIGHLKGASANWNNHR 216
DB 8 GGIPAV-----QAQAGWLQHDYGHLSVSTSKWNHLJHHFVIGHLKGASANWNNHM 58

QY 217 HFQHAKPNIFHKDPDNNMLH--VFVLGSEWQPIEYKQKLLKYLPNYHQHEYFFLIGPPLL 274
DB 59 HFQHAKPNCFKDPDNNM--HPFFALGKILSVLQKQKXMPYNNHQHYFFLIGPPAL 117

QY 275 IPMYFQYQIIMTVHKNWDLAWAVSYIRFIYIPYIGLQALLFNIRFLESHPF 334
DB 118 LPLFYQWYIFFYFIQKRWKVDLAWMITFYVRFLTYVPLGLKAFGLFFIVRFLESNWF 177

QY 335 VVYTMNHVMEIDQAYDWFSSQLTATCNVEQSFNDWFS 376
DB 178 VVYTMNHVPMHIDBNDWDSVTLQATCNVHKSAFNDWFS 219

RESULT 27
US-09-439-261-21
; Sequence 21, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradiip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1997-04-11
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (128)...(128)
; OTHER INFORMATION: Xaa = Unknown or other at position 128
US-09-439-261-21

US-09-227-613-19
; Sequence 19, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradiip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-227-613-19

Query Match 32.2%; Score 784; DB 4; Length 219;
Best Local Similarity 61.7%; Pred. No. 4.1e-79;
Matches 137; Conservative 27; Mismatches 46; Indels 12; Gaps 3;

QY 157 GMIPTLITAFVLATSAQAQAGWLQHDYGHLSVYRKPKXNHLVHKFVIGHLKGASANWNNHR 216
DB 8 GGIPAV-----QAQAGWLQHDYGHLSVSTSKWNHLJHHFVIGHLKGASANWNNHM 58

QY 217 HFQHAKPNIFHKDPDNNMLH--VFVLGSEWQPIEYKQKLLKYLPNYHQHEYFFLIGPPLL 274
DB 59 HFQHAKPNCFKDPDNNM--HPFFALGKILSVLQKQKXMPYNNHQHYFFLIGPPAL 117

QY 275 IPMYFQYQIIMTVHKNWDLAWAVSYIRFIYIPYIGLQALLFNIRFLESHPF 334
DB 118 LPLFYQWYIFFYFIQKRWKVDLAWMITFYVRFLTYVPLGLKAFGLFFIVRFLESNWF 177

QY 335 VVYTMNHVMEIDQAYDWFSSQLTATCNVEQSFNDWFS 376
DB 178 VVYTMNHVPMHIDBNDWDSVTLQATCNVHKSAFNDWFS 219

RESULT 27
US-09-439-261-21
; Sequence 21, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradiip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1997-04-11
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (128)...(128)
; OTHER INFORMATION: Xaa = Unknown or other at position 128
US-09-439-261-21

US-09-227-613-20
; Sequence 20, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradiip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: Xaa at position 128 is unknown or other.
US-09-227-613-20

Query Match 24.1%; Score 587.5; DB 4; Length 182;
Best Local Similarity 62.3%; Pred. No. 2.6e-57;
Matches 101; Conservative 22; Mismatches 36; Indels 3; Gaps 2;

QY 139 HIIALESIAWFTVFYFGNGWIPTLITAFVLATSAQAQAGWLQHDYGHLSVYRKPKXNHLVH 198
DB 2 HILLDGAALTLWVFGTSFLPFLLCVALLSAVQAQAGWLQHDYGHLSVSTSKWNHLH 61

QY 199 KFYVIGHLKGASANWNNHRFQHHAKPNIFHKDPDNNMLH--VFVLGSEWQPIEYKQKLLKY 256
DB 62 HFVIGHLKGASANWNNHMFQHHAKPNCFKDPDNNM--HPFFALGKILSVLQKQKXKY 120

QY 257 LPYNHQHEYFFLIGPPLLIPMYFQYQIIMTVHKNWVDLAW 298
DB 121 MPYNHQHYFFLIGPPLLIPMYFQYQIIMTVHKNWVDLAW 162

RESULT 28
US-09-227-613-20
; Sequence 20, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradiip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: Xaa at position 128 is unknown or other.
US-09-227-613-20

Query Match 24.1%; Score 587.5; DB 4; Length 182;
Best Local Similarity 62.3%; Pred. No. 2.6e-57;
Matches 101; Conservative 22; Mismatches 36; Indels 3; Gaps 2;

QY 139 HIIALESIAWFTVFYFGNGWIPTLITAFVLATSAQAQAGWLQHDYGHLSVYRKPKXNHLVH 198
DB 2 H
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; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-363-574-9

Query Match      20.6%; Score 502; DB 3; Length 131;
Best Local Similarity 69.4%; Pred. No. 5.4e-48;
Matches 86; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 296 LANAVSYIRFFITYIPFYGLGALLFLNFIREFSHFWVVTQNMHIWMEIDQAYRDW 355
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Db 8  LAMWTFYVRFFITYVPLGLKAFGLFFIVRFLESNNFWVTQNMHIFPHDHRNDW 67
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 356 FSSQLTATCNVQSFNDWFSGLNFQIEHHLFPTWPRNHLKIAPLVKSCLKAGHIEYQ 415
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 VSTQLQATCNVHKSADFNDWFSGLNFQIEHHLFPTWPRNHYHVAVLVQSLCAKHGIEYQ 127
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 416 EKPL 419
   |||
Db 128 SKPL 131
   |||

RESULT 33
US-08-834-655-11
; Sequence 11, Application US/08934655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-834-655-11

Query Match      20.3%; Score 496; DB 2; Length 143;
Best Local Similarity 66.7%; Pred. No. 2.9e-47;
Matches 86; Conservative 11; Mismatches 32; Indels 0; Gaps 0;

QY 267 MIVHKNVWDLAWASYVIRFFITYIPFYGLGALLFLNFIREFSHFWVVTQNMHIWME 346
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 14  MLVCMQWTDLLWASAFYSRFFLSISPFYGATGTLILFVAVRVLESFHWVITQNMHIKPE 73
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 347 IDQEAYRDWFSLSQTATCNVQSFNDWFSGLNFQIEHHLFPTWPRNHLKIAPLVKS 406
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 74 IGHEKRDWASSQLAATCNVPSLFIDWFSGLNFOIEHHLPFTWTRHNYRXVAPLVKAF 133
QY 407 CAXHGIEYQ 415
Db 134 CAXHGLHYE 142

RESULT 34
US-08-834-033A-12
; Sequence 12, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 11-APR-1997
; APPLICATION NUMBER: US/08/834.033A
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-834-033A-12

Query Match 20.3%; Score 496; DB 3; Length 143;
Best Local Similarity 66.7%; Pred. No. 2.9e-47;
Matches 86; Conservative 11; Mismatches 32; Indels 0; Gaps 0;

QY 287 MIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRFLESHFWVWVTOMNHVME 346
Db 14 MLVCMQWTDLLWAAAFYSRFFLSYSPFYGATGTLFLFVAVRVLESHFWVWVTOMNHIPKE 73

QY 347 IDOEAYRDMFSSQLATCNVPSLFIDWFSGLNFOIEHHLPFTWTRHNYRXVAPLVKSL 406
Db 74 IGHEKRDWASSQLAATCNVPSLFIDWFSGLNFOIEHHLPFTWTRHNYRXVAPLVKAF 133

QY 407 CAXHGIEYQ 415
Db 134 CAXHGLHYE 142

RESULT 35
US-09-363-574-11
; Sequence 11, Application US/09363574
; Patent No. 6136574
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/363,574
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-202 USA
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-363-574-11

Query Match 20.3%; Score 496; DB 3; Length 143;
Best Local Similarity 66.7%; Pred. No. 2.9e-47;
Matches 86; Conservative 11; Mismatches 32; Indels 0; Gaps 0;

QY 287 MIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRFLESHFWVWVTOMNHVME 346
Db 14 MLVCMQWTDLLWAAAFYSRFFLSYSPFYGATGTLFLFVAVRVLESHFWVWVTOMNHIPKE 73

QY 347 IDOEAYRDMFSSQLATCNVPSLFIDWFSGLNFOIEHHLPFTWTRHNYRXVAPLVKSL 406
Db 74 IGHEKRDWASSQLAATCNVPSLFIDWFSGLNFOIEHHLPFTWTRHNYRXVAPLVKAF 133

QY 407 CAXHGIEYQ 415
Db 134 CAXHGLHYE 142

RESULT 36
US-09-363-526-11
; Sequence 11, Application US/09363526
; Patent No. 6410288
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

```

; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,526
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-201 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-526-11

Query Match 20.3%; Score 496; DB 4; Length 143;
Best Local Similarity 66.7%; Pred. No. 2.9e-47;
Matches 86; Conservative 11; Mismatches 32; Indels 0; Gaps 0;

QY 287 MIVHKNVWDLAWAYVYIRPITYIPYIGILGALLFNFIREFLESHVFWVWTONHIVME 346
Db 14 MLVCNQMTDLWAAAFYSRFLSYSPFYGTGLLLFVAVRVLESHVFWVWITQNHIFKE 73
QY 347 IDQAYRDWFSQSQTATCNVEQSFNDWFSQHLNFQIEHHLFPTMPRHNLKHIAPLVKSL 406
Db 74 IGHEKGRDWASQLAACNVPSLFDWFSQHLNFQIEHHLFPTMTTEHNYRXVAPLVKAF 133
QY 407 CAKHGIEYQ 415
Db 134 CAKHGLHYE 142

RESULT 37
US-08-834-655-2
; Sequence 2, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-655-2

Query Match 18.8%; Score 459; DB 2; Length 457;
Best Local Similarity 24.9%; Pred. No. 2.3e-42;
Matches 118; Conservative 88; Mismatches 183; Indels 84; Gaps 14;

QY 17 SVPTFSWEEI-----QKHLRTDGLVIDRKVYNITKWSIQHPGQORVIGHYAGEDA 68
Db 6 SVRTFTRAEVLNAEALNEGKDAEAPFLMIIDNKVYDVREVPDPGGSVILTH-VGKDG 64
QY 69 TDAFAPHPDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEOMNLPKT 128
Db 65 TDVDFTHFP--EAAWETLANFYVGI--DESDRI-KNDDFAAEVRKURTLFQSLGYDS 119
QY 129 NHVFPDLLLHAIHIALESIAWFTVFYFG-NGWIPITLITAFVLATSOAQAGW-QHDPYHLSV 187
Db 120 SKAYAFKVSFNLICWGLSTVIVAKWGQSTLANVLSAALLGLEFWQCGWLHDFLHHQV 179
QY 188 YRKPKWHLVHKFVIGLKGASANKWNRHFFQHAKPNIHKDDVDNMLHVFLGEGWQPI 247
Db 180 FQDRFWGLFGAPLGVCGQGFSSSWKDKNTHHAAPNVHGEDPDDIDTHPLLTWSE---- 235
QY 248 EYGGKKLKYLPVNHQHEFFLIGPPLLIPIFYQIIMTMIVHKW-----VDLAWA 299
Db 236 -----HALEMFSVDPOBELTRMSRF-----WVLNQTFYFPILSPARLSWC 277
QY 300 VSYTRPFTIYIPYIGILGALLFNFI--FLESHVFW----- 336
Db 278 LQ-SILFVLPGQAHKPSGARVPISLVEQLSLAMHW-TWYLATMFLFKDPVNMMLVYFLV 335
QY 337 -----VTOMNHIVMEI---DQAYRDWFSQSQTATCNVEQSFNDWFSQHLNFQ 382
Db 336 SOAVCGNLLAIIVFSLNHNGMPVISKEAVDMDFFTKIITGRDVHPGLFANFWTGLGLNYQ 395
QY 383 IEHHLFPTMPRHNLKHIAPLVKSLCAKHGIEYQEKPLLRALLDIRSLKKGK 435
Db 396 IEHHLFPPSPRHNFSKIOPAVETLCKKYNVRVHTTGMIEGTAEVFSRLNEVSK 448

RESULT 38
US-08-834-033A-2
; Sequence 2, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

```


Db 336 SQAVCGNLLAIVPSLNHNGMPVISKEEAVDMDFTXQIITORDVHFGLPANWFTGGLNYQ 395
Qy 383 IEHHLFPTMPRHNLHKAIPLVKSLCAKHGIEYQCEKPLLRALLDIIIRSLKKSXK 435
Db 396 IEHHLFSPMRHNFHSKIQAPEVLCKKYNVRYHTTGMIEGTAEVFSRLNEVSK 448

RESULT 40

US-09-363-526-2
; Sequence 2, Application US/09363526
; Patent No. 6410288
; GENERAL INFORMATION:
; APPLICANT: KNUZON, DEBORAH
; APPLICANT: MURKERT, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,526
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-201 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-363-526-2

Query Match 18.8%; Score 459; DB 4; Length 457;
Best Local Similarity 24.9%; Pred. No. 2.3e-42;
Matches 118; Conservative 88; Mismatches 183; Indels 84; Gaps 14;
Qy 17 SVPTFSWEEI-----QKHLRTDSGLVIDRKVYMITKWSIOHPGQVRVIGHYAGEDA 68
Db 6 SVRTFTRAEVLNAEALNEGKDAEAPFLMIIDNKVYDVREFPVDPHGGSVILTH-VGKDG 64
Qy 59 TDAPRAEPDLEFVGKFKPLLIGELAPEEPSQHGKNSKITEDFRALRKTAEEDMNLFT 128
Db 65 TDVPTTFHP--EAWETLANYVVGDI--DESDRI-KNDPFAEVRKRLTFLQSLGYDS 119
Qy 129 NHVFFLLLAHIIALESIAWFTVYFG-NGWIPTLITAFVLATSCAQAGMLQHDYGLSLV 187
Db 120 SKAYYAFKVSFNLCIWLGLSTVIVAKWGQSTLANVLSAALLGLEFWQCGGLAHDFLHQV 179
Qy 188 YRKPKWHLVHKFVICHKLGASAWNNHRRHFQHHAKPNI FHKDPDVMNLHVFLVGEWQPI 247
Db 180 FQDFREWGLDFGAFLGGVCGGFSSWWKDKHNTHAAPNVHGEPDIDITHPLLTWSE---- 235

Qy 248 EYGGKKLKYPYNHQHIEYFFELIGPPLLIIPMYFQYQIIMTNIVHKNW-----VDLAWA 299
Db 236 -----HALEMFSDFVDEELTRMWSRF-----MVLNQTFYFPILSFARLSWC 277
Qy 300 VSYVIRFFITYIPFYGILGALLFLNFR--FLESHMFVM----- 336
Db 278 LQ-SILFVLPGQAHKPSGARVPISLVEQSLAMHW-TWYLATMFLFIKDPVNMVLYFLV 335
Qy 337 -----VTQMNHIVMEI---DOEAYRDWFSQLTATCNVQSFNDWFSGLHNFQ 382
Db 336 SQAVCGNLLAIVPSLNHNGMPVISKEEAVDMDFTXQIITGRDVHFGLPANWFTGGLNYQ 395
Qy 383 IEHHLFPTMPRHNLHKAIPLVKSLCAKHGIEYQCEKPLLRALLDIIIRSLKKSXK 435
Db 396 IEHHLFSPMRHNFHSKIQAPEVLCKKYNVRYHTTGMIEGTAEVFSRLNEVSK 448

Search completed: December 9, 2003, 10:20:08
Job time : 23 secs